

```
LIB3106-023-Q1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498280
BLAST score
                  150
E value
                   7.0e-10
Match length
                   98
                   33
% identity
NCBI Description
                  D15KZ1 PROTEIN >gi 90653 pir A30222 hypothetical D15Kz1
                  protein - mouse (fragment) >gi 576884 (M25773) D15Kzl [Mus
                  38703
Seq. No.
                  LIB3106-025-Q1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1055367
BLAST score
                  107
                  3.0e-53
E value
Match length
                  207
% identity
                  88
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
Seq. No.
                   38704
Seq. ID
                  LIB3106-025-Q1-K1-A2
Method
                  BLASTN
NCBI GI
                  q2565416
BLAST score
                  51
E value
                  8.0e-20
Match length
                  113
% identity
                  86
NCBI Description
                  Onobrychis viciifolia oxygen-evolving enhancer protein 3
                  precursor, mRNA, complete cds
Seq. No.
                  38705
Seq. ID
                  LIB3106-025-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  q4580395
BLAST score
                  352
                  2.0e-33
E value
Match length
                  144
% identity
                   49
NCBI Description
                   (AC007171) putative kinesin-related protein [Arabidopsis
                  thalianal
                  38706
Seq. No.
Seq. ID
                  LIB3106-025-Q1-K1-B7
Method
                  BLASTN
NCBI GI
                  g2257597
BLAST score
                  37
E value
                  1.0e-11
Match length
                  133
```

% identity 82

NCBI Description Robinia pseudoacacia mRNA for phosphoglycerate kinase,

partial cds

38707 Seq. No.

Seq. ID LIB3106-025-Q1-K1-C1



```
Method
                  BLASTX
NCBI GI
                  g3236238
BLAST score
                  142
                  7.0e-09
E value
                  47
Match length
% identity
                  62
NCBI Description
                  (AC004684) putative ARF1 GTPase activating protein
                  [Arabidopsis thaliana] >gi 4519792 dbj BAA75744.1
                  (AB017876) Aspl [Arabidopsis thaliana]
Seq. No.
                  38708
Seq. ID
                  LIB3106-025-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2529662
BLAST score
                  173
E value
                  5.0e-13
                  49
Match length
                  76
% identity
                  (AC002535) putative small nuclear ribonucleoprotein, Sm D2
NCBI Description
                  [Arabidopsis thaliana] >gi 3738278 (AC005309) putative
```

small nuclear ribonucleoprotein, Sm D2 [Arabidopsis thaliana]

38709

Seq. ID LIB3106-026-Q1-K1-A3 Method BLASTX NCBI GI q1709358 284 BLAST score E value 2.0e-25 Match length 85 59 % identity

NCBI Description

Seq. No.

NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE

PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859

nucleoside triphosphatase - garden pea

>gi 2129890 pir S65147 nucleoside triphosphatase

precursor, chromatin-associated - garden pea

>gi 563612 emb CAA83655 (Z32743) nucleoside triphosphatase

[Pisum sativum] >gi 4519173 dbj BAA75506.1 (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No. 38710

Seq. ID LIB3106-026-Q1-K1-C3

Method BLASTN NCBI GI q403326 BLAST score 51 E value 1.0e-19 Match length 127 85 % identity

T.repens TrMT1A mRNA for metallothionein-like protein NCBI Description

38711 Seq. No.

LIB3106-026-Q1-K1-C4 Seq. ID

Method BLASTX NCBI GI q3128168 BLAST score 255 E value 4.0e-22 Match length 96



```
% identity
                   (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  38712
Seq. ID
                  LIB3106-026-Q1-K1-F6
Method
                  BLASTX
                  g2529683
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
                  55
Match length
                  56
% identity
                  (AC002535) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  38713
                  LIB3106-027-Q1-K1-F12
Seq. ID
Method
                  BLASTN
                  g984307
NCBI GI
BLAST score
                  104
E value
                  9.0e-52
Match length
                  165
% identity
                  90
                  Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                  cds, beta-carboxyltransferase (accD), photosystem I
                  component (psaI), ORF 202 protein (ORF 203), ORF 151
                  protein (ORF 151), ORF 103 protein (ORF 103), ORF 229
                  precurso
Seq. No.
Seq. ID
                  38714
                  LIB3106-028-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2677830
BLAST score
                  251
                  1.0e-21
E value
                  112
Match length
                  54
% identity
                  (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
                  38715
Seq. No.
                  LIB3106-028-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q595768
BLAST score
                   148
                   1.0e-09
E value
Match length
                   46
% identity
                   63
                  (U13866) non-functional lacZ alpha peptide [Cloning vector]
NCBI Description
                  38716
Seq. No.
                  LIB3106-028-Q1-K1-E9
Seq. ID
Method
                  BLASTX
```

NCBI GI g2695711 96 BLAST score E value 8.0e-10 Match length 63 54 % identity

NCBI Description (AJ001370) cytochome b5 [Olea europaea]



```
Seq. No.
                    38717
  Seq. ID
                    LIB3106-028-Q1-K1-F10
  Method
                    BLASTN
  NCBI GI
                    g1053215
  BLAST score
                    120
 E value
                    6.0e-61
 Match length
                    292
% identity
                    85
 NCBI Description
                    Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
                    nuclear gene encoding chloroplast protein, complete cds
                    38718
  Seq. No.
                    LIB3106-028-Q1-K1-G6
  Seq. ID
  Method
                    BLASTN
                    g170089
  NCBI GI
  BLAST score
                    79
                    1.0e-36
 E value
 Match length
                    191
                    85
  % identity
 NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                    38719
  Seq. No.
  Seq. ID
                    LIB3106-028-Q1-K1-H2
  Method
                    BLASTX
                    q3090403
  NCBI GI
                    194
  BLAST score
                    7.0e-15
  E value
  Match length
                    75
                    57
  % identity
                    (AJ005671) cytochrome b6f complex subunit [Arabidopsis
  NCBI Description
                    thaliana]
                    38720
  Seq. No.
                    LIB3106-028-Q1-K1-H4
  Seq. ID
                    BLASTX
  Method
                    g4006876
  NCBI GI
                     283
  BLAST score
                    3.0e-25
  E value
                    140
  Match length
                     47
  % identity
                    (Z99707) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     38721
                    LIB3106-030-Q1-K1-B9
  Seg. ID
  Method
                    BLASTX
                     q1871577
  NCBI GI
  BLAST score
                     224
                     3.0e-18
  E value
                     50
  Match length
  % identity
                    (Y11553) putative 21kD protein precursor [Medicago sativa]
  NCBI Description
  Seq. No.
                     38722
                    LIB3106-030-Q1-K1-F9
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                     g2129740
```

6000



```
BLAST score 286
E value 8.0e-26
Match length 82
% identity 62
```

NCBI Description small nuclear ribonucleoprotein - Arabidopsis thaliana >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis

thaliana >gi 1255711 (M93439) small nuclear

ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

 Seq. No.
 38723

 Seq. ID
 LIB3106-031-Q1-K1-C8

 Method
 BLASTX

 NCBI GI
 g322663

BLAST score 328
E value 2.0e-41
Match length 128
% identity 65

NCBI Description S-receptor kinase-related protein - Chinese kale

>gi 17917 emb CAA79324 (Z18884) S-receptor kinase related

protein [Brassica oleracea]

Seq. No. 38724

Seq. ID LIB3106-031-Q1-K1-E10

Method BLASTN

NCBI GI g169897

BLAST score 268

E value 1.0e-149

Match length 411

% identity 92

NCBI Description G.max 28 kDa protein, complete cds

Seq. No.

Seq. ID

38725 LIB3106-031-Q1-K1-F1

Method BLASTN
NCBI GI g296444
BLAST score 72
E value 2.0e-32
Match length 215
% identity 84

NCBI Description G.max ADR6 mRNA

Seq. No.

38726

Seq. ID LIB3106-031-Q1-K1-F8

Method BLASTN
NCBI GI g169980
BLAST score 49
E value 1.0e-18
Match length 189
% identity 81

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No.

38727

Seq. ID LIB3106-032-Q1-K1-A3

Method BLASTN
NCBI GI g1055367
BLAST score 101

BLAST score

Match length

E value

239

299

1.0e-132



```
E value
Match length
                   173
 % identity
                   91
NCBI Description
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
Seq. No.
                   38728
Seq. ID
                   LIB3106-032-Q1-K1-B10
Method
                   BLASTX
NCBI GI
                   q595768
BLAST score
                   151
E value
                   8.0e-10
Match length
                   46
% identity
                   65
NCBI Description
                  (U13866) non-functional lacZ alpha peptide [Cloning vector]
Seq. No.
                   38729
Seq. ID
                   LIB3106-032-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   g3402704
BLAST score
                   267
E value
                   2.0e-23
Match length
                   132
% identity
                   42
NCBI Description
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   38730
Seq. ID
                   LIB3106-032-Q1-K1-B9
Method
                   BLASTX
NCBI GI
                   q4567201
BLAST score
                   175
E value
                   1.0e-12
Match length
                   62
% identity
                   63
NCBI Description
                   (AC007168) putative aspartate aminotransferase [Arabidopsis
                   thaliana]
Seq. No.
                   38731
Seq. ID
                   LIB3106-032-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g1477565
BLAST score
                   160
E value
                   7.0e-11
Match length
                   130
% identity
NCBI Description
                   (U50078) p532 [Homo sapiens]
                  >gi_4557026_ref_NP_003913.1_pHERC1_ hect (homologous to the
                  E6-AP (UBE3A) carboxyl terminus) domain and RCC1
                   (CHC1)-like domain (RLD)
Seq. No.
                  38732
Seq. ID
                  LIB3106-032-Q1-K1-D11
Method
                  BLASTN
NCBI GI
                  g347458
```



% identity 95

NCBI Description Glycine max brassinosteroid-regulated protein mRNA,

complete cds

Seq. No. 38733

Seq. ID LIB3106-032-Q1-K1-F11

Method BLASTX
NCBI GI g1076626
BLAST score 160
E value 2.0e-11
Match length 45
% identity 67

NCBI Description glycine rich protein - common tobacco

>gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich

protein [Nicotiana tabacum]

Seq. No. 38734

Seq. ID LIB3106-032-Q1-K1-G12

Method BLASTN
NCBI GI g1055367
BLAST score 153
E value 1.0e-80
Match length 185
% identity 96

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 38735

Seq. ID LIB3106-032-Q1-K1-G3

Method BLASTX
NCBI GI g2506443
BLAST score 426
E value 8.0e-46
Match length 136
% identity 76

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi 2117520 pir JQ1285

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde

3-phosphate dehydrogenase [Arabidopsis thaliana]

>gi 1402885 emb CAA66816 (X98130)

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

Seq. No. 38736

Seq. ID LIB3106-032-Q1-K1-G4

Method BLASTX
NCBI GI g2388582
BLAST score 291
E value 2.0e-30
Match length 112
% identity 68

NCBI Description (AC000098) Contains similarity to Rattus O-GlcNAc

transferase (gb_U76557). [Arabidopsis thaliana]

Seq. No. 38737



```
LIB3106-032-Q1-K1-H7
Seq. ID
                  BLASTN
Method
                  g4103958
NCBI GI
BLAST score
                  121
                  1.0e-61
E value
                  213
Match length
                  89
% identity
NCBI Description Phaseolus vulgaris calmodulin (CaM) mRNA, PvCaM-2 allele,
                  complete cds
                  38738
Seq. No.
                  LIB3106-033-Q1-K1-A12
Seq. ID
                  BLASTX
Method
                  g2384669
NCBI GI
BLAST score
                  404
E value
                  1.0e-39
Match length
                  103
% identity
                   69
                  (AF012656) putative potassium transporter AtKT1p
NCBI Description
                   [Arabidopsis thaliana]
                   38739
Seq. No.
                   LIB3106-033-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   g4566614
NCBI GI
BLAST score
                   206
                   3.0e-16
E value
Match length
                   87
% identity
                   49
                  (AF112887) actin depolymerizing factor [Populus alba x
NCBI Description
                   Populus tremula]
                   38740
Seq. No.
                   LIB3106-033-Q1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3367531
                   178
BLAST score
                   6.0e-13
E value
Match length
                   102
                   38
% identity
                   (AC004392) Strong similarity to gi_2160138 F19K23.6 gene
NCBI Description
                   product from A. thaliana BAC gb_AC000375. [Arabidopsis
                   thaliana]
                   38741
Seq. No.
                   LIB3106-033-Q1-K1-E6
Seq. ID
                   BLASTN
Method
                   g1055367
NCBI GI
                   158
BLAST score
E value
                   1.0e-83
Match length
                   274
% identity
                   89
```

Seq. No. 38742

LIB3106-033-Q1-K1-F11 Seq. ID

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

W. .



```
BLASTX
Method
                   g3024874
NCBI GI
                   226
BLAST score
                   1.0e-18
E value
                   96
Match length
% identity
                   46
                   HYPOTHETICAL 50.0 KD PROTEIN SLR0076
NCBI Description
                   >gi_1001707_dbj_BAA10544_ (D64004) hypothetical protein
                   [Synechocystis sp.]
                   38743
Seq. No.
                   LIB3106-033-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g3152594
NCBI GI
BLAST score
                   169
E value
                   4.0e-12
                   101
Match length
% identity
                    (AC002986) Contains repeats similar to RECA protein
NCBI Description
                   gb L26100 from Acinetobacter calcoaceticus. [Arabidopsis
                   thaliana]
                    38744
Seq. No.
                   LIB3106-033-Q1-K1-G6
Seq. ID
                    BLASTX
Method
                    g115577
NCBI GI
                    406
BLAST score
                    1.0e-39
E value
                    140
Match length
                    61
% identity
                   PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME
NCBI Description
                    (PEPCASE) >gi_348536_pir__S28614 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sugarcane hybrid H32-8560
                    >gi_169844 (M86661) phosphoenolpyruvate carboxylase
                    [Saccharum sp.]
                    38745
Seq. No.
                    LIB3106-033-Q1-K1-H1
Seq. ID
                    BLASTN
Method
                    g2695930
NCBI GI
```

Method BLASTN
NCBI GI g269593
BLAST score 34
E value 1.0e-09
Match length 58
% identity 90

NCBI Description Hordeum vulgare mRNA for hypothetical protein, clone RG49

Seq. No. 38746

Seq. ID LIB3106-034-Q1-K1-A1

Method BLASTN
NCBI GI g1055367
BLAST score 239
E value 1.0e-132
Match length 374
% identity 91

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds



```
Seq. No.
                  38747
                  LIB3106-034-Q1-K1-A4
Seq. ID
Method
                  BLASTN
                  g169190
NCBI GI
                  79
BLAST score
                  9.0e-37
E value
                  79
Match length
                  100
% identity
                  P.hybrida 5-enolpyruvylshikimate 3-phosphate synthase mRNA,
NCBI Description
                  complete cds
                  38748
Seq. No.
                  LIB3106-034-Q1-K1-C6
Seq. ID
Method
                  BLASTN
                  g4204758
NCBI GI
                  64
BLAST score
                  2.0e-27
E value
                   64
Match length
                  100
% identity
NCBI Description Glycine max peroxidase precursor (sEPa1) mRNA, partial cds
                  38749
Seq. No.
                  LIB3106-034-Q1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2498731
                   159
BLAST score
                   6.0e-11
E value
                   97
Match length
% identity
                   34
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                   >gi_1362013_pir__S57611 zeta-crystallin homolog -
                   Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                   zeta-crystallin homologue [Arabidopsis thaliana]
                   38750
Seq. No.
                   LIB3106-034-Q1-K1-E8
Seq. ID
Method
                   BLASTN
                   q1053215
NCBI GI
                   390
BLAST score
                   0.0e+00
E value
Match length
                   409
                   99
% identity
                   Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                   nuclear gene encoding chloroplast protein, complete cds
Seq. No.
                   38751
                   LIB3106-034-Q1-K1-F6
Seq. ID
Method
                   BLASTN
                   g18761
NCBI GI
                   135
BLAST score
E value
                   8.0e-70
                   267
Match length
```

% identity

Seq. No.

LIB3106-034-Q1-K1-G6 Seq. ID

38752

NCBI Description Soybean stem mRNA for 31 kD glycoprotein



```
Method
NCBI GI
                  q170087
BLAST score
                  107
E value
                  4.0e-53
                  299
Match length
                  84
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
                  38753
Seq. No.
                  LIB3106-034-Q1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  9.0e-11
Match length
                  45
                  65
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  38754
Seq. No.
Seq. ID
                  LIB3106-034-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3152613
BLAST score
                  176
E value
                  1.0e-12
Match length
                  61
                  54
% identity
                  (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  38755
Seq. No.
                  LIB3106-035-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g3152572
NCBI GI
BLAST score
                  181
E value
                  3.0e-13
Match length
                  92
                  46
% identity
NCBI Description
                   (AC002986) Contains homology to DNAJ heatshock protein
                  gb U32803 from Haemophilus influenzae. [Arabidopsis
                  thaliana]
                  38756
Seq. No.
Seq. ID
                  LIB3106-035-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3335374
BLAST score
                  186
```

E value 4.0e-14 Match length 62

55 % identity

NCBI Description (AC003028) glutaredoxin-like protein [Arabidopsis thaliana]

Seq. No.

38757

LIB3106-035-Q1-K1-D10 Seq. ID

Method BLASTX NCBI GI g2982452 BLAST score 285 2.0e-25 E value Match length 141



% identity 6

NCBI Description (AL022223) receptor protein kinase-like protein [Arabidopsis thaliana]

Seq. No. 38758 Seq. ID LIB3106-035-Q1-K1-E3

Method BLASTN
NCBI GI g2905777
BLAST score 121
E value 2.0e-61
Match length 225
% identity 89

NCBI Description Glycine max ribosomal protein L41 mRNA, partial cds

Seq. No. 38759

Seq. ID LIB3106-035-Q1-K1-E7

Method BLASTX
NCBI GI g2191175
BLAST score 169
E value 5.0e-12
Match length 105
% identity 40

NCBI Description (AF007270) A_IG002P16.24 gene product [Arabidopsis

thaliana]

Seq. No. 38760

Seq. ID LIB3106-035-Q1-K1-E8

Method BLASTN
NCBI GI g984307
BLAST score 179
E value 4.0e-96
Match length 368
% identity 87

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 38761

Seq. ID LIB3106-035-Q1-K1-F6

Method BLASTN
NCBI GI g1055367
BLAST score 222
E value 1.0e-122
Match length 341
% identity 92

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 38762

Seq. ID LIB3106-035-Q1-K1-H5

Method BLASTN
NCBI GI g669002
BLAST score 75
E value 4.0e-34
Match length 193

6008

% identity



```
% identity
                                                                                m.
                  Glycine max calnexin mRNA, complete cds
NCBI Description
                  38763
Seq. No.
                  LIB3106-036-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  q131773
NCBI GI
BLAST score
                  119
                  8.0e-09
E value
                  64
Match length
% identity
                  66
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                  >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                  38764
Seq. No.
                  LIB3106-036-Q1-K1-A5
Seq. ID
Method
                  BLASTX
                  q1363479
NCBI GI
                  235
BLAST score
                   8.0e-20
E value
Match length
                   91
% identity
                   58
                  photosystem I protein psaL - cucumber
NCBI Description
                   >gi 801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]
                   38765
Seq. No.
                   LIB3106-036-Q1-K1-B2
Seq. ID
                   BLASTX
Method
                   g4115534
NCBI GI
BLAST score
                   357
                   5.0e-34
E value
                   110
Match length
                   64
% identity
                  (AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                   mungo]
                   38766
Seq. No.
                   LIB3106-036-Q1-K1-E5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q169897
                   218
BLAST score
E value
                   1.0e-119
                   413
Match length
                   89
 % identity
 NCBI Description G.max 28 kDa protein, complete cds
                   38767
 Seq. No.
                   LIB3106-036-Q1-K1-F11
 Seq. ID
                   BLASTX
 Method
                   g2982445
 NCBI GI
                   208
 BLAST score
                   1.0e-16
 E value
                   82
 Match length
                   52
```

NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                  LIB3106-036-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1076421
                   200
BLAST score
                  1.0e-15
E value
Match length
                   62
% identity
                   68
                  transcription factor TGA3 - Arabidopsis thaliana >gi_304113
NCBI Description
                   (L10209) transcription factor [Arabidopsis thaliana]
                   38769
Seq. No.
Seq. ID
                  LIB3106-036-Q1-K1-F9
Method
                  BLASTN
                   g169897
NCBI GI
BLAST score
                   350
                   0.0e + 00
E value
Match length
                   370
% identity
                   99
NCBI Description G.max 28 kDa protein, complete cds
                   38770
Seq. No.
                   LIB3106-036-Q1-K1-G11
Seq. ID
Method
                   BLASTX
                   q2347189
NCBI GI
                   367
BLAST score
                   4.0e-35
E value
Match length
                   82
                   82
% identity
                   (AC002338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3150399 (AC004165) hypothetical protein [Arabidopsis
                   thaliana]
                   38771
Seq. No.
                   LIB3106-036-Q1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4206622 ·
BLAST score
                   199
E value
                   1.0e-15
Match length
                   93
% identity
                   46
                   (AF066857) ATP synthase beta subunit [Swietenia
NCBI Description
                   macrophylla]
Seq. No.
                   38772
Seq. ID
                   LIB3106-036-Q1-K1-H3
Method
                   BLASTX
```

NCBI GI g2252846
BLAST score 198
E value 2.0e-15
Match length 63
% identity 62

NCBI Description (AF013293) Similar to phospholipase D [Arabidopsis

thaliana]

Seq. No.

38773

Seq. ID

LIB3106-036-Q1-K1-H5

E value

7.0e-98



```
Method
  NCBI GI
                     g130271
  BLAST score
                     219
                     8.0e-18
  E value
                     86
  Match length
                     57
  % identity
                     PLASTOCYANIN PRECURSOR >gi_100238_pir__S05303 plastocyanin
  NCBI Description
                     precursor - tomato >gi_19300_emb_CAA32121_ (X13934)
                     pre-plastocyanin (AA -64 to \overline{106}) [Lycopersicon esculentum]
                     38774
  Seq. No.
                     LIB3106-036-Q1-K1-H9
  Seq. ID
  Method
                     BLASTX
                     g3850920
  NCBI GI
  BLAST score
                     230
                     2.0e-19
  E value
  Match length
                     91
                     55
  % identity
                     (AF060400) ATP synthase beta subunit [Franklandia
  NCBI Description
                     fucifolia]
                     38775
  Seq. No.
                     LIB3106-037-Q1-K1-A10
  Seq. ID
                     BLASTN
  Method
  NCBI GI
                     g169974
                     145
  BLAST score
                     7.0e-76
  E value
                     293
  Match length
                     87
  % identity
  NCBI Description Glycine max vspA gene, complete cds
                     38776
  Seq. No.
                     LIB3106-037-Q1-K1-A8
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g4006878
  BLAST score
                     212
  E value
                     3.0e-17
  Match length
                     69
                     55
   % identity
  NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
                     38777
   Seq. No.
                     LIB3106-037-Q1-K1-B12
   Seq. ID
  Method
                     BLASTN
  NCBI GI
                     q454178
                     139
  BLAST score
                     4.0e-72
  E value
  Match length
                     235
   % identity
                     90
   NCBI Description Glycine max rubisco-associated protein mRNA, complete cds
                     38778
   Seq. No.
                     LIB3106-037-Q1-K1-C1
   Seq. ID
   Method
                     BLASTN
   NCBI GI
                     g1055367
   BLAST score
                     182
```



Match length % identity Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description subunit mRNA, complete cds 38779 Seq. No. Seq. ID LIB3106-037-Q1-K1-C6 Method BLASTN q18741 176 2.0e-94

NCBI GI BLAST score E value Match length 309 % identity

Glycine max gene encoding ribulose-1,5-bisphosphate NCBI Description

carboxylase small subunit

Seq. No. 38780

Seq. ID LIB3106-037-Q1-K1-E11

BLASTX Method q1374991 NCBI GI 184 BLAST score 9.0e-14 E value Match length 101 % identity 42

(D83177) furostanol glycoside 26-0-beta-glucosidase (F26G) NCBI Description

[Costus speciosus]

38781 Seq. No.

Seq. ID LIB3106-037-Q1-K1-E12

Method BLASTN NCBI GI q1079735 49 BLAST score 2.0e-18 E value Match length 179 % identity 86

Glycine soja ribulose 1,5-bisphosphate carboxylase small NCBI Description

subunit precursor (rbcS) gene, nuclear gene encoding

chloroplast protein, complete cds

Seq. No. 38782

LIB3106-037-Q1-K1-E6 Seq. ID

Method BLASTN NCBI GI g441205 BLAST score 89 1.0e-42 E value Match length 225 % identity

NCBI Description Soybean lox1gm4 gene encoding lipxygenase L-4

Seq. No. 38783

LIB3106-037-Q1-K1-F3 Seq. ID

Method BLASTN NCBI GI g1053215 BLAST score 393 0.0e+00E value Match length 413 % identity 99



NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 38784

Seq. ID LIB3106-037-Q1-K1-G10

Method BLASTN
NCBI GI g1055367
BLAST score 107
E value 2.0e-53
Match length 119
% identity 97

% identity 97 NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 38785

Seq. ID LIB3106-037-Q1-K1-G12

Method BLASTX
NCBI GI g2464880
BLAST score 145
E value 1.0e-10
Match length 78
% identity 51

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 38786

Seq. ID LIB3106-038-Q1-K1-A5

Method BLASTX
NCBI GI g2564066
BLAST score 219
E value 5.0e-18
Match length 69
% identity 67

NCBI Description (D45900) LEDI-3 protein [Lithospermum erythrorhizon]

Seq. No. 38787

Seq. ID LIB3106-038-Q1-K1-A7

Method BLASTX
NCBI GI g3885884
BLAST score 140
E value 6.0e-13
Match length 85
% identity 55

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 38788

Seq. ID LIB3106-038-Q1-K1-B10

Method BLASTX
NCBI GI g3128228
BLAST score 232
E value 9.0e-20
Match length 57
% identity 77

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 38789

6013

```
Seq. ID
                   LIB3106-038-Q1-K1-B3
Method
                   BLASTX
 NCBI GI
                   g4469025
BLAST score
                   260
E value
                   9.0e-23
Match length
                   84
 % identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   38790
Seq. ID
                   LIB3106-038-Q1-K1-B9
Method
                   BLASTN
NCBI GI
                   g1055367
BLAST score
                   320
E value
                   1.0e-180
Match length
                   384
% identity
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
Seq. No.
                   38791
Seq. ID
                   LIB3106-038-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   q3335372
BLAST score
                   191
E value
                   8.0e-21
Match length
                   97
% identity
                   53
NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]
Seq. No.
                   38792
Seq. ID
                  LIB3106-038-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   g3402690
BLAST score
                   320
E value
                   1.0e-29
Match length
                   111
% identity
                   59
NCBI Description
                  (AC004697) hypothetical protein, 3' partial [Arabidopsis
                  thaliana]
Seq. No.
                  38793
Seq. ID
                  LIB3106-038-Q1-K1-C6
Method
                  BLASTN
NCBI GI
                  g18644
BLAST score
                  307
E value
                  1.0e-172
Match length
                  341
% identity
                  97
NCBI Description Soybean mRNA for HMG-1 like protein
```

Seq. No. 38794

Seq. ID LIB3106-038-Q1-K1-C7

Method BLASTX NCBI GI g2511715 BLAST score 243 E value 1.0e-20



Match length 75 % identity 12

NCBI Description (AF019380) putative phosphatidylinositol-4-phosphate

5-kinase [Arabidopsis thaliana]

Seq. No. 38795

Seq. ID LIB3106-038-Q1-K1-E8

Method BLASTN
NCBI GI g3982595
BLAST score 118
E value 8.0e-60
Match length 246
% identity 89

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 38796

Seq. ID LIB3106-038-Q1-K1-F1

Method BLASTN
NCBI GI g1236948
BLAST score 97
E value 3.0e-47
Match length 273
% identity 84

NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds

Seq. No. 38797

Seq. ID LIB3106-038-Q1-K1-F2

Method BLASTX
NCBI GI g4567242
BLAST score 244
E value 2.0e-22
Match length 79
% identity 72

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 38798

Seq. ID LIB3106-038-Q1-K1-F8

Method BLASTN
NCBI GI g1277165
BLAST score 102
E value 4.0e-50
Match length 201
% identity 88

NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No. 38799

Seq. ID LIB3106-038-Q1-K1-G10

Method BLASTX
NCBI GI g505100
BLAST score 176
E value 7.0e-13
Match length 106
% identity 38

NCBI Description (D31886) KIAA0066 [Homo sapiens]

Seq. No. 38800

Seq. ID LIB3106-038-Q1-K1-H1



```
Method BLASTX
NCBI GI g4218113
BLAST score 203
E value 6.0e-16
Match length 94
% identity 49
```

NCBI Description (AL035353) xyloglucan endotransglycosylase-like protein [Arabidopsis thaliana]

Seq. No. 38801

Seq. ID LIB3106-039-Q1-K1-A11

Method BLASTX
NCBI GI g3819708
BLAST score 165
E value 1.0e-11
Match length 59
% identity 47

NCBI Description (AJ224160) delta-8 sphingolipid desaturase [Brassica napus]

Seq. No. 38802

Seq. ID LIB3106-039-Q1-K1-A9

Method BLASTX
NCBI GI g1172664
BLAST score 349
E value 4.0e-33
Match length 115
% identity 67

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR

(LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi_419791_pir__S31165 photosystem I chain III precursor Flaveria trinervia >gi_298482_bbs_127083 photosystem I
reaction center subunit III, PSI-RC PsaF [Flaveria

trinervia, Peptide, 232 aa] >gi 168173 (M83119) photosystem

I subunit III [Flaveria trinervīa]

Seq. No. 38803

Seq. ID LIB3106-039-Q1-K1-C1

Method BLASTX
NCBI GI g2492514
BLAST score 532
E value 2.0e-54
Match length 118
% identity 88

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR

>gi 1483215 emb CAA68141 (X99808) chloroplast FtsH

protease [Arabidopsis thaliana]

Seq. No. 38804

Seq. ID LIB3106-039-Q1-K1-D5

Method BLASTX
NCBI GI g3288109
BLAST score 164
E value 1.0e-11
Match length 83
% identity 39

NCBI Description (AJ002057) calreticulin [Beta vulgaris]



```
Seq. No.
                  38805
                  LIB3106-039-Q1-K1-D6
Seq. ID
Method
                  BLASTX
                  g3947735
NCBI GI
BLAST score
                  210
                  1.0e-16
E value
                  115
Match length
% identity
                  39
                  (AJ009720) NL27 [Solanum tuberosum]
NCBI Description
                  38806
Seq. No.
                  LIB3106-039-Q1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  173
                  5.0e-21
E value
                  99
Match length
                  57
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                  38807
Seq. No.
                  LIB3106-039-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1236961
BLAST score
                  315
                  3.0e-29
E value
Match length
                  72
                  74
% identity
                  (U50201) prunasin hydrolase precursor [Prunus serotina]
NCBI Description
                   38808
Seq. No.
                  LIB3106-039-Q1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1277163
BLAST score
                   96
E value
                   1.0e-46
Match length
                   248
% identity
                   85
NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds
Seq. No.
                   38809
                  LIB3106-040-Q1-K1-A6
Seq. ID
Method
                   BLASTX
                   g129231
NCBI GI
BLAST score
                   170
                   1.0e-12
E value
                   45
Match length
                   69
% identity
                  ORYZAIN ALPHA CHAIN PRECURSOR >gi 67644 pir KHRZOA oryzain
NCBI Description
                   (EC 3.4.22.-) alpha precursor - rice
                   >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor
                   [Oryza sativa]
```

Seq. No. 38810

Seq. ID LIB3106-040-Q1-K1-A7

Method BLASTX NCBI GI g4455169

E value

Match length

% identity

9.0e-11

68

49



```
BLAST score
                  4.0e-23
E value
Match length
                  92
                  53
% identity
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  38811
Seq. No.
                  LIB3106-040-Q1-K1-E2
Seq. ID
                  BLASTX
Method
                  g2459420
NCBI GI
                  330
BLAST score
                  6.0e-31
E value
Match length
                  100
% identity
                  66
                  (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                  thaliana]
                  38812
Seq. No.
                  LIB3106-040-Q1-K1-F12
Seq. ID
                  BLASTX
Method
                  g1848214
NCBI GI
BLAST score
                  220
                  5.0e-18
E value
Match length
                  60
                  73
% identity
                  (Y11210) uracil phosphoribosyltransferase [Nicotiana
NCBI Description
                  tabacum]
                  38813
Seq. No.
                  LIB3106-040-Q1-K1-F3
Seq. ID
                  BLASTN
Method
                  g1680711
NCBI GI
BLAST score
                  114
                   1.0e-57
E value
                   161
Match length
                   93
% identity
NCBI Description Glycine max gamma glutamyl hydrolase mRNA, complete cds
                   38814
Seq. No.
                   LIB3106-040-Q1-K1-G4
Seq. ID
Method
                   BLASTN
                   g303900
NCBI GI
                   182
BLAST score
E value
                   5.0e-98
                   286
Match length
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                   38815
Seq. No.
                   LIB3106-041-Q1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3335335
BLAST score
                   156
```

6018



(AC004512) ESTs gb F14113 and gb T42122 come from this NCBI Description region. [Arabidopsis thaliana]

38816 Seq. No.

Seq. ID LIB3106-041-Q1-K1-C12

Method BLASTN NCBI GI g169897 301 BLAST score 1.0e-169 E value 371 Match length % identity 96

NCBI Description G.max 28 kDa protein, complete cds

38817 Seq. No.

LIB3106-041-Q1-K1-C5 Seq. ID

Method BLASTX q2554675 NCBI GI BLAST score 167 E value 9.0e-12 Match length 94 44 % identity

Three-Dimensional Structure Of Glycolate Oxidase With Bound NCBI Description

Active-Site Inhibitors >gi_2624594_pdb_1AL7

Three-Dimensional Structures Of Glycolate Oxidase With

Bound Active-Site Inhibitors

38818 Seq. No.

LIB3106-041-Q1-K1-D11 Seq. ID

Method BLASTX g484531 NCBI GI BLAST score 222 2.0e-18 E value Match length 79

% identity 62

NCBI Description H3.3 like histone MH321 - mouse

Seq. No. 38819

LIB3106-041-Q1-K1-F10 Seq. ID

Method BLASTN NCBI GI q533691 BLAST score 97 3.0e-47 E value Match length 193 % identity 88

NCBI Description Glycine max Essex protease inhibitor mRNA, complete cds

38820 Seq. No.

LIB3106-041-Q1-K1-F8 Seq. ID

BLASTN Method g169897 NCBI GI 124 BLAST score 3.0e-63 E value 312 Match length % identity 85

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 38821

```
Seq. ID
                   LIB3106-041-Q1-K1-G9
Method
                   BLASTN
NCBI GI
                   q18764
BLAST score
                   179
E value
                   3.0e - 96
Match length
                   222
% identity
NCBI Description
                   G.max tefS1 gene for elongation factor EF-1a
                   38822
Seq. No.
Seq. ID
                   LIB3106-041-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   q131199
BLAST score
                   143
                   4.0e-09
E value
Match length
                   82
% identity
                   37
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                   >gi_81470_pir__S00453 photosystem I protein psaH precursor
- spinach >gi_21287_emb_CAA34749_ (X16858) psaH [Spinacia
                   oleracea]
Seq. No.
                   38823
Seq. ID
                   LIB3106-042-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   q2499966
BLAST score
                   209
E value
                   7.0e-17
Match length
                   64
% identity
                   69
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E
                   A) >gi_632722_bbs_151001 (S72356) photosystem I subunit
                   PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,
                   141 aa] [Nicotiana sylvestris]
Seq. No.
                   38824
Seq. ID
                   LIB3106-042-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   q1296955
BLAST score
                   145
                   4.0e-09
E value
Match length
                   114
% identity
                   20
NCBI Description
                   (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.
                   38825
```

Seq. ID LIB3106-042-Q1-K1-E7

38826

Method BLASTX NCBI GI q3885884 BLAST score 264 5.0e-23 E value 53 Match length 94 % identity

(AF093630) 60S ribosomal protein L21 [Oryza sativa] NCBI Description

Seq. No.

6020



```
LIB3106-042-Q1-K1-G8
Seq. ID
Method
                  BLASTN
                  g170087
NCBI GI
                  245
BLAST score
                  1.0e-135
E value
Match length
                  257
                  99
% identity
                  G.max vegetative storage protein mRNA (VSP25 gene)
NCBI Description
                  38827
Seq. No.
                  LIB3106-042-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263704
BLAST score
                  350
                  3.0e-33
E value
Match length
                  99
                  70
% identity
                  (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
                  38828
Seq. No.
                  LIB3106-043-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q133793
BLAST score
                   228
                   3.0e-19
E value
                   80
Match length
                   62
% identity
                  40S RIBOSOMAL PROTEIN S15A (PPCB8) >gi 99825 pir S20945
NCBI Description
                   ribosomal protein S15a - rape >gi_17863_emb CAA42599
                   (X59983) r-protein BnS15a [Brassica napus]
                   38829
Seq. No.
Seq. ID
                   LIB3106-043-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   q2739002
BLAST score
                   229
                   6.0e-19
E value
Match length
                   112
% identity
                   40
                  (AF022460) CYP83D1p [Glycine max]
NCBI Description
                   38830
Seq. No.
Seq. ID
                   LIB3106-043-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   g2981475
BLAST score
                   252
E value
                   9.0e-22
                   72
Match length
% identity
                   65
                   (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
NCBI Description
                   domestica]
```

Seq. No. 38831

Seq. ID LIB3106-043-Q1-K1-D10

Method BLASTX NCBI GI g1172995



BLAST score 238
E value 5.0e-20 **
Match length 117
% identity 46

NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal

protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)

ribosomal protein L22 [Rattus norvegicus]

>gi 1093952 prf 2105193A ribosomal protein L22 [Rattus

norvegicus]

Seq. No. 38832

Seq. ID LIB3106-043-Q1-K1-D6

Method BLASTX
NCBI GI g166708
BLAST score 241
E value 1.0e-20
Match length 92
% identity 59

NCBI Description (M64118) glyceraldehyde-3-phosphate dehydrogenase

[Arabidopsis thaliana]

Seq. No. 38833

Seq. ID LIB3106-043-Q1-K1-E7

Method BLASTX
NCBI GI g4454484
BLAST score 192
E value 2.0e-28
Match length 104
% identity 63

NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No. 38834

Seq. ID LIB3106-043-Q1-K1-F2

Method BLASTX
NCBI GI g2501356
BLAST score 334
E value 3.0e-31
Match length 92
% identity 87

NCBI Description TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)

>gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor

[Solanum tuberosum]

Seq. No. 38835

Seq. ID LIB3106-043-Q1-K1-H10

Method BLASTN
NCBI GI g1053215
BLAST score 39
E value 7.0e-13
Match length 127
% identity 83

NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA,

nuclear gene encoding chloroplast protein, complete cds

Seq. No. 38836

Seq. ID LIB3106-045-Q1-K1-A4



```
Method
NCBI GI
                   g3075398
BLAST score
                   190
                   2.0e-14
E value
                   132
Match length
                   37
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
                   38837
Seq. No.
                  LIB3106-045-Q1-K1-B10
Seq. ID
                  BLASTN
Method
                   g2286199
NCBI GI
BLAST score
                   278
E value
                   1.0e-155
Match length
                   437
                   91
% identity
                  Pisum sativum polynucleotide phosphorylase (pnp) mRNA,
NCBI Description
                   complete cds
                   38838
Seq. No.
                   LIB3106-045-Q1-K1-D4
Seq. ID
Method
                   BLASTX
                   g4468979
NCBI GI
BLAST score
                   462
E value
                   3.0e-46
                   91
Match length
% identity
                   92
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
                   38839
Seq. No.
                   LIB3106-045-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1055368
BLAST score
                   268
E value
                   6.0e-41
Match length
                   115
                   74
% identity
                   (U39567) ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Glycine max]
                   38840
Seq. No.
Seq. ID
                   LIB3106-046-Q1-K1-E1
Method
                   BLASTN
NCBI GI
                   q3183639
BLAST score
                   33
                   4.0e-09
E value
Match length
                   61
                   89
% identity
NCBI Description
                  Cicer arietinum mRNA for putative transmembrane channel
                   protein, partial
Seq. No.
                   38841
                   LIB3106-046-Q1-K1-E9
Seq. ID
```

Method BLASTX NCBI GI g3434971 239 BLAST score 3.0e-20 E value



```
Match length 53 % identity 81
```

NCBI Description (AB008105) ethylene responsive element binding factor 3

[Arabidopsis thaliana]

Seq. No. 38842

Seq. ID LIB3106-046-Q1-K1-F10

Method BLASTN
NCBI GI g169897
BLAST score 42
E value 9.0e-15
Match length 134
% identity 83

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 38843

Seq. ID LIB3106-046-Q1-K1-F2

Method BLASTX
NCBI GI g4104816
BLAST score 149
E value 3.0e-21
Match length 93
% identity 62

NCBI Description (AF039662) ferredoxin-like protein [Capsicum annuum]

Seq. No. 38844

Seq. ID LIB3106-046-Q1-K1-F3

Method BLASTX
NCBI GI g3876805
BLAST score 145
E value 4.0e-09
Match length 100
% identity 38

NCBI Description (Z81532) similar to Zinc finger, C3HC4 type (RING finger),

Zinc finger, CCHC class; cDNA EST EMBL:D76268 comes from this gene; cDNA EST EMBL:D68142 comes from this gene; cDNA

EST EMBL:C13529 comes from this gene; cDNA EST yk208

Seq. No. 38845

Seq. ID LIB3106-046-Q1-K1-G11

Method BLASTN
NCBI GI g531832
BLAST score 43
E value 4.0e-15
Match length 103
% identity 85

NCBI Description Cloning vector pSport2, complete sequence

Seq. No.

38846

Seq. ID LIB3106-046-Q1-K1-G8

Method BLASTX
NCBI GI g3892059
BLAST score 411
E value 2.0e-40
Match length 114
% identity 70

NCBI Description (AC002330) predicted protein of unknown function



[Arabidopsis thaliana]

```
38847
Seq. No.
                  LIB3106-047-Q1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170091
BLAST score
                   44
                  1.0e-15
E value
Match length
                  48
                  98
% identity
NCBI Description
                  Glycine max vegetative storage protein (vspB) gene,
                  complete cds
Seq. No.
                   38848
                  LIB3106-047-Q1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2460298
BLAST score
                  205
E value
                   3.0e-16
Match length
                   121
% identity
                   38
                  (AF022152) AP-3 complex beta3B subunit [Homo sapiens]
NCBI Description
                   38849
Seq. No.
Seq. ID
                  LIB3106-047-Q1-K1-C5
Method
                  BLASTX
                   g4454470
NCBI GI
BLAST score
                   399
E value
                   5.0e-44
Match length
                   140
% identity
                   69
                   (AC006234) putative sugar transporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   38850
Seq. ID
                   LIB3106-047-Q1-K1-D3
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   5.0e-11
E value
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   38851
Seq. ID
                   LIB3106-047-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   q1087073
BLAST score
                   509
E value
                   7.0e-52
Match length
                   101
% identity
                   92
                   (S79243) calmodulin-binding heat-shock protein, CaMBP
NCBI Description
                   [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa]
```

Seq. No. 38852

[Nicotiana tabacum]

BLAST score

E value

77

3.0e-35

```
Seq. ID
                    LIB3106-047-Q1-K1-D9
 Method
                    BLASTN
 NCBI GI
                    g2055227
 BLAST score
                    42
 E value
                    3.0e-14
 Match length
                   177
 % identity
                   90
 NCBI Description Glycine max mRNA for SRC1, complete cds
 Seq. No.
                   38853
                   LIB3106-047-Q1-K1-E11
 Seq. ID
 Method
                   BLASTX
NCBI GI
                   g4567275
BLAST score
                   191
E value
                   8.0e-15
Match length
                   83
 % identity
                   54
NCBI Description
                   (AC006841) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   38854
Seq. ID
                   LIB3106-048-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   g541950
BLAST score
                   158
E value
                   6.0e-11
Match length
                   69
% identity
                   55
NCBI Description
                   SPCP1 protein - soybean >gi_310576 (L12257) nodulin-26
                   [Glycine max]
Seq. No.
                   38855
Seq. ID
                   LIB3106-048-Q1-K1-B2
Method
                   BLASTN
NCBI GI
                   g2062691
BLAST score
                   36
E value
                   4.0e-11
Match length
                   39
% identity
                   65
NCBI Description
                  Human sodium phosphate transporter (NPT4) mRNA, complete
Seq. No.
                   38856
Seq. ID
                   LIB3106-048-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1085953
BLAST score
                  227
E value
                  1.0e-18
Match length
                  99
% identity
                  41
NCBI Description
                  hypothetical protein S2 - Phalaris coerulescens
Seq. No.
                  38857
Seq. ID
                  LIB3106-048-Q1-K1-D11
Method
                  BLASTN
NCBI GI
                  g3420043
```

6026



Match length 176 % identity 86

NCBI Description Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 38858

Seq. ID LIB3106-048-Q1-K1-F12

Method BLASTX
NCBI GI g836954
BLAST score 591
E value 2.0e-61
Match length 139
% identity 81

NCBI Description (U20948) receptor protein kinase [Ipomoea trifida]

Seq. No. 38859

Seq. ID LIB3106-048-Q1-K1-G10

Method BLASTX
NCBI GI g4455338
BLAST score 597
E value 4.0e-62
Match length 139
% identity 76

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 38860

Seq. ID LIB3106-048-Q1-K1-G7

Method BLASTN
NCBI GI g1680711
BLAST score 33
E value 2.0e-09
Match length 105
% identity 83

NCBI Description Glycine max gamma glutamyl hydrolase mRNA, complete cds

Seq. No. 38861

Seq. ID LIB3106-048-Q1-K1-H8

Method BLASTX
NCBI GI g1711036
BLAST score 153
E value 1.0e-10
Match length 57
% identity 58

NCBI Description (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum

sativum]

Seq. No.

38862

Seq. ID LIB3106-049-Q1-K1-B2 Method BLASTN

NCBI GI g533691 BLAST score 52 E value 3.0e-20 Match length 52 % identity 100

NCBI Description Glycine max Essex protease inhibitor mRNA, complete cds

Seq. No.

38863



```
LIB3106-049-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3036801
BLAST score
                  150
                  1.0e-09
E value
                  73
Match length
% identity
                  48
NCBI Description
                  (AL022373) putative ascorbate peroxidase [Arabidopsis
                  thaliana] >gi_3805863_emb_CAA21483_ (AL031986) putative
                  ascorbate peroxidase [Arabidopsis thaliana]
Seq. No.
                  38864
Seq. ID
                  LIB3106-049-Q1-K1-C9
Method
                  BLASTX
                  q4098517
NCBI GI
                  171
BLAST score
                  9.0e-13
E value
Match length
                  57
% identity
                  63
NCBI Description (U79114) auxin-binding protein ABP19 [Prunus persica]
                  38865
Seq. No.
Seq. ID
                  LIB3106-049-Q1-K1-E1
Method
                  BLASTN
NCBI GI
                  q19498
                  199
BLAST score
                  1.0e-108
E value
                  397
Match length
% identity
NCBI Description L.polyphyllus pPLB08 mRNA
                  38866
Seq. No.
                  LIB3106-049-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3033379
BLAST score
                  291
E value
                  4.0e-26
Match length
                  66
                  74
% identity
NCBI Description
                  (AC004238) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  38867
Seq. ID
                  LIB3106-049-Q1-K1-F3
Method
                  BLASTN
NCBI GI
                  g170087
BLAST score
                  141
E value
                  2.0e-73
Match length
                  289
% identity
                  88
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
```

38868 Seq. No.

Seq. ID LIB3106-049-Q1-K1-G6

Method BLASTX g1709358 NCBI GI BLAST score 250



E value Match length 64 % identity

NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE NCBI Description

PHOSPHOHYDROLASE) (NTPASE) >qi 629638 pir S48859

nucleoside triphosphatase - garden pea

>gi_2129890_pir__S65147 nucleoside triphosphatase

precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase

[Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No. 38869

LIB3106-049-Q1-K1-H12 Seq. ID

BLASTX Method NCBI GI q729671 BLAST score 214 E value 5.0e-23 87 Match length % identity 76

NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]

38870 Seq. No.

Seq. ID LIB3106-049-Q1-K1-H9

Method BLASTX g3451068 NCBI GI 397 BLAST score 1.0e-38 E value Match length 106 % identity 69

(AL031326) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

38871

Seq. ID LIB3106-050-Q1-K1-B4

Method BLASTX NCBI GI q4337197 BLAST score 314 E value 7.0e-29 Match length 115 % identity

(AC006403) putative AIG2 protein [Arabidopsis thaliana] NCBI Description

Seq. No.

38872

Seq. ID LIB3106-050-Q1-K1-C11

Method BLASTN NCBI GI g169897 BLAST score 267 E value 1.0e-148 Match length 423 % identity 91

NCBI Description G.max 28 kDa protein, complete cds

Seq. No.

38873

Seq. ID LIB3106-050-Q1-K1-D6

Method BLASTX NCBI GI q421826 BLAST score 276



2.0e-24 E value Match length 118 % identity 49 NCBI Description

chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi 298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 38874

LIB3106-050-Q1-K1-G1 Seq. ID

Method BLASTX NCBI GI g4567205 BLAST score 305 E value 3.0e-28 Match length 82 72 % identity

(AC007168) putative trehalose-6-phosphate phosphatase NCBI Description

[Arabidopsis thaliana]

Seq. No. 38875

LIB3106-050-Q1-K1-H10 Seq. ID

Method BLASTN g170089 NCBI GI BLAST score 61 E value 1.0e-25 Match length 211 85 % identity

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

38876 Seq. No.

Seq. ID LIB3106-050-Q1-K1-H8

Method BLASTX NCBI GI g4056480 BLAST score 253 E value 4.0e-22 Match length 90 64 % identity

NCBI Description (AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.

38877

Seq. ID LIB3106-050-Q1-K1-H9

Method BLASTN NCBI GI g170089 BLAST score 409 0.0e + 00E value Match length 449 % identity 98

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No.

38878

Seq. ID LIB3106-051-Q1-K1-B4

Method BLASTN NCBI GI q170087 BLAST score 154 E value 3.0e-81 Match length 325 % identity 88

NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)



38879 Seq. No. Seq. ID

LIB3106-051-Q1-K1-C5

Method BLASTX NCBI GI q2129774 BLAST score 152 4.0e-10 E value Match length 63. 52 % identity

xyloglucan endotransglycosylase-related protein XTR4 -NCBI Description

Arabidopsis thaliana (fragment) >gi_1244754 (U43486) xyloglucan endotransglycosylase-related protein

[Arabidopsis thaliana]

38880 Seq. No.

LIB3106-051-Q1-K1-C6 Seq. ID

BLASTX Method NCBI GI g115471 BLAST score 156 1.0e-10 E value Match length 75 52 % identity

CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE NCBI Description

DEHYDRATASE) >gi 100078_pir__S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792 (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

38881 Seq. No.

LIB3106-051-Q1-K1-C9 Seq. ID

Method BLASTX q115492 NCBI GI BLAST score 155 9.0e-15 E value Match length 85

% identity 62

NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)

calmodulin-related protein [Petunia hybrida]

38882 Seq. No.

Seq. ID LIB3106-051-01-K1-D12

Method BLASTX NCBI GI q131166 BLAST score 184 E value 7.0e-14 Match length 87 61 % identity

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi 82100 pir S00449

photosystem I chain II precursor - tomato >gi_170492 (M21344) photosystem I subunit II protein precursor [Lycopersicon esculentum] >gi_226544_prf__1601516A photosystem I reaction center II [Lycopersicon esculentum]

Seq. No. 38883

Seq. ID LIB3106-051-Q1-K1-E8

BLASTX Method NCBI GI g3860331



BLAST score 257 E value 3.0e-22 Match length 77 % identity 68

NCBI Description (AJ012692) hypothetical protein [Cicer arietinum]

Seq. No.

38884

Seq. ID LIB3106-051-Q1-K1-F1

Method BLASTN
NCBI GI g169897
BLAST score 109
E value 2.0e-54
Match length 309
% identity 84

NCBI Description G.max 28 kDa protein, complete cds

Seq. No.

38885

Seq. ID

LIB3106-052-Q1-K1-A7

Method BLASTX
NCBI GI g136638
BLAST score 184
E value 8.0e-14
Match length 80
% identity 41

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) (HR6B)

>gi_108017_pir__ B41222 ubiquitin-conjugating enzyme HHR6B human >gi_284677_pir__ A42416 ubiquitin carrier protein E2 rabbit >gi_2143552_pir__ I51913_14 kDa ubiquitin conjugating
enzyme - rat >gi_30954_emb_CAA37339_ (X53251) E2 protein

[Homo sapiens] >gi 165780 (M62387) ubiquitin

conjugating-protein [Oryctolagus cuniculus] >gi_184046 (M74525) HHR6B (Human homologue of yeast RAD 6); putative

[Homo sapiens] >gi_207555 (M62388) ubiquitin

conjugating-protein [Rattus norvegicus] >gi_476117 (U04308) 14 kDa ubiquitin conjugating enzyme [Rattus norvegicus] >gi_1237240_emb_CAA65602_ (X96859) ubiquitin-conjugating enzym [Mus musculus] >gi_1373353 (U57690) E214K [Mus musculus] >gi_745378_prf__2016220A ubiquitin-conjugating

enzyme:ISOTYPE=E2-14k [Rattus norvegicus]

>gi_4507771_ref_NP_003328.1_pUBE2B_ ubiquitin-conjugating

enzyme E2B (RAD6 homolog)

Seq. No. 38886

Seq. ID LIB3106-052-Q1-K1-A8

Method BLASTX
NCBI GI g4262154
BLAST score 174
E value 6.0e-13
Match length 79
% identity 44

NCBI Description (AC005275) putative protein phosphatase regulatory subunit

[Arabidopsis thaliana]

Seq. No.

38887

Seq. ID LIB3106-052-Q1-K1-D11

Method

BLASTX



NCBI GI g3024434
BLAST score 216
E value 2.0e-17
Match length 68
% identity 71

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_

(D88663) Tat binding protein 1 [Brassica rapa]

Seq. No. 38888

Seq. ID LIB3106-052-Q1-K1-D12

Method BLASTN
NCBI GI g170089
BLAST score 220
E value 1.0e-120
Match length 287
% identity 94

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 38889

Seq. ID LIB3106-052-Q1-K1-D4

Method BLASTX
NCBI GI g126151
BLAST score 164
E value 7.0e-13
Match length 112
% identity 46

NCBI Description LECTIN PRECURSOR (AGGLUTININ) (SBA) >gi_282898_pir__S27365

lectin precursor - soybean >gi_170006 (K00821) lectin

prepeptide [Glycine max]

Seq. No. 38890

Seq. ID LIB3106-052-Q1-K1-E2

Method BLASTX
NCBI GI g1408471
BLAST score 248
E value 2.0e-21
Match length 71
% identity 69

NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis

thaliana] >gi 3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]

Seq. No. 38891

Seq. ID LIB3106-054-Q1-K1-A3

Method BLASTN
NCBI GI g475599
BLAST score 112
E value 4.0e-56
Match length 164
% identity 94

NCBI Description Glycine max Century 84 BiP isoform B mRNA, complete cds

Seq. No. 38892

Seq. ID LIB3106-054-Q1-K1-A4

Method BLASTN NCBI GI g20061

```
BLAST score
E value
                  2.0e-67
                  278
Match length
                  87
% identity
                  Oenothera elata subsp. hookeri mRNA for protein kinase C
NCBI Description
                  inhibitor homologue
Seq. No.
                  38893
                  LIB3106-054-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q531829
BLAST score
                  173
E value
                  2.0e-12
Match length
                  63
                  52
% identity
                  (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
Seq. No.
                  38894
                  LIB3106-054-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                   g3953473
NCBI GI
BLAST score
                  130
E value
                  1.0e-10
Match length
                  106
% identity
                   44
NCBI Description (AC002328) F2202.18 [Arabidopsis thaliana]
                   38895
Seq. No.
                  LIB3106-054-Q1-K1-E11
Seq. ID
                  BLASTN
Method
                   q1236948
NCBI GI
BLAST score
                   53
E value
                   5.0e-21
                   166
Match length
% identity
                   89
NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds
                   38896
Seq. No.
                   LIB3106-054-Q1-K1-H2
```

Seq. ID

Method BLASTX NCBI GI g3341685 BLAST score 390 E value 1.0e-37 Match length 105 72 % identity

(AC003672) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

38897

Seq. ID LIB3106-054-Q1-K1-H4

Method BLASTN g2529228 NCBI GI BLAST score 340 0.0e+00E value Match length 420 95 % identity

NCBI Description Glycine max mRNA for 6-phosphogluconate dehydrogenase,



complete cds

```
38898
Seq. No.
                  LIB3106-054-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  g4539394
NCBI GI
BLAST score
                  259
                  2.0e-22
E value
Match length
                  140
                  9
% identity
NCBI Description (AL035526) putative protein [Arabidopsis thaliana]
                  38899
Seq. No.
                  LIB3106-055-Q1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191138
BLAST score
                  161
E value
                  6.0e-11
Match length
                  59
                  56
% identity
                  (AF007269) A_IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  38900
                  LIB3106-056-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                  g2961346
NCBI GI
BLAST score
                  346
E value
                  1.0e-32
Match length
                  148
                  80
% identity
                  (AL022140) pectinesterase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  38901
Seq. ID
                  LIB3106-056-Q1-K1-B8
Method
                  BLASTN
                  q2765444
NCBI GI
BLAST score
                  72
E value
                  1.0e-32
Match length
                  156
% identity
NCBI Description Glycine max mRNA for ferredoxin thioredoxin reductase
Seq. No.
                  38902
Seq. ID
                  LIB3106-056-Q1-K1-C2
Method
                  BLASTN
NCBI GI
                  q497119
BLAST score
                  124
                  3.0e-63
E value
Match length
                  284
% identity
                  86
NCBI Description Pisum sativum monodehydroascorbate reductase mRNA, complete
```

38903 Seq. No.

LIB3106-056-Q1-K1-D5 Seq. ID

6035



```
Method
                  BLASTX
NCBI GI
                  q2344903
BLAST score
                  301
                  3.0e-27
E value
Match length
                  87
                  61
% identity
NCBI Description
                   (AC002388) triacyglycerol lipase isolog [Arabidopsis
                  thaliana] >gi_3341700 (AC003672) putative triacyglycerol
                  lipase [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3106-056-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q4027897
BLAST score
                  514
E value
                  2.0e-52
Match length
                  100
% identity
                  87
NCBI Description
                  (AF049353) alpha-expansin precursor [Nicotiana tabacum]
Seq. No.
Seq. ID
                  LIB3106-056-Q1-K1-F10
Method
                  BLASTN
NCBI GI
                  q2765444
BLAST score
                  172
E value
                  7.0e-92
Match length
                  216
                  95
% identity
NCBI Description Glycine max mRNA for ferredoxin thioredoxin reductase
Seq. No.
                  38906
Seq. ID
                  LIB3106-056-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  g4218008
BLAST score
                  203
                  8.0e-16
E value
Match length
                  64
% identity
                  58
NCBI Description
                  (AC006135) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  38907
Seq. ID
                  LIB3106-057-Q1-K1-A6
                  BLASTN
Method
NCBI GI
                  g343344
BLAST score
                  65
E value
                  2.0e-28
Match length
                  125
% identity
                  89
                  Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end),
NCBI Description
                  Ile-tRNA, and Ala-tRNA genes
                  38908
Seq. No.
Seq. ID
                  LIB3106-057-Q1-K1-C6
```

Method BLASTX NCBI GI g2827143 BLAST score 205 1.0e-16 E value

Match length 64 % identity 66

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 38909

Seq. ID LIB3106-057-Q1-K1-E8

Method BLASTN
NCBI GI g2961297
BLAST score 37
E value 2.0e-11
Match length 162
% identity 81

NCBI Description Cicer arietinum mRNA for unidentified protein

Seq. No. 38910

Seq. ID LIB3106-057-Q1-K1-F10

Method BLASTN
NCBI GI g1277165
BLAST score 85
E value 6.0e-40
Match length 125
% identity 92

NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No. 38911

Seq. ID LIB3106-057-Q1-K1-H1

Method BLASTX
NCBI GI g2832625
BLAST score 234
E value 4.0e-20
Match length 55
% identity 78

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 38912

Seq. ID LIB3106-058-Q1-K1-B10

Method BLASTX
NCBI GI g2500354
BLAST score 514
E value 2.0e-52
Match length 99
% identity 95

NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj_BAA19462_

(AB001891) QM family protein [Solanum melongena]

Seq. No.

38913

Seq. ID LIB3106-058-Q1-K1-C10

Method BLASTX
NCBI GI g3645985
BLAST score 276
E value 2.0e-24
Match length 49
% identity 98

NCBI Description (AL031581) 1-evidence=predicted by content;

1-method=genefinder;084; 1-method_score=23.36;
1-evidence_end; 2-evidence=predicted by match;



2-match accession=AA141041;

2-match_description=CK01110.3prime CK Drosophila

melanogaster

Seq. No. 38914

Seq. ID LIB3106-058-Q1-K1-C3

Method BLASTN
NCBI GI g18764
BLAST score 35
E value 3.0e-10
Match length 99
% identity 84

NCBI Description G.max tefS1 gene for elongation factor EF-la

Seq. No. 38915

Seq. ID LIB3106-058-Q1-K1-C4

Method BLASTX
NCBI GI 94432858
BLAST score 190
E value 2.0e-14
Match length 117
% identity 6

NCBI Description (AC006300) putative disease resistance protein [Arabidopsis

thaliana]

Seq. No. 38916

Seq. ID LIB3106-058-Q1-K1-D4

Method BLASTX
NCBI GI g1076315
BLAST score 140
E value 1.0e-08
Match length 32
% identity 69

NCBI Description cytochrome P450 - Arabidopsis thaliana

>gi_853719_emb_CAA60793_ (X87367) CYP90 protein

[Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)

CYP90 protein [Arabidopsis thaliana]

Seq. No. 38917

Seq. ID LIB3106-058-Q1-K1-D9

Method BLASTX
NCBI GI g3860255
BLAST score 212
E value 6.0e-17
Match length 134
% identity 40

NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No. 38918

Seq. ID LIB3106-058-Q1-K1-E8

Method BLASTN
NCBI GI g18761
BLAST score 284
E value 1.0e-159
Match length 324
% identity 97

NCBI Description Soybean stem mRNA for 31 kD glycoprotein



38919 Seq. No. LIB3106-058-Q1-K1-F11 Seq. ID Method BLASTX

q3790587 NCBI GI 213 BLAST score 4.0e-17 E value 79 Match length 58 % identity

(AF079182) RING-H2 finger protein RHF2a [Arabidopsis NCBI Description

thaliana]

38920 Seq. No.

LIB3106-058-Q1-K1-F12 Seq. ID

Method BLASTN NCBI GI g167283 BLAST score 55 5.0e-22 E value 103 Match length % identity 88

C.vulgaris glyoxysomal malate dehydrogenase mRNA, complete NCBI Description

38921 Seq. No.

LIB3106-058-Q1-K1-G6 Seq. ID

Method BLASTN g170091 NCBI GI BLAST score 282 E value 1.0e-157 373 Match length 94 % identity

Glycine max vegetative storage protein (vspB) gene, NCBI Description

complete cds

Seq. No.

38922 LIB3106-058-Q1-K1-G8 Seq. ID

BLASTN Method NCBI GI q169190 BLAST score 90 5.0e-43 E value Match length 202 % identity . 86

NCBI Description P.hybrida 5-enolpyruvylshikimate 3-phosphate synthase mRNA,

complete cds

38923 Seq. No.

LIB3106-059-Q1-K1-A1 Seq. ID

BLASTX Method g2117303 NCBI GI 174 BLAST score E value 2.0e-12 75 Match length 45 % identity

(Z95620) n-acetylglucosaminyl-phosphatidylinositol NCBI Description

[Schizosaccharomyces pombe]

38924 Seq. No.



```
LIB3106-059-Q1-K1-A11
 Seq. ID
                     BLASTX
 Method
                     g131390
 NCBI GI
BLAST score
                     275
                     3.0e-24
 E value
 Match length
                     84
                     70
 % identity
                     OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD
 NCBI Description
                     SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II)
                     >gi 280396 pir__JS0771 photosystem II oxygen-evolving
                     complex protein 2 precursor - garden pea
                     >gi 20617 emb CAA33557 (X15552) precursor polypeptide (AA
                     -73 to 186) [Pisum sativum] >gi_344006_dbj BAA02553
                     (D13296) precursor for 23-kDa protein of photosystem II
                     [Pisum sativum]
 Seq. No.
                     38925
                     LIB3106-059-Q1-K1-A8
 Seq. ID
 Method
                     BLASTX
                     g730449
 NCBI GI
 BLAST score
                     328
                     9.0e-31
 E value
 Match length
                     65
                     89
 % identity
                     60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)
 NCBI Description
                     >gi 480647_pir__S37132 ribosomal protein L13.A - rape
                     >gi 398918 emb CAA80341 (Z22618) cold induced protein
                     (BnC24A) [Brassica napus]
                     38926
 Seq. No.
                     LIB3106-059-Q1-K1-B11
 Seq. ID
                     BLASTN
 Method
 NCBI GI
                     q3821780
 BLAST score
                     36
 E value
                     9.0e-11
 Match length
                     36
                     100
 % identity
                     Xenopus laevis cDNA clone 27A6-1
 NCBI Description
                     38927
 Seq. No.
                     LIB3106-059-Q1-K1-C7
 Seq. ID
 Method
                     BLASTX
                     g4337175
 NCBI GI
                     209
 BLAST score
                     5.0e-17
 E value
 Match length
                     68
  % identity
                     57
                     (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
 NCBI Description
                     gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
```

Seq. No.

38928

Seq. ID

LIB3106-059-Q1-K1-E2

Method BLASTN
NCBI GI g169974
BLAST score 193



1.0e-104 E value Match length 381 % identity

Glycine max vspA gene, complete cds NCBI Description

Seq. No.

38929

38930

Seq. ID

LIB3106-059-Q1-K1-E9

Method BLASTX NCBI GI q4538926 536 BLAST score E value 7.0e-55 Match length 144 % identity 71

(ALO49483) putative phosphatidylserine decarboxylase NCBI Description

[Arabidopsis thaliana]

Seq. No.

Seq. ID

LIB3106-059-Q1-K1-F5

Method BLASTN g1055367 NCBI GI BLAST score 366 0.0e + 00E value Match length 449 % identity 95

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No.

38931

Seq. ID LIB3106-059-Q1-K1-F7 BLASTN Method NCBI GI q1055367 BLAST score 244 E value 1.0e-135 Match length 337

99 % identity

Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description

subunit mRNA, complete cds

Seq. No.

38932

Seq. ID LIB3106-059-Q1-K1-H3

Method BLASTN NCBI GI g2055227 BLAST score 178 E value 2.0e-95 Match length 358 87 % identity

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No.

38933

Seq. ID

LIB3106-060-Q1-K1-D7

Method BLASTX g4218120 NCBI GI BLAST score 234 1.0e-19 E value Match length 62 69 % identity

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

% identity

NCBI Description

75



thaliana]

```
38934
Seq. No.
                  LIB3106-060-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                  g4406812
NCBI GI
BLAST score
                  338
E value
                  9.0e-32
Match length
                  69
                  83
% identity
                   (AC006201) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  38935
                  LIB3106-061-Q1-K1-B10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1055367
BLAST score
                  109
                  1.0e-54
E value
Match length
                  189
                  89
% identity
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
Seq. No.
                  38936
                  LIB3106-061-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                   g2129698
NCBI GI
BLAST score
                   264
                   2.0e-23
E value
Match length
                  76
                   71
% identity
                  protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi 1054633 emb CAA63387_ (X92728) protein kinase
                   [Arabidopsis thaliana]
                   38937
Seq. No.
Seq. ID
                   LIB3106-061-Q1-K1-B7
Method
                   BLASTN
                   g456713
NCBI GI
BLAST score
                   128
E value
                   1.0e-65
Match length
                   276
                   35
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
Seq. No.
                   38938
                   LIB3106-061-Q1-K1-D8
Seq. ID
Method
                   BLASTX
                   g585565
NCBI GI
BLAST score
                   437
                   2.0e-43
E value
Match length
                   118
```

6042

RIBOSOME RECYCLING FACTOR HOMOLOG (NUCLEAR LOCATED PROTEIN

>gi_297891_emb_CAA51077_ (X72384) nuclear located protein

ا دالا

D2) >gi_629661_pir__S32716 nuclear protein - carrot



[Daucus carota]

```
38939
Seq. No.
                  LIB3106-061-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3738319
BLAST score
                  168
                  5.0e-12
E value
Match length
                  94
                  46
% identity
NCBI Description
                  (AC005170) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  38940
                  LIB3106-061-Q1-K1-E6
Seq. ID
Method
                  BLASTN
                  g1658321
NCBI GI
BLAST score
                  52
E value
                  3.0e-20
Match length
                  152
                  84
% identity
NCBI Description S.tuberosum mRNA for transketolase
                  38941
Seq. No.
Seq. ID
                  LIB3106-061-Q1-K1-G5
                  BLASTN
Method
                  g2995454
NCBI GI
BLAST score
                  74
E value
                  2.0e-33
Match length
                  170
% identity
                  86
NCBI Description L.luteus mRNA for tRNA-glutamine synthetase
Seq. No.
                  38942
Seq. ID
                  LIB3106-062-Q1-K1-D7
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  35
E value
                  3.0e-10
Match length
                  35
% identity
                  59
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  38943
Seq. ID
                  LIB3106-062-Q1-K1-E10
Method
                  BLASTN
NCBI GI
                  g1055367
BLAST score
                  304
E value
                  1.0e-171
Match length
                  328
% identity
                  98
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
```

Seq. No. 38944

Seq. ID LIB3106-062-Q1-K1-F1

Method BLASTX NCBI GI g2213594

6043



```
BLAST score 337

E value 8.0e-32

Match length 95

% identity 66

NCBI Description (AC000348) T7N9.1
```

38945

NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. ID LIB3106-062-Q1-K1-F9
Method BLASTN
NCBI GI g169974
BLAST score 256
E value 1.0e-142
Match length 304

Seq. No.

% identity 96
NCBI Description Glycine max vspA gene, complete cds

Seq. No. 38946

Seq. ID LIB3106-063-Q1-K1-B11

Method BLASTX
NCBI GI g1171579
BLAST score 274
E value 3.0e-24
Match length 71
% identity 76

NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 38947

Seq. ID LIB3106-063-Q1-K1-D11

Method BLASTX
NCBI GI g266936
BLAST score 248
E value 8.0e-23
Match length 114
% identity 58

NCBI Description 50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27)

>gi_282960_pir__A42840 ribosomal protein L27 - common

tobacco >gi 170306 (M98473) ribosomal protein L27

[Nicotiana tabacum] >gi_170326 (M75731) ribosomal protein

L27 [Nicotiana tabacum]

Seq. No. 38948

Seq. ID LIB3106-063-Q1-K1-E1

Method BLASTN
NCBI GI g18741
BLAST score 72
E value 2.0e-32
Match length 175
% identity 88

NCBI Description Glycine max gene encoding ribulose-1,5-bisphosphate

carboxylase small subunit

Seq. No. 38949

Seq. ID LIB3106-063-Q1-K1-F12

Method BLASTX
NCBI GI g131385
BLAST score 416
E value 6.0e-41



38950

Match length 106
% identity 82

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN)

Seq. ID LIB3106-063-Q1-K1-F4
Method BLASTX
NCBI GI g537313
BLAST score 138
E value 2.0e-14
Match length 89
% identity 58

NCBI Description (L36159) unknown protein [Medicago sativa]

Seq. No. 38951

Seq. No.

Seq. ID LIB3106-064-Q1-K1-A10

Method BLASTX
NCBI GI g2245054
BLAST score 202
E value 1.0e-15
Match length 123
% identity 40

NCBI Description (Z97342) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 38952

Seq. ID LIB3106-064-Q1-K1-A6

Method BLASTN
NCBI GI g310575
BLAST score 35
E value 1.0e-10
Match length 83
% identity 86

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 38953

Seq. ID LIB3106-064-Q1-K1-B10

Method BLASTX
NCBI GI g531829
BLAST score 148
E value 2.0e-09
Match length 67
% identity 49

NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector

pSport1]

Seq. No. 38954

Seq. ID LIB3106-064-Q1-K1-C12

Method BLASTX
NCBI GI g2673908
BLAST score 403
E value 2.0e-39
Match length 128
% identity 55

NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                   LIB3106-064-Q1-K1-D1
Method
                   BLASTX
NCBI GI
                   g1931638
BLAST score
                   292
E value
                   3.0e-26
Match length
                   74
                   77
% identity
                   (U95973) transcription factor RUSH-lalpha isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   38956
Seq. ID
                   LIB3106-064-Q1-K1-D11
Method
                   BLASTN
NCBI GI
                   q170091
                   347
BLAST score
                   0.0e + 00
E value
Match length
                   407
% identity
                   96
                   Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
Seq. No.
                   38957
Seq. ID
                   LIB3106-065-P1-K1-A7
Method
                   BLASTN
NCBI GI
                   q170089
BLAST score
                   85
E value
                   3.0e-40
Match length
                   214
                   80
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
Seq. No.
                   38958
Seq. ID
                   LIB3106-065-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g3377507
BLAST score
                   175
                   6.0e-13
E value
Match length
                   47
% identity
                   72
NCBI Description
                   (AF056026) auxin transport protein EIR1 [Arabidopsis
                   thaliana] >gi_3661620 (AF093241) putative auxin efflux
                   carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1
                   [Arabidopsis thaliana] >gi 4206709 (AF086906) root
                   gravitropism control protein [Arabidopsis thaliana]
Seq. No.
                   38959
Seq. ID
                   LIB3106-065-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q1363487
BLAST score
                   233
```

2.0e-19 E value Match length 67

75 % identity

IAA7 protein - Arabidopsis thaliana >gi_972917 (U18409) NCBI Description

IAA7 [Arabidopsis thaliana]

Seq. No.

Seq. ID

Method

38965

BLASTN

LIB3106-067-P1-K1-B5



```
38960
Seq. No.
                  LIB3106-065-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  q3283996
NCBI GI
BLAST score
                  151
                  5.0e-10
E value
                  105
Match length
                  36
% identity
                  (AF072908) calcium-dependent protein kinase [Nicotiana
NCBI Description
                  tabacum]
                  38961
Seq. No.
                  LIB3106-066-P1-K1-A5
Seq. ID
                  BLASTX
Method
                  g3851636
NCBI GI
                  173
BLAST score
                   8.0e-13
E value
Match length
                  77
                   49
% identity
                  (AF098519) unknown [Avicennia marina] >gi_4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   38962
Seq. No.
                  LIB3106-066-P1-K1-C4
Seq. ID
Method
                  BLASTN
                   q2317899
NCBI GI
                   46
BLAST score
                   7.0e-17
E value
Match length
                   122
                   85
% identity
NCBI Description Glycine max Sali3-2 mRNA, complete cds
                   38963
Seq. No.
                   LIB3106-066-P1-K1-E8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1055367
                   57
BLAST score
E value
                   9.0e-24
Match length
                   109
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   38964
                   LIB3106-066-P1-K1-H2
Seq. ID
                   BLASTN
Method
                   q457688
NCBI GI
BLAST score
                   87
                   4.0e-41
E value
Match length
                   307
                   82
% identity
NCBI Description M.crystallinum mRNA for protein kinase
```

6047



```
NCBI GI
                  q2288900
BLAST score
                  56
                  6.0e-23
E value
Match length
                  92
                  90
% identity
NCBI Description Chenopodium quinoa partial chloroplast genome
                  38966
Seq. No.
                  LIB3106-067-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539459
BLAST score
                  153
E value
                  4.0e-10
Match length
                  49
                  51
% identity
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                  38967
                  LIB3106-067-P1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1217641
BLAST score
                  38
E value
                  4.0e-12
Match length
                  98
                  85
% identity
                  L.esculentum mRNA for 10kDa polypeptide precursor of
NCBI Description
                  photosystem II
Seq. No.
                  38968
Seq. ID
                  LIB3106-067-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g4056488
BLAST score
                  397
                  1.0e-38
E value
Match length
                  86
% identity
                  78
                  (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  38969
                  LIB3106-067-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  g1491931
NCBI GI
BLAST score
                  449
                  1.0e-44
E value
                  145
Match length
% identity
                  64
                  (U52078) kinesin-like protein [Nicotiana tabacum]
NCBI Description
                  38970
Seq. No.
Seq. ID
                  LIB3106-067-P1-K1-F10
                  BLASTN
Method
                  g170067
NCBI GI
BLAST score
                  114
                  2.0e-57
E value
Match length
                  133
                  97
% identity
```

NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)



gene, complete cds

Seq. No. 38971 LIB3106-068-P1-K1-D7 Seq. ID Method BLASTN NCBI GI g984307 BLAST score 147 E value 4.0e-77 196 Match length 93 % identity Glycine max ribosomal protein S16 (rps16) gene, partial NCBI Description cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 38972 Seq. ID LIB3106-068-P1-K1-E10

Method BLASTX
NCBI GI g2501647
BLAST score 363
E value 8.0e-35
Match length 77
% identity 86

NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)

>gi 1362120_pir__S55732 uroporphyrinogen decarboxylase -

common tobacco >gi_1009429 emb_CAA58040 (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]

Seq. No. 38973

Seq. ID LIB3106-068-P1-K1-E3

Method BLASTN
NCBI GI g170071
BLAST score 258
E value 1.0e-143
Match length 342
% identity 94

NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds

Seq. No. 38974

Seq. ID LIB3106-068-P1-K1-G11

Method BLASTX
NCBI GI g3024021
BLAST score 140
E value 7.0e-09
Match length 39
% identity 72

NCBI Description INITIATION FACTOR 5A-4 (EIF-5A) (EIF-4D)

>gi 2225883 dbj BAA20878 (AB004825) eukaryotic initiation

factor 5A4 [Solanum tuberosum]

Seq. No. 38975

Seq. ID LIB3106-068-P1-K1-G7

Method BLASTN
NCBI GI g19701
BLAST score 100
E value 4.0e-49



Match length % identity 86

N.plumbaginifolia mRNA NeIF-5A2 for initiation factor 5A(2) NCBI Description

Seq. No.

LIB3106-068-P1-K1-H11 Seq. ID

Method BLASTX q4139502 NCBI GI 192 BLAST score 1.0e-14 E value Match length 100 % identity 54

NCBI Description Chain A, Db58, A Legume Lectin From Dolichos Biflorus

>qi 4139503 pdb 1LUL B Chain B, Db58, A Legume Lectin From Dolichos Biflorus >gi_4139504_pdb_1LUL_C Chain C, Db58, A Legume Lectin From Dolichos Biflorus >gi 4139505 pdb_1LUL D Chain D, Db58, A Legume Lectin From Dolichos Biflorus >gi_4139506_pdb_1LUL_E Chain E, Db58, A Legume Lectin From Dolichos Biflorus >gi_4139507_pdb_1LUL_F Chain F, Db58, A

Legume Lectin From Dolichos Biflorus

38977 Seq. No.

Seq. ID LIB3106-068-P1-K1-H7

Method BLASTX NCBI GI q4490341 BLAST score 492 E value 6.0e-50 Match length 115 % identity 80

(AL035656) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

Seq. ID LIB3106-068-P1-K1-H9

Method BLASTX NCBI GI g4263795 BLAST score 401 E value 3.0e-39 Match length 113 % identity

(AC006068) putative glucosyltransferase [Arabidopsis NCBI Description

thaliana]

Seq. No.

38979 Seq. ID LIB3106-069-P1-K1-C6

Method BLASTX NCBI GI g3885344

BLAST score 197 E value 4.0e-15 102 Match length % identity 37

(AC005623) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 4557057 gb AAD22497.1 AC007154_1 (AC007154) unknown

protein [Arabidopsis thaliana]

38980 Seq. No.

LIB3106-069-P1-K1-C8 Seq. ID

Method BLASTX



```
NCBI GI
BLAST score
                   586
E value
                   9.0e-61
Match length
                   152
                   70
% identity
                  (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No. .
                   38981
                   LIB3106-069-P1-K1-E4
Seq. ID
Method
                   BLASTN
                   g3043429
NCBI GI
BLAST score
                   73
E value
                   5.0e-33
Match length
                   193
% identity
                   84
NCBI Description Cicer arietinum mRNA for annexin
                   38982
Seq. No.
                   LIB3106-069-P1-K1-F3
Seq. ID
Method
                   BLASTX
                   q1350680
NCBI GI
                   209
BLAST score
E value
                   7.0e-17
                - 57
Match length
% identity
                   70
NCBI Description 60S RIBOSOMAL PROTEIN L1
                   38983
Seq. No.
Seq. ID
                   LIB3106-070-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g2773184
BLAST score
                   157
E value
                   1.0e-10
Match length
                   86
                   43
% identity
                  (AF039720) similar to the "DEAD" box family of helicases;
NCBI Description
                   most similar to eukaryotic initiation factor 4A
                   [Caenorhabditis elegans]
                   38984
Seq. No.
Seq. ID
                   LIB3106-070-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g541943
BLAST score
                   305
                   8.0e-28
E value
Match length
                   56
% identity
                   95
                  metallothionein - soybean >gi_228682_prf__1808316A
metallothionein-like protein [Glycine max]
NCBI Description
                   38985
Seq. No.
Seq. ID
                   LIB3106-070-P1-K1-F6
                   BLASTN
Method
NCBI GI
                   g170087
BLAST score
                   145
```

6051

7.0e-76

217

E value Match length

```
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
Seq. No.
                  38986
Seq. ID
                  LIB3106-071-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g18741
BLAST score
                  124
E value
                  2.0e-63
Match length
                  253
% identity
                  90
NCBI Description
                  Glycine max gene encoding ribulose-1,5-bisphosphate
                  carboxylase small subunit
                  38987
Seq. No.
Seq. ID
                  LIB3106-071-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q3080415
                  214
```

BLAST score E value 4.0e-17 Match length 57 67 % identity NCBI Description

(AL022604) cysteine proteinase - like protein [Arabidopsis thaliana]

Seq. No. 38988

Seq. ID LIB3106-071-P1-K1-B7

Method BLASTX NCBI GI a2194117 BLAST score 239 E value 5.0e-20 Match length 106 % identity 50

NCBI Description (AC002062) Strong similarity to Arabidopsis receptor protein kinase PR5K (gb_ATU48698). [Arabidopsis thaliana]

Seq. No. 38989

Seq. ID LIB3106-071-P1-K1-C3

Method BLASTX g3402689 NCBI GI BLAST score 174 6.0e-16 E value Match length 88 % identity 60

(AC004697) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 38990

Seq. ID LIB3106-071-P1-K1-D7

Method BLASTX NCBI GI q3668097 BLAST score 162 1.0e-11 E value Match length 58 59 % identity

(AC004667) putative glycine cleavage system protein H NCBI Description

precursor [Arabidopsis thaliana]



```
Seq. No.
                  LIB3106-071-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4151066
BLAST score
                  171
E value
                  3.0e-13
Match length
                  102
% identity
                  49
                  (Y10861) ribonucleotide reductase [Nicotiana tabacum]
NCBI Description
Seq. No.
                  38992
Seq. ID
                  LIB3106-071-P1-K1-E8
Method
                  BLASTN
NCBI GI
                  g2815245
BLAST score
                  75
E value
                  5.0e-34
Match length
                  242
% identity
                  84
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                  CanMT-2)
Seq. No.
                  38993
Seq. ID
                  LIB3106-071-P1-K1-G12
Method
                  BLASTN
NCBI GI
                  g531832
BLAST score
                  37
E value
                  2.0e-11
Match length
                  129
% identity
                  82
                  Cloning vector pSport2, complete sequence
NCBI Description
Seq. No.
                  38994
                  LIB3106-071-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2347088
BLAST score
                  387
E value
                  2.0e-37
Match length
                  117
% identity
                   68
                  (U72765) non-specific lipid transfer protein PvLTP-24
NCBI Description
                   [Phaseolus vulgaris]
Seq. No.
                  38995
                  LIB3106-071-P1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2304954
BLAST score
                  145
                  9.0e-76
E value
Match length
                  352
% identity
                  86
NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds
```

Seq. No.

38996

Seq. ID LIB3106-071-P1-K1-H10

Method BLASTN NCBI GI g169974 BLAST score 65



E value 4.0e-28 Match length 73 97 % identity Glycine max vspA gene, complete cds NCBI Description 38997 Seq. No. Seq. ID LIB3106-071-P1-K1-H11 Method BLASTX NCBI GI q3914472 245 BLAST score E value 5.0e-21Match length 61 % identity 77 PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) NCBI Description >gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana tabacum] 38998 Seq. No. LIB3106-072-P1-K1-D4 Seq. ID Method BLASTN NCBI GI q1044867 BLAST score 69 E value 1.0e-30 Match length 248 % identity 83 NCBI Description Glycine max mRNA for cinnamic acid 4-hydroxylase (CYP73) Seq. No. 38999 Seq. ID LIB3106-072-P1-K1-E12 Method BLASTN g20728 NCBI GI BLAST score 72 E value 3.0e-32 Match length 231 % identity 87 NCBI Description Pea chloroplast GAPA mRNA encoding qlyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A (EC 1.2.1.13) 39000 Seq. No. Seq. ID LIB3106-072-P1-K1-F12 Method BLASTX NCBI GI g4455301 BLAST score 192 4.0e-18 E value Match length 81 % identity 57 (AL035528) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 39001 Seq. ID LIB3106-072-P1-K1-G8

Method BLASTN NCBI GI g18274

BLAST score 158
E value 2.0e-83
Match length 350



% identity

Cucumis sativus mRNA for NAPH-dependent hydroxypyruvate NCBI Description

reductase (EC 1.1.1.29)

39002 Seq. No.

LIB3106-072-P1-K1-G9 Seq. ID

BLASTN Method g169897 NCBI GI BLAST score 274 1.0e-153 E value 420 Match length 92 % identity

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 39003

LIB3106-072-P1-K1-H10 Seq. ID

Method BLASTX g3075488 NCBI GI BLAST score 251 E value 1.0e-21 Match length 93 57 % identity

(AF058796) chlorophyll a/b-binding protein [Oryza sativa] NCBI Description

Seq. No.

39004 LIB3106-073-Q1-K1-F8

Seq. ID Method BLASTX NCBI GI g2462733 BLAST score 380

1.0e-36 E value Match length 122 65 % identity

(AC002292) Putative enoyl-CoA hydratase/isomerase NCBI Description

[Arabidopsis thaliana]

39005 Seq. No.

LIB3106-074-Q1-K1-A10 Seq. ID

Method BLASTN NCBI GI q2815245 BLAST score 70 5.0e-31 E value Match length 242 82 % identity

C.arietinum mRNA for class I type 2 metallothionein (clone: NCBI Description

CanMT-2)

Seq. No.

39006

LIB3106-074-Q1-K1-A3 Seq. ID

Method BLASTX NCBI GI g4115534 BLAST score 239 E value 2.0e-40

Match length 112 % identity

NCBI Description (AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna

mungo]

E value

Match length

9.0e-28

116



```
Seq. No.
                   LIB3106-074-Q1-K1-A5
 Seq. ID
 Method
                   BLASTN
                   g18644
 NCBI GI
                   52
 BLAST score
                   1.0e-20
 E value
                   100
Match length
                   88
% identity
 NCBI Description Soybean mRNA for HMG-1 like protein
                   39008
 Seq. No.
                   LIB3106-074-Q1-K1-A6
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   g18644
 BLAST score
                   151
                   2.0e-79
 E value
                   219
 Match length
                   92
 % identity
 NCBI Description Soybean mRNA for HMG-1 like protein
                    39009
 Seq. No.
                   LIB3106-074-Q1-K1-A9
 Seq. ID
                   BLASTX
 Method
                    g2425066
 NCBI GI
 BLAST score
                    338
                    1.0e-31
 E value
 Match length
                    114
                    52
 % identity
 NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]
                    39010
 Seq. No.
                    LIB3106-074-Q1-K1-C2
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g2558961
 BLAST score
                    106
 E value
                    2.0e-52
 Match length
                    194
                    89
 % identity
 NCBI Description Gossypium hirsutum histone H2B1 mRNA, complete cds
                    39011
 Seq. No.
 Seq. ID
                    LIB3106-074-Q1-K1-E1
 Method
                    BLASTX
                    g2980788
 NCBI GI
 BLAST score
                    188
                    4.0e-14
 E value
                    92
 Match length
                    50
 % identity
                   (AL022197) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    39012
                    LIB3106-075-Q1-K1-B12
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g168492
 BLAST score
                    64
```

6056



% identity NCBI Description Corn histone H3 (H3C3) gene, complete cds 39013 Seq. No. LIB3106-075-Q1-K1-E2 Seq. ID Method BLASTX NCBI GI g462195

BLAST score 215 8.0e-18 E value 68 Match length 68 % identity

PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) NCBI Description

>gi 100682_pir__S21636 GOS2 protein - rice

>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza

satīva]

39014 Seq. No.

LIB3106-075-Q1-K2-A10 Seq. ID

Method BLASTN g1196896 NCBI GI 188 BLAST score 1.0e-101 E value Match length 210

% identity 98

NCBI Description Glycine max acidic ribosomal protein PO mRNA, complete cds

39015 Seq. No.

LIB3106-075-Q1-K2-A7 Seq. ID

Method BLASTX g3747050 NCBI GI BLAST score 142 2.0e-16 E value Match length 76 67 % identity

NCBI Description (AF093540) ribosomal protein L26 [Zea mays]

39016 Seq. No.

Seq. ID LIB3106-075-01-K2-C1

Method BLASTN q441205 NCBI GI 37 BLAST score 2.0e-11 E value 57 Match length % identity 91

NCBI Description Soybean lox1gm4 gene encoding lipxygenase L-4

39017 Seq. No.

LIB3106-075-Q1-K2-C12 Seq. ID

Method BLASTX NCBI GI q4262151 BLAST score 444 E value 1.0e-48 Match length 143 % identity 72

NCBI Description (AC005275) putative receptor kinase [Arabidopsis thaliana]



```
Seq. No.
                  LIB3106-075-Q1-K2-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q136057
                  186
BLAST score
                  4.0e-14
E value
                  76
Match length
                  55
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                  Coptis japonica >gi_556171 (J04121) triosephosphate
                  isomerase [Coptis japonica]
```

Seq. No. 39019 LIB3106-075-Q1-K2-D2 Seq. ID BLASTN Method g439856 NCBI GI

39020

134 BLAST score 3.0e-69 E value 266 Match length 88 % identity

NCBI Description Glycine max Williams 82 lipoxygenase mRNA, complete cds

Seq. No. Seq. ID LIB3106-075-Q1-K2-E11 BLASTN Method g288187 NCBI GI 151 BLAST score 1.0e-79 E value Match length 211 % identity 93

NCBI Description V.unguiculata cysteine proteinase inhibitor mRNA

Seq. No. 39021

LIB3106-075-Q1-K2-E12 Seq. ID

Method BLASTN NCBI GI g508303 BLAST score 40 4.0e-13 E value Match length 71 % identity 89

NCBI Description Alfalfa bimodular protein (corC) mRNA, complete cds

39022 Seq. No.

Seq. ID LIB3106-075-Q1-K2-G7

Method BLASTN g454178 NCBI GI 246 BLAST score E value 1.0e-136 302 Match length % identity

NCBI Description Glycine max rubisco-associated protein mRNA, complete cds

39023 Seq. No.

Seq. ID LIB3106-076-Q1-K1-A3

Method BLASTN NCBI GI g3821780



```
BLAST score
                  6.0e-11
E value
Match length
                  37
                  61
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  39024
Seq. No.
                  LIB3106-076-Q1-K1-D10
Seq. ID
                  BLASTX
Method
                  g2191152
NCBI GI
                  171
BLAST score
                  2.0e-12
E value
Match length
                  61
% identity
                  66
                  (AF007269) A_IG002N01.31 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  39025
Seq. No.
                  LIB3106-076-Q1-K1-D12
Seq. ID
Method
                  BLASTX
                  g2494119
NCBI GI
                  356
BLAST score
                  9.0e-34
E value
                  97
Match length
                  72
% identity
                  (AC002376) EST gb T04104 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  39026
Seq. No.
                  LIB3106-076-Q1-K1-F11
Seq. ID
                  BLASTN
Method
                  g169899
NCBI GI
BLAST score
                  287
E value
                  1.0e-160
Match length
                   367
                   95
% identity
NCBI Description G.max 31 kDa protein mRNA, 3' end
                   39027
Seq. No.
Seq. ID
                  LIB3106-076-Q1-K1-F12
                  BLASTN
Method
                   g170089
NCBI GI
                   89
BLAST score
                   2.0e-42
E value
Match length
                   217
% identity
                   85
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
Seq. No.
                   39028
Seq. ID
                   LIB3106-076-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   q4056456
BLAST score
                   250
                   2.0e-21
E value
Match length
                   119
% identity
                   50
NCBI Description (AC005990) Strong similarity to gb_U20808 auxin-induced
```



39029

protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb AA395179 come from this gene. [Arabidopsis thaliana]

Seq. ID LIB3106-077-P1-K1-C8 Method BLASTN
NCBI GI g303900
BLAST score 272
E value 1.0e-151
Match length 360
% identity 28

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 39030

Seq. No.

Seq. ID LIB3106-078-P1-K1-A2

Method BLASTN
NCBI GI g14146
BLAST score 279
E value 1.0e-155
Match length 434
% identity 91

NCBI Description Oenothera elata subsp. hookeri plastid DNA for psbB, psbH

and psbN genes for chlorophyll a-binding apoprotein, 10 kDa

phosphoprotein, and unknown protein of photosystem II,

respectively

Seq. No. 39031

Seq. ID LIB3106-078-P1-K1-A3

Method BLASTX
NCBI GI g136636
BLAST score 463
E value 2.0e-46
Match length 107
% identity 84

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 39032

Seq. ID LIB3106-078-P1-K1-E10

Method BLASTX
NCBI GI g1709651
BLAST score 142
E value 3.0e-09
Match length 75
% identity 48

NCBI Description PLASTOCYANIN A PRECURSOR >gi_2117431_pir__S58209

plastocyanin a precursor - black poplar

>gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus

nigra]

Match length

NCBI Description

% identity

152 58

[Arabidopsis thaliana]



```
Seq. No.
                  39033
                  LIB3106-078-P1-K1-F7
Seq. ID
Method
                  BLASTN
                  q169974
NCBI GI
                  160
BLAST score
E value
                  8.0e-85
                  332
Match length
% identity
                  87
NCBI Description Glycine max vspA gene, complete cds
                  39034
Seq. No.
Seq. ID
                  LIB3106-078-P1-K1-G10
Method
                  BLASTN
                  a984307
NCBI GI
                  39
BLAST score
                  1.0e-12
E value
Match length
                  229
% identity
                  78
                  Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                  cds, beta-carboxyltransferase (accD), photosystem I
                  component (psaI), ORF 202 protein (ORF 203), ORF 151
                  protein (ORF 151), ORF 103 protein (ORF 103), ORF 229
                  precurso
Seq. No.
                  39035
                  LIB3106-078-P1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170087
BLAST score
                  153
E value
                  1.0e-80
Match length
                  245
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
Seq. No.
                  39036
                  LIB3106-078-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709825
BLAST score
                  215
E value
                  3.0e-17
Match length
                  110
% identity
                   46
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  39037
Seq. ID
                  LIB3106-079-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4204284
BLAST score
                  480
                  3.0e-48
E value
```

(AC003027) lcl_prt_seq No definition line found



```
Seq. No.
                  LIB3106-079-P1-K1-D5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2598656
                  92
BLAST score
                  1.0e-44
E value
                  120
Match length
                   94
% identity
NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
Seq. No.
                   39039
Seq. ID
                   LIB3106-079-P1-K1-F4
Method
                   BLASTX
                   q2129753
NCBI GI
                   427
BLAST score
                   3.0e-42
E value
                   133
Match length
% identity
                   77
                  threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                   thaliana (fragment) >gi 1448917 (L41666) threonine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   39040
Seq. ID
                   LIB3106-079-P1-K1-G3
                   BLASTN
Method
                   q1055367
NCBI GI
                   339
BLAST score
E value
                   0.0e + 00
Match length
                   407
                   96
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   39041
Seq. ID
                   LIB3106-079-P1-K1-H2
Method
                   BLASTN
                   q347454
NCBI GI
BLAST score
                   225
                   1.0e-123
E value
Match length
                   334
                   96
% identity
                   Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'
NCBI Description
                   end
                   39042
Seq. No.
                   LIB3106-080-P1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3337356
                   199
BLAST score
                   8.0e-16
E value
                   62
Match length
                   65
% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
```

Seq. No. 39043

Seq. ID LIB3106-080-P1-K1-C12



```
Method
  NCBI GI
                    q1053215
  BLAST score
                    354
                    0.0e+00
  E value
                    400
  Match length
                    97
  % identity
                    Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
  NCBI Description
                    nuclear gene encoding chloroplast protein, complete cds
                    39044
  Seq. No.
  Seq. ID
                    LIB3106-080-P1-K1-E11
  Method
                    BLASTX
  NCBI GI
                    q4455232
                    485
BLAST score
  E value
                    2.0e-49
                    131
  Match length
                    73
  % identity
  NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                    39045
  Seq. No.
                    LIB3106-080-P1-K1-G10
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                    g18761
  BLAST score
                    240
  E value
                    1.0e-132
  Match length
                    364
  % identity
                    91
  NCBI Description Soybean stem mRNA for 31 kD glycoprotein
  Seq. No.
                    39046
                    LIB3106-085-Q1-K1-A11
  Seq. ID
  Method
                    BLASTX
                    g2160173
  NCBI GI
  BLAST score
                    172
                    3.0e-12
  E value
  Match length
                    105
  % identity
                    (AC000132) Similar to N. tabacum salt-inducible protein
  NCBI Description
                     (gb U08285). [Arabidopsis thaliana]
  Seq. No.
                    39047
                    LIB3106-085-Q1-K1-A5
  Seq. ID
                    BLASTN
  Method
  NCBI GI
                    g170087
  BLAST score
                    294
                    1.0e-164
  E value
                     326
  Match length
  % identity
  NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
  Seq. No.
                     39048
                    LIB3106-085-Q1-K1-B8
  Seq. ID
  Method
                    BLASTX
```

NCBI GI g2281107
BLAST score 287
E value 9.0e-26
Match length 107

% identity

% identity

84

```
(ACO02333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   39049
Seq. No.
                   LIB3106-085-Q1-K1-D7
Seq. ID
                   BLASTX
Method
                   q464621
NCBI GI
BLAST score
                   351
                   2.0e-33
E value
                   93
Match length
                   70
% identity
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir__S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   39050
Seq. No.
                   LIB3106-085-Q1-K1-F10
Seq. ID
Method
                   BLASTX
                   g3023752
NCBI GI
                   401
BLAST score
                   4.0e-39
E value
                   106
Match length
                   72
% identity
                   FERREDOXIN I PRECURSOR >gi_1418982_emb_CAA99756_ (Z75520)
NCBI Description
                   ferredoxin-I [Lycopersicon esculentum]
                   39051
Seq. No.
                   LIB3106-085-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   q4325338
NCBI GI
BLAST score
                   139
                   6.0e-09
E value
                   30
Match length
                   83
% identity
                   (AF128392) No definition line found [Arabidopsis thaliana]
NCBI Description
                   39052
Seq. No.
Seq. ID
                   LIB3106-085-Q1-K1-H6
Method
                   BLASTN
                   q2815245
NCBI GI
                   70
BLAST score
                   5.0e-31
E value
                   242
Match length
% identity
                   82
                   C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                   CanMT-2)
Seq. No.
                   39053
                   LIB3106-086-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2924772
                    325
BLAST score
                    3.0e - 30
E value
Match length
                    69
```

NCBI Description (AC002334) unknown protein [Arabidopsis thaliana]

NCBI GI



```
Seq. No.
                  39054
                  LIB3106-086-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738316
                  281
BLAST score
E value
                   3.0e-25
                   86
Match length
% identity
                  (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                   39055
Seq. No.
Seq. ID
                  LIB3106-086-Q1-K1-D4
Method
                  BLASTX
                   q3935167
NCBI GI
                   150
BLAST score
                   3.0e-10
E value
Match length
                   43
                   72
% identity
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
                   39056
Seq. No.
                   LIB3106-086-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   q3122724
NCBI GI
                   169
BLAST score
                   3.0e-12
E value
                   46
Match length
% identity
                   72
                   60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
NCBI Description
                   protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                   39057
Seq. ID
                   LIB3106-086-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   q4263716
BLAST score
                   220
                   6.0e-18
E value
Match length
                   117
% identity
                   40
                   (AC006223) putative alanine acetyl transferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   39058
                   LIB3106-086-Q1-K1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   9.0e-11
E value
                   45
Match length
% identity
                   65
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   39059
Seq. No.
                   LIB3106-086-Q1-K1-G6
Seq. ID
                   BLASTX
Method
```

6065

g2662343

```
BLAST score 163
E value 2.0e-11
Match length 86
% identity 50
NCBI Description (D63581
```

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. Seq. ID

39060 LIB3106-086-Q1-K1-H12

Method BLASTX
NCBI GI g3341679
BLAST score 352
E value 3.0e-33
Match length 121
% identity 57

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No.

39061

Seq. ID

LIB3106-087-Q1-K1-A12

Method BLASTX
NCBI GI g2347088
BLAST score 252
E value 1.0e-21
Match length 76
% identity 64

NCBI Description (U72765) non-specific lipid transfer protein PvLTP-24

[Phaseolus vulgaris]

Seq. No.

39062

Seq. ID

LIB3106-087-Q1-K1-A5

Method BLASTX
NCBI GI g3927836
BLAST score 455
E value 2.0e-45
Match length 125
% identity 70

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.

39063

Seq. ID Method LIB3106-087-Q1-K1-B7

Method BLASTX
NCBI GI g1723894
BLAST score 160
E value 5.0e-11
Match length 96
% identity 36

NCBI Description HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION >gi 2131584 pir S64106 hypothetical protein YGL099w

- yeast (Saccharomyces cerevisiae)

>gi_1322637_emb_CAA96805_ (Z72621) ORF YGL099w

[Saccharomyces cerevisiae]

Seq. No.

39064

Seq. ID

LIB3106-087-Q1-K1-C9

Method BLASTN
NCBI GI g1055367
BLAST score 246



```
E value
Match length
                  342
                  93
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  39065
Seq. No.
                  LIB3106-087-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                  g2501850
NCBI GI
                  330
BLAST score
                  1.0e-39
E value
                  145
Match length
% identity
                  65
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
                  39066
Seq. No.
                  LIB3106-087-Q1-K1-E2
Seq. ID
                  BLASTN
Method
                  g3600062
NCBI GI
BLAST score
                  38
                  7.0e-12
E value
                  194
Match length
                  80
% identity
NCBI Description Arabidopsis thaliana BAC T25C13
                  39067
Seq. No.
                  LIB3106-087-Q1-K1-H6
Seq. ID
                  BLASTX
Method
                  g3024017
NCBI GI
                   153
BLAST score
                   3.0e-10
E value
                   52
Match length
                   60
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
NCBI Description
                   (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation
                   initiation factor eIF-1A [Onobrychis viciifolia]
                   39068
Seq. No.
                   LIB3106-088-Q1-K1-A4
Seq. ID
Method
                   BLASTX
                   g1001649
NCBI GI
                   372
BLAST score
E value
                   1.0e-35
Match length
                   153
% identity
                   37
                  (D64002) DNA gyrase A subunit [Synechocystis sp.]
NCBI Description
                   39069
Seq. No.
Seq. ID
                   LIB3106-088-Q1-K1-B4
Method
```

BLASTX

NCBI GI q3024503 BLAST score 218 1.0e-17 E value 58 Match length % identity 71

NCBI Description RAS-RELATED PROTEIN RAB11C >gi 623576 (L29268) putative

Match length

% identity

395 88



[Nicotiana tabacum]

```
Seq. No.
                  39070
Seq. ID
                  LIB3106-088-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g1351974
BLAST score
                  270
                  7.0e-24
E value
Match length
                  91
                  68
% identity
NCBI Description
                  ADP-RIBOSYLATION FACTOR >gi 1076788 pir $49325
                  ADP-ribosylation factor - maize >gi 1076789 pir S53486
                  ADP-ribosylation factor - maize >gi 556686 emb CAA56351
                  (X80042) ADP-ribosylation factor [Zea mays]
                  39071
Seq. No.
                  LIB3106-088-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006860
                  230
BLAST score
E value
                  5.0e-19
Match length
                  55
% identity
                  82
NCBI Description
                  (Z99707) thiol-disulfide interchange like protein
                  [Arabidopsis thaliana]
Seq. No.
                  39072
Seq. ID
                  LIB3106-088-Q1-K1-E12
Method
                  BLASTN
NCBI GI
                  g310575
BLAST score
                  159
E value
                  3.0e-84
Match length
                  321
                  89
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
Seq. No.
                  39073
Seq. ID
                  LIB3106-088-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  g4185513
BLAST score
                  230
                  3.0e-19
E value
Match length
                  83
                  63
% identity
NCBI Description
                  (AF102823) actin depolymerizing factor 5 [Arabidopsis
                  thaliana] >gi 4185517 (AF102825) actin depolymerizing
                  factor 5 [Arabidopsis thaliana]
                  39074
Seq. No.
Seq. ID
                  LIB3106-088-Q1-K1-H6
Method
                  BLASTN
NCBI GI
                  g871507
BLAST score
                  196
E value
                  1.0e-106
```



```
Seq. No.
                  39075
                  LIB3106-088-Q1-K1-H7
Seq. ID
                  BLASTX
Method
                  g643469
NCBI GI
                  335
BLAST score
                  2.0e-31
E value
                  90
Match length
                  67
% identity
                  (U19886) unknown [Lycopersicon esculentum]
NCBI Description
                  39076
Seq. No.
                  LIB3106-088-Q1-K1-H8
Seq. ID
                  BLASTN
Method
                  g1055367
NCBI GI
                  133
BLAST score
                   6.0e-69
E value
                   133
Match length
                   100
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   39077
Seq. No.
                   LIB3106-089-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   g4406759
NCBI GI
                   215
BLAST score
                   2.0e-17
E value
                   105
Match length
                   48
% identity
                   (AC006836) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   39078
Seq. No.
                   LIB3106-089-Q1-K1-B3
Seq. ID
                   BLASTX
Method
                   g1055368
NCBI GI
                   203
BLAST score
                   6.0e-16
E value
Match length
                   103
                   48
% identity
                   (U39567) ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Glycine max]
                   39079
Seq. No.
                   LIB3106-089-Q1-K1-C11
Seq. ID
Method
                   BLASTN
                   g18569
NCBI GI
                   42
BLAST score
                   1.0e-14
E value
Match length
                   118
% identity
                   86
NCBI Description G.max coxII gene for cytochrome oxidase subunit
                   39080
Seq. No.
```

Seq. ID LIB3106-089-Q1-K1-D7

Method BLASTN NCBI GI g3510337

Match length

% identity

81

38



```
BLAST score
E value
                 $3.0e-16
Match length
                  265
                  85
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19E20, complete sequence [Arabidopsis thaliana]
                  39081
Seq. No.
                  LIB3106-089-Q1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1652323
                  162
BLAST score
E value
                  5.0e-11
Match length
                  139
% identity
                  35
NCBI Description (D90904) fibrillin [Synechocystis sp.]
                  39082
Seq. No.
                  LIB3106-089-Q1-K1-E9
Seq. ID
Method
                  BLASTX
                  g2253442
NCBI GI
BLAST score
                  216
                  2.0e-17
E value
Match length
                  52
% identity
                  63
NCBI Description
                  (AF007784) LTCOR11 [Lavatera thuringiaca]
                  39083
Seq. No.
                  LIB3106-089-Q1-K1-F9
Seq. ID
Method
                  BLASTX
                  q1351033
NCBI GI
BLAST score
                  214
E value
                  1.0e-17
                   95
Match length
% identity_
                   52
                  STEM 31 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                  PROTEIN VSP25) >gi_170088 (M20037) vegetative storage
                  protein [Glycine max]
Seq. No.
                   39084
                   LIB3106-090-Q1-K1-A12
Seq. ID
Method
                   BLASTX
                   g2462756
NCBI GI
                   281
BLAST score
E value
                   5.0e-25
Match length
                   149
% identity
                   45
                   (AC002292) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                   39085
Seq. No.
Seq. ID
                   LIB3106-090-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   q1777386
BLAST score
                   144
E value
                   3.0e-09
```

```
(U39301) caffeic acid O-methyltransferase [Pinus taeda]
NCBI Description
                  39086
Seq. No.
                  LIB3106-090-Q1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1171579
BLAST score
                  207
                  3.0e-16
E value
                  52
Match length
                  75
% identity
NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]
                   39087
Seq. No.
                  LIB3106-090-Q1-K1-D4
Seq. ID
                  BLASTN
Method
                   g1370199
NCBI GI
                   55
BLAST score
                   3.0e-22
E value
                   195
Match length
                   86
% identity
```

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC1

39088 Seq. No. LIB3106-090-Q1-K1-F2 Seq. ID Method BLASTN g169974 NCBI GI BLAST score 127

3.0e-65 E value 223 Match length 89 % identity

NCBI Description Glycine max vspA gene, complete cds

39089 Seq. No.

LIB3106-090-Q1-K1-F5 Seq. ID

Method BLASTX g2062176 NCBI GI BLAST score 330 1.0e-30 E value Match length 83 77 % identity

(AC001645) Myb-related transcription activator (MybSt1) NCBI Description

isolog [Arabidopsis thaliana]

39090 Seq. No.

LIB3106-090-Q1-K1-G12 Seq. ID

Method BLASTX g2842480 NCBI GI 165 BLAST score E value 3.0e-2497 Match length % identity 61

(AL021749) ADP, ATP carrier-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No.

39091

LIB3106-090-Q1-K1-H5 Seq. ID

Method BLASTX

```
g3075391
NCBI GI
                  152
BLAST score
                  7.0e-10
E value
                  72
Match length
                  50
% identity
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
                  39092
Seq. No.
                  LIB3106-091-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g1679658
NCBI GI
```

159 BLAST score 4.0e-11 E value 56 Match length 62

% identity

(U63726) gamma glutamyl hydrolase [Glycine max] NCBI Description

39093 Seq. No. LIB3106-091-Q1-K1-B7 Seq. ID BLASTX Method

g1703088 NCBI GI 267 BLAST score 2.0e-23 E value 100 Match length 60 % identity

ACYL CARRIER PROTEIN 4 PRECURSOR (ACP) NCBI Description

>gi_1166431_emb_CAA64542_ (X95253) acyl carrier protein

[Cuphea lanceolata]

39094 Seq. No.

LIB3106-091-Q1-K1-C6 Seq. ID

BLASTX Method g3122724 NCBI GI 173 BLAST score 6.0e-13 E value 61

Match length 59 % identity

60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal NCBI Description

protein L38 isolog [Arabidopsis thaliana]

39095 Seq. No.

LIB3106-091-Q1-K1-E9 Seq. ID

BLASTN Method q12139 NCBI GI BLAST score 284 E value 1.0e-158 396 Match length 93 % identity

Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and NCBI Description trnG coding for ribosomal protein S2, one CF(1) and three

CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

39096 Seq. No.

LIB3106-091-Q1-K1-F10 Seq. ID

Method BLASTX NCBI GI g541943 291 BLAST score

```
3.0e-26
E value
                  68
Match length
% identity
                  75
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                  39097
Seq. No.
                  LIB3106-091-Q1-K1-F4
Seq. ID
                  BLASTN
Method
                  g3900979
NCBI GI
                  33
BLAST score
                  3.0e-09
E value
                  33
Match length
                  100
% identity
                  Eichhornia crassipes mRNA for metallothionein-like protein,
NCBI Description
                  clone A
                  39098
Seq. No.
                  LIB3106-091-Q1-K1-H2
Seq. ID
                  BLASTN
Method
                  g829118
NCBI GI
                   147
BLAST score
                   6.0e-77
E value
                   322
Match length
                   86
% identity
NCBI Description P.vulgaris gene for cyclophilin
                   39099
Seq. No.
                   LIB3106-092-Q1-K1-A8
Seq. ID
                   BLASTN
Method
                   q403326
NCBI GI
BLAST score
                   32
                   1.0e-08
E value
                   120
Match length
% identity
NCBI Description T.repens TrMT1A mRNA for metallothionein-like protein
                   39100
Seq. No.
                   LIB3106-092-Q1-K1-B3
Seq. ID
Method
                   BLASTX
                   q3650368
NCBI GI
                   195
BLAST score
                   3.0e-15
E value
                   84
Match length
% identity
                   50
                   (AJ011398) profucosidase [Pisum sativum]
NCBI Description
                   39101
Seq. No.
                   LIB3106-092-Q1-K1-C3
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3947854
BLAST score 173
E value 2.0e-12
Match length 101
% identity 41

NCBI Description (AL034381) conserved hypothetical PFAM UPF0031 containing

protein [Schizosaccharomyces pombe]



```
39102
Seq. No.
                  LIB3106-092-Q1-K1-D10
Seq. ID
                  BLASTN
Method
                  g1675195
NCBI GI
                  52
BLAST score
                  2.0e-20
E value
                  218
Match length
% identity
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                  complete cds
                  39103
Seq. No.
                  LIB3106-092-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334112
BLAST score
                  139
                  1.0e-08
E value
                  57
Match length
                  45
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1938236 emb CAA70200
NCBI Description
                   (Y08996) acyl-CoA-binding protein [Ricinus communis]
                   39104
Seq. No.
                  LIB3106-092-Q1-K1-E1
Seq. ID
Method
                  BLASTX
                   g2104679
NCBI GI
BLAST score
                   142
                   3.0e-09
E value
                   50
Match length
                   60
% identity
                  (X97906) transcription factor [Vicia faba]
NCBI Description
                   39105
Seq. No.
                   LIB3106-092-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   g2078350
NCBI GI
                   157
BLAST score
                   5.0e-18
E value
                   96
Match length
                   57
% identity
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
                   39106
Seq. No.
                   LIB3106-092-Q1-K1-F12
Seq. ID
Method
                   BLASTX
                   q4544453
NCBI GI
                   230
BLAST score
                   2.0e-19
E value
                   89
Match length
% identity
                   62
                   (AC006592) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 39107

Seq. ID LIB3106-092-Q1-K1-F9

Method BLASTX NCBI GI g2245097



```
BLAST score
                  7.0e-25
E value
Match length
                  104
                   61
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  LIB3106-092-Q1-K1-G1
Seq. ID
Method
                  BLASTX
                  q3805845
NCBI GI
BLAST score
                   406
E value
                  8.0e-40
Match length
                  101
% identity
                   71
                  (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                   39109
Seq. No.
Seq. ID
                  LIB3106-092-Q1-K1-H11
Method
                  BLASTN
NCBI GI
                   q18764
BLAST score
                  86
                   6.0e-41
E value
Match length
                   154
% identity
                   89
                  G.max tefS1 gene for elongation factor EF-1a
NCBI Description
                   39110
Seq. No.
                   LIB3106-092-Q1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g399333
BLAST score
                   301
E value
                   2.0e-27
Match length
                   89
% identity
                   69
                  CYSTEINE SYNTHASE CHLOROPLAST PRECURSOR (O-ACETYLSERINE
NCBI Description
                   SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                   >qi 322740 pir A43407 cysteine synthase (EC 4.2.99.8)
                   precursor - pepper >gi 17944 emb CAA46086 (X64874)
                   O-acetylserine (thiol) - lyase [Capsicum annuum]
                   39111
Seq. No.
Seq. ID
                   LIB3106-093-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g3094012
BLAST score
                   166
                   2.0e-11
E value
Match length
                   68
% identity
                   50
                  (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
NCBI Description
                   39112
Seq. No.
```

Seq. ID LIB3106-093-Q1-K1-B5

Method BLASTX
NCBI GI g445613
BLAST score 324
E value 4.0e-30
Match length 113



% identity NCBI Description ribosomal protein L7 [Solanum tuberosum]

39113 Seq. No.

LIB3106-093-Q1-K1-C8 Seq. ID

BLASTX Method g2501647 NCBI GI 173 BLAST score 2.0e-12 E value 64 Match length 61 % identity

UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) NCBI Description

>gi_1362120_pir__S55732 uroporphyrinogen decarboxylase -

common tobacco >gi_1009429_emb_CAA58040_ (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]

39114 Seq. No.

LIB3106-093-Q1-K1-D2 Seq. ID

BLASTX Method q2129752 NCBI GI 174 BLAST score 2.0e-12 E value 72 Match length 49 % identity

thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_ NCBI Description

(Z35475) thioredoxin [Arabidopsis thalīana]

39115 Seq. No.

LIB3106-093-Q1-K1-D9 Seq. ID

BLASTX Method q2829927 NCBI GI 206 BLAST score 3.0e-16 E value 80 Match length 53 % identity

(AC002291) Unknown protein [Arabidopsis thaliana] NCBI Description

39116 Seq. No.

LIB3106-093-Q1-K1-E1 Seq. ID

BLASTX Method g1353352 NCBI GI BLAST score 351 3.0e-33 E value 121 Match length 54 % identity

(U31975) alanine aminotransferase [Chlamydomonas NCBI Description

reinhardtii]

39117 Seq. No.

LIB3106-093-Q1-K1-E3 Seq. ID

Method BLASTX NCBI GI q2447107 BLAST score 227 E value 7.0e-19 83 Match length % identity 57

NCBI Description (U42580) A638R [Paramecium bursaria Chlorella virus 1]



```
39118
Seq. No.
                  LIB3106-093-Q1-K1-G4
Seq. ID
                  BLASTN
Method
                  g1055367
NCBI GI
BLAST score
                  289
                  1.0e-162
E value
                  372
Match length
% identity
                  94
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                  39119
                  LIB3106-094-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3242659
BLAST score
                  284
                  2.0e-25
E value
Match length
                  120
                   49
% identity
                  (AB015599) spermidine synthase [Coffea arabica]
NCBI Description
Seq. No.
                   39120
                  LIB3106-094-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4415908
BLAST score
                   246
E value
                   4.0e-21
                   70
Match length
                   71
% identity
                   (AC006282) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   LIB3106-094-Q1-K1-D5
Seq. ID
Method
                   BLASTX
                   g2702284
NCBI GI
BLAST score
                   194
                   6.0e-15
E value
Match length
                   89
                   34
% identity
                   (AC003033) Argonaute (AG01)-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   39122
                   LIB3106-094-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g2347088
NCBI GI
BLAST score
                   265
                   3.0e-23
E value
                   80
Match length
                   66
% identity
                   (U72765) non-specific lipid transfer protein PvLTP-24
NCBI Description
                   [Phaseolus vulgaris]
                   39123
Seq. No.
```

6077

LIB3106-094-Q1-K1-F10

BLASTX

÷.-

Seq. ID

Method

```
g3292827
NCBI GI
                  392
BLAST score
                  3.0e-38
E value
                  97
Match length
                  80
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                  39124
Seq. No.
                  LIB3106-094-Q1-K1-F4
Seq. ID
                  BLASTX
Method
                  g2739375
NCBI GI
                  263
BLAST score
                   6.0e-23
E value
                  91
Match length
                   63
% identity
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
                   39125
Seq. No.
                  LIB3106-094-Q1-K1-G11
Seq. ID
                  BLASTN
Method
                   g1236950
NCBI GI
                   47
BLAST score
                   1.0e-17
E value
                   71
Match length
                   92
% identity
NCBI Description Glycine max nucleoside diphosphate kinase mRNA, complete
                   cds
                   39126
Seq. No.
                   LIB3106-094-Q1-K1-G4
Seq. ID
                   BLASTN
Method
                   g3885510
NCBI GI
                   150
BLAST score
                   9.0e-79
E value
                   274
Match length
                   89
% identity
NCBI Description Medicago sativa clone MS28 unknown mRNA
                   39127
Seq. No.
                   LIB3106-094-Q1-K1-H5
Seq. ID
                   BLASTN
Method
                   g19747
NCBI GI
                   64
BLAST score
                   1.0e-27
E value
                   131
Match length
                   87
 % identity
NCBI Description N.sylvestris psaDa gene for PSI-D2
                   39128
 Seq. No.
                   LIB3106-094-Q1-K1-H9
 Seq. ID
 Method
                   BLASTX
                   q1706958
 NCBI GI
 BLAST score
                   186
                   6.0e-14
 E value
 Match length
                   35
 % identity
 NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
```

% identity

NCBI Description

89



```
39129
Seq. No.
                  LIB3106-095-Q1-K1-A1
Seq. ID
Method
                  BLASTX
                  g82078
NCBI GI
                  141
BLAST score
                  4.0e-09
E value
                  63
Match length
                  56
% identity
                  chlorophyll a/b-binding protein type I precursor (cab-6A) -
NCBI Description
                  tomato >gi_170388 (M17633) chlorophyll a/b-binding protein
                   [Lycopersicon esculentum] >gi_225895_prf__1402358A
                  photosystem I protein CAB [Lycopersicon esculentum]
                  39130
Seq. No.
                  LIB3106-095-Q1-K1-A11
Seq. ID
                  BLASTN
Method
                  g1055367
NCBI GI
BLAST score
                  251
                  1.0e-139
E value
                  299
Match length
                   96
% identity
NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
                   39131
Seq. No.
                  LIB3106-095-Q1-K1-A2
Seq. ID
                  BLASTN
Method
                   q1173641
NCBI GI
                   156
BLAST score
                   2.0e-82
E value
                   200
Match length
% identity
NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds
                   39132
Seq. No.
                   LIB3106-095-Q1-K1-A5
Seq. ID
                   BLASTX
Method
                   q4185513
NCBI GI
BLAST score
                   258
                   8.0e-23
E value
                   79
Match length
% identity
                   (AF102823) actin depolymerizing factor 5 [Arabidopsis
NCBI Description
                   thaliana] >gi 4185517 (AF102825) actin depolymerizing
                   factor 5 [Arabidopsis thaliana]
                   39133
Seq. No.
                   LIB3106-095-Q1-K1-A8
Seq. ID
Method
                   BLASTX
                   q4417271
NCBI GI
                   138
BLAST score
                   1.0e-08
E value
                   28
Match length
```

[Arabidopsis thaliana]

(AC007019) putative cellulose synthase catalytic subunit

Seq. ID

NCBI GI

Method



```
Seq. No.
                   39134
Seq. ID
                   LIB3106-095-Q1-K1-A9
Method
                   BLASTX
NCBI GI
                   g3021348
BLAST score
                   530
E value
                   3.0e-54
Match length
                   120
% identity
                   87
NCBI Description
                  (AJ004961) ribosomal protein L18 [Cicer arietinum]
Seq. No.
                   39135
Seq. ID
                   LIB3106-095-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   g1709970
BLAST score
                   189
E value
                   2.0e-14
Match length
                   54
% identity
                   69
NCBI Description 60S RIBOSOMAL PROTEIN L10A
Seq. No.
                   39136
Seq. ID
                   LIB3106-095-Q1-K1-H4
Method
                ⇒ BLASTN
NCBI GI
                   g310575
BLAST score
                   72
E value
                   2.0e-32
Match length
                   164
% identity
                   92
NCBI Description
                  Glycine max nodulin-26 mRNA, complete cds
Seq. No.
                   39137
Seq. ID
                   LIB3106-096-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   q1053057
BLAST score
                   390
E value
                   8.0e-38
Match length
                   124
% identity
                   69
NCBI Description
                  (U38422) histone H3 [Triticum aestivum]
Seq. No.
                   39138
Seq. ID
                  LIB3106-096-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q464981
BLAST score
                  225
E value
                  1.0e-18
Match length
                  56
% identity
                  79
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                  39139
```

6080

LIB3106-096-Q1-K1-C10

BLASTX

q567893



```
BLAST score
                  1.0e-09
E value
                  89
Match length
                  40
% identity
NCBI Description (L37382) beta-galactosidase-complementation protein
                  [Cloning vector]
                  39140
Seq. No.
                  LIB3106-096-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g3121825
NCBI GI
                  200
BLAST score
                  1.0e-15
E value
                  93
Match length
% identity
                  53
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                  ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                  bas1 protein [Spinacia oleracea]
                   39141
Seq. No.
                  LIB3106-096-Q1-K1-D8
Seq. ID
                  BLASTN
Method
                   g343480
NCBI GI
                   96
BLAST score
                   9.0e-47
E value
                   176
Match length
                   89
% identity
NCBI Description tobacco chloroplast atpase gene (b and e subunits) and
                   flanks
                   39142
Seq. No.
                   LIB3106-096-Q1-K1-E8
Seq. ID
                   BLASTX
Method
                   q1351279
NCBI GI
BLAST score
                   273
                   3.0e-24
E value
                   111
Match length
                   57
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi 602590_emb_CAA58230_ (X83227) triosephosphate isomerase
                   [Petunia x hybrida]
                   39143
 Seq. No.
                   LIB3106-096-Q1-K1-F5
 Seq. ID
                   BLASTX
```

Method g3023436 NCBI GI 214 BLAST score 3.0e-17 E value 109 Match length

39 % identity

CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA NCBI Description 3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT) >gi_857578 (U27116) caffeoyl-CoA 3-O-methyltransferase [Populus

tremuloides]

Seq. No. 39144

LIB3106-096-Q1-K1-F9 Seq. ID

```
BLASTX
Method
NCBI GI
                  q2342735
BLAST score
                  385
                  3.0e-37
E value
                  109
Match length
% identity
                  71
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                  39145
Seq. No.
                  LIB3106-096-Q1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170089
BLAST score
                   373
                  0.0e + 00
E value
                   445
Match length
                  96
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
Seq. No.
                   39146
                  LIB3106-096-Q1-K1-H6
Seq. ID
Method
                  BLASTN
                   q1769904
NCBI GI
BLAST score
                   53
                   7.0e-21
E value
Match length
                   85
% identity
                   91
NCBI Description A.thaliana psbP gene
Seq. No.
                   39147
                   LIB3106-097-Q1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2674203
BLAST score
                   200
E value
                   2.0e-15
Match length
                   46
% identity
                   83
                   (AF036328) CLP protease regulatory subunit CLPX
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   39148
                   LIB3106-097-Q1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g134145
BLAST score
                   325
                   2.0e-30
E value
Match length
                   105
% identity
                   61
                   STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                   PROTEIN A) >gi_99886_pir__S08511 28K protein - soybean
                   >gi_169898 (M37530) 28 kDa protein [Glycine max] >gi_169975
                   (M76981) vegetative storage protein [Glycine max]
                   >qi 226867 prf 1609232B 28kD glycoprotein [Glycine max]
                   >gi 444325 prf 1906374A vegetative storage protein
                   [Glycine max]
```

Seq. No. 39149

Seq. ID LIB3106-097-Q1-K1-A5

BLAST score

E value

129 3.0e-66



```
BLASTN
Method
                  g20657
NCBI GI
                  85
BLAST score
                  5.0e-40
E value
                  195
Match length
                  89
% identity
NCBI Description P.sativum Cab II gene for chlorophyll a/b-binding protein
                  39150
Seq. No.
                  LIB3106-097-Q1-K1-B5
Seq. ID
                  BLASTX
Method
                  g1076668
NCBI GI
                   249
BLAST score
                   7.0e-35
E value
Match length
                  119
% identity
                   64
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                  >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
                   39151
Seq. No.
                   LIB3106-097-Q1-K1-E10
Sea. ID
                   BLASTN
Method
                   g169190
NCBI GI
                   95
BLAST score
                   4.0e-46
E value
                   203
Match length
% identity
                   87
                   P.hybrida 5-enolpyruvylshikimate 3-phosphate synthase mRNA,
NCBI Description
                   complete cds
                   39152
Seq. No.
                   LIB3106-097-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g4104457
NCBI GI
                   234
BLAST score
                   2.0e-19
E value
                   51
Match length
                   75
 % identity
                   (AF036172) 2-oxoglutarate/malate translocator [Zea mays]
 NCBI Description
                   39153
 Seq. No.
                   LIB3106-097-Q1-K1-F4
 Seq. ID
                   BLASTN
Method
                   q170089
NCBI GI
                   71
 BLAST score
                   9.0e-32
 E value
                   155
 Match length
 % identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                   39154
 Seq. No.
                   LIB3106-097-Q1-K1-F6
 Seq. ID
                   BLASTN
 Method
                    g170089
 NCBI GI
```

6083



% identity 88 G.max vegetative storage protien mRNA (VSP27), complete cds NCBI Description

39155 Seq. No.

Match length

Seq. ID LIB3106-097-Q1-K1-H9

Method BLASTX NCBI GI g3355487 BLAST score 176 1.0e-12 E value Match length 113 % identity 38

(AC004218) unknown protein [Arabidopsis thaliana] NCBI Description

39156 Seq. No.

LIB3106-098-Q1-K1-A2 Seq. ID

Method BLASTX NCBI GI g481812 BLAST score 255 4.0e-22 E value 56 Match length % identity 41

NCBI Description DNA-binding protein GT-2 - Arabidopsis thaliana

>gi 416490 emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis

thaliana]

39157 Seq. No.

Seq. ID LIB3106-098-Q1-K1-B12

Method BLASTX g2980761 NCBI GI 429 BLAST score 2.0e-42 E value 108 Match length % identity 69

(AL022198) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

39158

LIB3106-098-Q1-K1-B4 Seq. ID

Method BLASTX NCBI GI q3309575 BLAST score 387 E value 2.0e-37 Match length 119 65 % identity

(AF060553) calcium sensor homolog [Arabidopsis thaliana] NCBI Description

>gi 4538989 emb CAB39731.1_ (Y18870) CBL4 protein

[Arabidopsis thaliana]

39159 Seq. No.

Seq. ID LIB3106-098-Q1-K1-D2

Method BLASTN q20899 NCBI GI 91 BLAST score 1.0e-43 E value Match length 223 88 % identity

NCBI Description Pea mRNA for Cu/Zn superoxide dismutase II (SOD9)



39160 Seq. No. LIB3106-098-Q1-K1-D5 Seq. ID BLASTX Method g2982432 NCBI GI 325 BLAST score 3.0e-30 E value 73 Match length % identity 81 NCBI Description (AL022224) putative protein [Arabidopsis thaliana] 39161 Seq. No. LIB3106-098-Q1-K1-E10 Seq. ID Method BLASTX q4263795 NCBI GI 353 BLAST score 2.0e-33 E value 93 Match length 70 % identity (AC006068) putative glucosyltransferase [Arabidopsis NCBI Description thaliana] 39162 Seq. No. LIB3106-098-Q1-K1-E5 Seq. ID Method BLASTN g2565339 NCBI GI 140 BLAST score 9.0e-73 E value 283 Match length 87 % identity NCBI Description Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete 39163 Seq. No. LIB3106-098-Q1-K1-E6 Seq. ID BLASTX Method g3492806 NÇBI GI 181 BLAST score 2.0e-13 E value 72 Match length 49 % identity (AJ225045) adventitious rooting related oxygenase [Malus NCBI Description domestica] 39164 Seq. No. LIB3106-098-Q1-K1-F1 Seq. ID BLASTX Method g625547 NCBI GI BLAST score 309 3.0e-28 E value Match length 62 % identity 89 chlorophyll a/b-binding protein type I - common tobacco NCBI Description

>gi_493723_emb_CAA45523_ (X64198) photosystem I

light-harvesting chlorophyll a/b-binding protein [Nicotiana

tabacum]

% identity

NCBI Description

74



```
Seq. No.
                   39165
Seq. ID
                   LIB3106-098-Q1-K1-H3
Method
                   BLASTX
NCBI GI
                   g401142
BLAST score
                   191
                   1.0e-14
E value
Match length
                   83
% identity
                   48
NCBI Description
                  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
                   >gi 322721 pir S31479 sucrose synthase (EC 2.4.1.13) -
                   fava bean >gi 22038 emb CAA49428 (X69773) sucrose synthase
                   [Vicia faba] >gi 295426 (M97551)
                   UDP-glucose:D-fructose-2-glucosyltransferase [Vicia faba]
Seq. No.
                   39166
Seq. ID
                   LIB3106-099-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g3746059
BLAST score
                   306
E value
                   3.0e-28
Match length
                   92
                   71
% identity
                   (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana] >gi 4432812 gb AAD20662 (AC006593) putative
                   cysteinyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                   39167
Seq. ID
                  LIB3106-099-Q1-K1-B7
Method
                  BLASTN
NCBI GI
                   g1732468
BLAST score
                   156
E value
                   2.0e-82
Match length
                  269
% identity
                   92
NCBI Description
                  Soybean mRNA for Mg chelatase subunit (46 kD), complete cds
Seq. No.
                  39168
Seq. ID
                  LIB3106-099-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g134597
BLAST score
                  230
E value
                  4.0e-19
                  117
Match length
                  44
% identity
NCBI Description
                  SUPEROXIDE DISMUTASE-4A (CU-ZN) >gi 100926 pir S07007
                  superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4, cytosolic -
                  maize
Seq. No.
                  39169
Seq. ID
                  LIB3106-099-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2924363
BLAST score
                  158
E value
                  1.0e-10
Match length
                  42
```

(AJ224683) zeta-carotene desaturase [Narcissus

Method

NCBI GI

BLASTX g3893822



pseudonarcissus]

```
39170
Seq. No.
                  LIB3106-099-Q1-K1-H6
Seq. ID
                  BLASTN
Method
                  g2924257
NCBI GI
                  96
BLAST score
                  1.0e-46
E value
                  204
Match length
                  87
% identity
NCBI Description Tobacco chloroplast genome DNA
                  39171
Seq. No.
                  LIB3106-100-Q1-K1-A10
Seq. ID
                  BLASTN
Method
                   g3341442
NCBI GI
                   108
BLAST score
                   9.0e-54
E value
                   212
Match length
                   89
% identity
NCBI Description Glycine max mRNA for root nodule acid phosphatase
                   39172
Seq. No.
                   LIB3106-100-Q1-K1-B4
Seq. ID
                   BLASTX
Method
                   g628902
NCBI GI
                   154
BLAST score
                   4.0e-10
E value
                   60
Match length
                   43
% identity
NCBI Description thioredoxin - Chloroflexus aurantiacus
                   39173
Seq. No.
                   LIB3106-100-Q1-K1-C7
Seq. ID
                   BLASTX
Method
                   g687677
NCBI GI
                   163
BLAST score
                   3.0e-11
E value
                   104
Match length
                   37
% identity
                   (U19925) unknown [Arabidopsis thaliana]
NCBI Description
                   39174
Seq. No.
                   LIB3106-100-Q1-K1-E1
Seq. ID
                   BLASTN
Method
                   g1399379
NCBI GI
BLAST score
                   62
                   2.0e-26
E value
                   79
Match length
                   91
 % identity
                   Glycine max S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                   methyltransferase mRNA, complete cds
                   39175
 Seq. No.
                   LIB3106-100-Q1-K1-E5
 Seq. ID
```

Match length

% identity

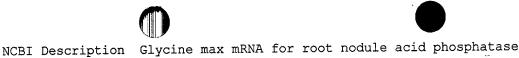
131

95



```
BLAST score
                  1.0e-22
E value
                  111
Match length
                  57
% identity
                  (U96498) ATPase beta subunit [Nicotiana sylvestris]
NCBI Description
                  39176
Seq. No.
                  LIB3106-100-Q1-K1-G9
Seq. ID
                  BLASTN
Method
                  g1326160
NCBI GI
                  69
BLAST score
                  2.0e-30
E value
                  179
Match length
                   94
% identity
NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds
                   39177
Seq. No.
                   LIB3106-100-Q1-K1-H4
Seq. ID
                   BLASTN
Method
                   g1055367
NCBI GI
                   371
BLAST score
                   0.0e+00
E value
                   399
Match length
                   98
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   39178
Seq. No.
                   LIB3106-101-Q1-K1-D10
Seq. ID
                   BLASTN
Method
                   g1055367
NCBI GI
                   65
BLAST score
                   3.0e-28
E value
                   208
Match length
                   91
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   39179
Seq. No.
                   LIB3106-101-Q1-K1-H6
Seq. ID
                   BLASTX
Method
                   q4538923
NCBI GI
BLAST score
                   202
                   6.0e-16
E value
                   56
Match length
                   70
% identity
                   (AL049483) predicted protein destination factor
NCBI Description
                    [Arabidopsis thaliana]
                   39180
 Seq. No.
                   LIB3106-102-Q1-K1-A5
 Seq. ID
                   BLASTN
Method
                   q3341442
NCBI GI
                   57
BLAST score
                   2.0e-23
E value
```

6088



```
39181
Seq. No.
                  LIB3106-102-Q1-K1-B7
Seq. ID
                  BLASTX
Method
                  g2330649
NCBI GI
                  286
BLAST score
                  1.0e-25
E value
                  141
Match length
                  43
% identity
NCBI Description (Y14558) topoisomerase I [Pisum sativum]
                  39182
Seq. No.
                  LIB3106-102-Q1-K1-C10
Seq. ID
Method
                  BLASTX
                  g2388565
NCBI GI
                  381
BLAST score
                  1.0e-36
E value
                  135
Match length
                   56
% identity
                  (AC000098) Similar to Prunus pectinesterase (gb_X95991).
NCBI Description
                   [Arabidopsis thaliana]
                   39183
Seq. No.
                  LIB3106-102-Q1-K1-C2
Seq. ID
                  BLASTX
Method
                   g2569938
NCBI GI
                   176
BLAST score
                   1.0e-12
E value
                   140
Match length
                   39
% identity
                  (Y15193) GAI [Arabidopsis thaliana]
NCBI Description
                   39184
Seq. No.
                   LIB3106-102-Q1-K1-E11
Seq. ID
                   BLASTN
Method
                   g2351070
NCBI GI
BLAST score
                   128
                   1.0e-65
E value
                   312
Match length
                   85
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTH12, complete sequence [Arabidopsis thaliana]
                   39185
Seq. No.
                   LIB3106-102-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   q2224663
NCBI GI
BLAST score
                   283
E value
                   2.0e-25
Match length
                   113
                   50
% identity
                  (AB002359) KIAA0361 [Homo sapiens]
NCBI Description
```

6089

39186

BLASTX

LIB3106-102-Q1-K1-H2

Seq. No.

Seq. ID Method

BLAST score

E value

92

2.0e-44



```
NCBI GI
                   q393707
BLAST score
                  206
                  3.0e-16
E value
Match length
                  80
                  54
% identity
NCBI Description
                  (X67696) acetyl-CoA acyltransferase [Cucumis sativus]
                  39187
Seq. No.
Seq. ID
                  LIB3106-103-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g100069
BLAST score
                  183
                  1.0e-13
E value
Match length
                  58
% identity
                  60
                  cysteine proteinase tpp (EC 3.4.22.-) - garden pea
NCBI Description
                  >gi_3980198_emb_CAA46863 (X66061) thiolprotease [Pisum
                  sativum]
Seq. No.
                  39188
Seq. ID
                  LIB3106-103-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                  g1055367
BLAST score
                  53
E value
                  3.0e-21
Match length
                  89
% identity
                  90
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
Seq. No.
                  39189
Seq. ID
                  LIB3106-103-Q1-K1-B10
Method
                  BLASTN
NCBI GI
                  g18755
BLAST score
                  113
                  9.0e-57
E value
Match length
                  121
% identity
                  98
                  Soybean SRS4 mRNA for ribulose-1,5-bisphosphate carboxylase
NCBI Description
                  (Rubisco) small subunit, partial cds
Seq. No.
                  39190
Seq. ID
                  LIB3106-103-Q1-K1-B5
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  42
E value
                  2.0e-14
Match length
                  82
% identity
                  88
NCBI Description
                  Cloning vector pSport1, complete cds
Seq. No.
                  39191
Seq. ID
                  LIB3106-103-Q1-K1-B8
Method
                  BLASTN
                  g169974
NCBI GI
```



143

39193

```
Match length
% identity
                  85
NCBI Description Glycine max vspA gene, complete cds
                  39192
Seq. No.
Seq. ID
                  LIB3106-103-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2832657
BLAST score
                  402
                  3.0e-39
E value
```

% identity 13 NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. LIB3106-103-Q1-K1-F1 Seq. ID Method BLASTN NCBI GI q170067 BLAST score 126 2.0e-64 E value Match length 342

% identity NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)

gene, complete cds

Seq. No. 39194

Match length

Seq. ID LIB3106-103-Q1-K1-G12

85

Method BLASTN NCBI GI q1055367 BLAST score 246 E value 1.0e-136 Match length 366 % identity 92

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 39195

Seq. ID LIB3106-103-Q1-K1-G4

Method BLASTX NCBI GI g1173198 BLAST score 499 E value 1.0e-50 Match length 104 % identity 93

NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal

protein S13.e - garden pea >gi_396639_emb_CAA80974_

(Z25509) ribosomal protein S13 [Pisum sativum]

Seq. No.

39196

Seq. ID LIB3106-103-Q1-K1-G5 Method BLASTX

NCBI GI g2392769 BLAST score 195 E value 6.0e-15 Match length 96 % identity 47

NCBI Description (AC002534) putative histone deacetylase [Arabidopsis



thaliana]

```
39197
Seq. No.
Seq. ID
                  LIB3106-103-Q1-K1-H11
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
                  9.0e-11
E value
                  48
Match length
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  39198
                  LIB3106-103-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914467
BLAST score
                  201
E value
                   7.0e-16
                  89
Match length
% identity
                   51
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                  >gi 1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana
                   tabacum]
                   39199
Seq. No.
                  LIB3106-104-Q1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2815245
BLAST score
                   86
E value
                   2.0e-40
Match length
                   242
                   84
% identity
NCBI Description
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
                   CanMT-2)
                   39200
Seq. No.
Seq. ID
                   LIB3106-104-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   g4371280
BLAST score
                   164
                   2.0e-11
E value
                   56
Match length
% identity
                   66
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   39201
Seq. ID
                   LIB3106-104-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   q3790102
BLAST score
                   144
                   6.0e-16
E value
                   82
Match length
                   60
% identity
                   (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
```

Seq. No. 39202

alpha subunit [Citrus X paradisi]



```
LIB3106-104-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  q2982243
NCBI GI
BLAST score
                  148
                  2.0e-09
E value
                  33
Match length
                  79
% identity
                  (AF051204) hypothetical protein [Picea mariana]
NCBI Description
                  39203
Seq. No.
                  LIB3106-104-Q1-K1-B2
Seq. ID
                  BLASTX
Method
                  g3193293
NCBI GI
                  339
BLAST score
                  7.0e-32
E value
                  121
Match length
                  56
% identity
                   (AF069298) contains a short region of similarity to another
NCBI Description
                  Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)
                   [Arabidopsis thaliana]
                  39204
Seq. No.
                  LIB3106-104-Q1-K1-D2
Seq. ID
Method
                  BLASTX
                   q1262440
NCBI GI
                   246
BLAST score
                   4.0e-21
E value
                   112
Match length
                   51
% identity
                  (U26457) lipoxygenase [Glycine max]
NCBI Description
                   39205
Seq. No.
                   LIB3106-104-Q1-K1-F2
Seq. ID
Method
                   BLASTN
                   q3821780
NCBI GI
BLAST score
                   36
E value
                   8.0e-11
                   48
Match length
                   67
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   39206
Seq. No.
                   LIB3106-104-Q1-K1-F6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g602358
BLAST score
                   86
E value
                   1.0e-40
Match length
                   203
% identity
                   89
NCBI Description P.sativum mRNA for type II chlorophyll a/b binding protein
                   39207
Seq. No.
                   LIB3106-104-Q1-K1-G1
Seq. ID
                   BLASTX
Method
                   g1109699
NCBI GI
```

6093

165

2.0e-17

BLAST score

E value



```
Match length 101 % identity 49
```

NCBI Description (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3106-104-Q1-K1-G3

39208

Method BLASTX
NCBI GI g2688820
BLAST score 257
E value 3.0e-22
Match length 121
% identity 44

NCBI Description (U93271) enoyl-CoA hydratase [Prunus armeniaca]

Seq. No. 39209

Seq. ID LIB3106-104-Q1-K1-H5

Method BLASTX
NCBI GI g2864608
BLAST score 296
E value 8.0e-27
Match length 99
% identity 61

NCBI Description (AL021811) ferredoxin--NADP+ reductase - like protein

[Arabidopsis thaliana] >gi 4049338 emb CAA22563 (AL034567)

ferredoxin-NADP+ reductase-like protein [Arabidopsis

thaliana]

Seq. No. 39210

Seq. ID LIB3106-104-Q1-K1-H8

Method BLASTX
NCBI GI g3776559
BLAST score 146
E value 3.0e-09
Match length 94
% identity 40

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 39211

Seq. ID LIB3106-105-Q1-K1-A2

Method BLASTX
NCBI GI 9441457
BLAST score 549
E value 2.0e-56
Match length 105
% identity 97

NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon

esculentum]

Seq. No. 39212

Seq. ID LIB3106-105-Q1-K1-A8

MethodBLASTNNCBI GIg169974BLAST score227E value1.0e-125



Match length 319 % identity 93

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 39213

Seq. ID LIB3106-105-Q1-K1-D11

Method BLASTX
NCBI GI g1946358
BLAST score 411
E value 3.0e-40
Match length 120
% identity 63

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 39214

Seq. ID LIB3106-105-Q1-K1-E11

Method BLASTN
NCBI GI 94204764
BLAST score 34
E value 1.0e-09
Match length 34
% identity 100

NCBI Description Glycine max peroxidase (sEPb2) mRNA, partial cds

Seq. No. 39215

Seq. ID LIB3106-105-Q1-K1-E5

Method BLASTN
NCBI GI g1196896
BLAST score 36
E value 3.0e-11
Match length 52
% identity 92

NCBI Description Glycine max acidic ribosomal protein PO mRNA, complete cds

Seq. No. 39216

Seq. ID LIB3106-105-Q1-K1-G11

Method BLASTX
NCBI GI g3158476
BLAST score 214
E value 2.0e-17
Match length 62
% identity 73

NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 39217

Seq. ID LIB3106-106-Q1-K1-C11

Method BLASTX
NCBI GI g417444
BLAST score 192
E value 7.0e-15
Match length 74
% identity 55

NCBI Description PHENYLALANINE AMMONIA-LYASE 2 >gi_217984_dbj_BAA00887_

(D10003) phenylalanine ammonia-lyase [Pisum sativum]

Seq. No. 39218

Seq. ID LIB3106-106-Q1-K1-C8

% identity

42

```
Method
NCBI GI
                   g1362108
BLAST score
                   156
E value
                   2.0e-10
Match length
                   89
% identity
                   42
NCBI Description histone H3 homolog - common tobacco
Seq. No.
                   39219
Seq. ID
                   LIB3106-106-Q1-K1-E3
Method
                   BLASTN
NCBI GI
                   g1055367
BLAST score
                   442
E value
                   0.0e+00
Match length
                   478
                   98
% identity
NCBI Description
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
Seq. No.
                   39220
Seq. ID
                   LIB3106-106-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g3269288
BLAST score
                   191
E value
                   1.0e-14
Match length
                   56
% identity
                   70
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                   39221
Seq. ID
                   LIB3106-106-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g4539662
BLAST score
                   257
E value
                   5.0e-24
Match length
                   117
% identity
                   60
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
Seq. No.
                   39222
Seq. ID
                  LIB3106-106-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4098517
BLAST score
                   230
E value
                   3.0e-19
Match length
                   68
% identity
NCBI Description (U79114) auxin-binding protein ABP19 [Prunus persica]
Seq. No.
                  39223
Seq. ID
                  LIB3106-107-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1653702
BLAST score
                  259
E value
                  2.0e-22
Match length
                  136
```





```
(D90915) dihydrolipoamide acetyltransferase component (E2)
NCBI Description
                  of pyruvate dehydrogenase complex [Synechocystis sp.]
Seq. No.
                   39224
                  LIB3106-107-Q1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                   g18551
BLAST score
                   360
                   0.0e + 00
E value
```

% identity Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding NCBI Description protein

Match length

39225 Seq. No. LIB3106-107-Q1-K1-G3 Seq. ID

360

100

Method BLASTX g4375832 NCBI GI BLAST score 484 6.0e-49 E value Match length 123 72 % identity

(AJ006961) peroxidase [Arabidopsis thaliana] NCBI Description

Seq. No. 39226

LIB3106-107-Q1-K1-G8 Seq. ID

Method BLASTN NCBI GI g3600029 BLAST score 34 2.0e-09 E value Match length 50 % identity 54

NCBI Description Arabidopsis thaliana BAC T12H2O

Seq. No.

Seq. ID LIB3106-108-Q1-K1-B5

39227

Method BLASTX NCBI GI q130010 BLAST score 164 E value 3.0e-11 64 Match length 50 % identity

NCBI Description LEUCOAGGLUTINATING PHYTOHEMAGGLUTININ PRECURSOR (PHA-L)

>gi 169339 (K03289) phytohemagglutinin prepeptide

[Phaseolus vulgaris] >gi_758252_emb_CAA26257_ (X02409) leucoagglutinating phytohemagglutinin [Phaseolus vulgaris]

Seq. No. 39228

Seq. ID LIB3106-108-Q1-K1-D6

Method BLASTX NCBI GI q3702964 BLAST score 770 E value 3.0e-82 Match length 155 % identity 92

(AF079485) rac GTP binding protein Aracl0 [Arabidopsis NCBI Description

thaliana]



```
39229
Seq. No.
                  LIB3106-108-Q1-K1-D8
Seq. ID
Method
                  BLASTX
                  g541943
NCBI GI
                  311
BLAST score
E value
                  2.0e-28
Match length
                  79
                  73
% identity
NCBI Description metallothionein - soybean >gi_228682_prf__1808316A
                  metallothionein-like protein [Glycine max]
Seq. No.
                  39230
Seq. ID
                  LIB3106-108-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1350984
BLAST score
                  373
                  9.0e-36
E value
Match length
                  88
                  84
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A >gi 469248 (L31645) ribosomal
                  protein S3a [Helianthus annuus]
                  39231
Seq. No.
Seq. ID
                  LIB3106-108-Q1-K1-G11
Method
                  BLASTX
                  g4567285
NCBI GI
                  267
BLAST score
                  2.0e-23
E value
Match length
                  72
                  72
% identity
                  (AC006841) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  39232
Seq. No.
                  LIB3106-109-Q1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3033375
                  176
BLAST score
                  2.0e-15
E value
Match length
                  83
% identity
                  55
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  39233
                  LIB3106-109-Q1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1769905
BLAST score
                   161
                   3.0e-23
E value
Match length
                   113
                   54
% identity
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 39234

Seq. ID LIB3106-109-Q1-K1-C8



```
Method
                   BLASTN
NCBI GI
                  q1055367
BLAST score
                   229
E value
                   1.0e-126
Match length
                   312
% identity
                   94
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
Seq. No.
                  39235
Seq. ID
                  LIB3106-109-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1524383
BLAST score
                  242
E value
                  1.0e-20
Match length
                  103
% identity
NCBI Description
                  (X63374) 3-phosphoshikimate 1-carboxyvinyltransferase [Zea
                  mays]
Seq. No.
                  39236
Seq. ID
                  LIB3106-109-Q1-K1-F7
Method
                  BLASTN
NCBI GI
                  q1053215
BLAST score
                  36
                  3.0e-11
E value
Match length
                  124
% identity
                  82
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
Seq. No.
                  39237
Seq. ID
                  LIB3106-109-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  q1370287
BLAST score
                  214
E value
                   3.0e-17
Match length
                   58
                  76
% identity
NCBI Description
                  (Z73553) core protein [Pisum sativum]
Seq. No.
                  39238
                  LIB3106-110-Q1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3236242
BLAST score
                  230
E value
                   3.0e-19
Match length
                  87
% identity
NCBI Description
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
                  thaliana]
Seq. No.
```

39239

Seq. ID

LIB3106-110-Q1-K1-C10

Method BLASTX NCBI GI g3377509 BLAST score 456



```
E value
Match length
                  147
% identity
                  57
NCBI Description (AF056027) auxin transport protein REH1 [Oryza sativa]
Seq. No.
                  39240
Seq. ID
                  LIB3106-110-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q3738329
BLAST score
                  190
E value
                  2.0e-14
Match length
                  47
% identity
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
                  39241
Seq. No.
                  LIB3106-110-Q1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4469023
                  210
BLAST score
                  2.0e-17
E value
                  70
Match length
% identity
                  67
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                  39242
Seq. No.
                  LIB3106-110-01-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170089
BLAST score
                  45
E value
                  3.0e-16
Match length
                  141
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
Seq. No.
                  39243
Seq. ID
                  LIB3106-110-Q1-K1-E7
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  69
                  2.0e-30
E value
Match length
                  368
% identity
                  80
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                  39244
Seq. ID
                  LIB3106-110-Q1-K1-F12
Method
                  BLASTN
NCBI GI
                  g170089
BLAST score
                  55
```

Method BLASTN
NCBI GI g170089
BLAST score 55
E value 4.0e-22
Match length 218
% identity 85

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 39245

Seq. ID LIB3106-110-Q1-K1-F3



```
Method
                  q633604
NCBI GI
BLAST score
                  35
                  2.0e-10
E value
Match length
                  64
                  87
% identity
                  P.sativum mRNA for gibberellin-responsive ovary protein
NCBI Description
                  39246
Seq. No.
                  LIB3106-110-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351033
BLAST score
                  178
                   3.0e-13
E value
                   64
Match length
                   61
% identity
                  STEM 31 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                  PROTEIN VSP25) >gi 170088 (M20037) vegetative storage
                  protein [Glycine max]
                   39247
Seq. No.
Seq. ID
                   LIB3106-110-Q1-K1-G11
                   BLASTX
Method
                   g2864616
NCBI GI
BLAST score
                   227
                   1.0e-18
E value
Match length
                   77
                   62
% identity
                  (AL021811) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   39248
Seq. No.
                   LIB3106-110-Q1-K1-G5
Seq. ID
                   BLASTN
Method
                   g169897
NCBI GI
                   222
BLAST score
                   1.0e-121
E value
Match length
                   365
                   92
% identity
                  G.max 28 kDa protein, complete cds
NCBI Description
                   39249
Seq. No.
                   LIB3106-111-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   g4510400
NCBI GI
                   396
BLAST score
                   2.0e-42
E value
Match length
                   106
                   80
% identity
                   (AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis
NCBI Description
                   thaliana]
                   39250
Seq. No.
                   LIB3106-111-Q1-K1-A7
```

Seq. ID

BLASTX Method q2129889 NCBI GI 287 BLAST score 2.0e-52 E value



Match length 126 % identity 83

NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea

Seq. No. 39251

Seq. ID LIB3106-111-Q1-K1-B10

Method BLASTN
NCBI GI g169974
BLAST score 160
E value 8.0e-85
Match length 308
% identity 88

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 39252

Seq. ID LIB3106-111-Q1-K1-B2

Method BLASTX
NCBI GI g3789952
BLAST score 177
E value 6.0e-13
Match length 46
% identity 70

NCBI Description (AF094775) chlorophyll a/b-binding protein presursor [Oryza

sativa]

Seq. No. 39253

Seq. ID LIB3106-111-Q1-K1-B8

Method BLASTN
NCBI GI g347454
BLAST score 96
E value 1.0e-46
Match length 208
% identity 87

NCBI Description Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'

end

Seq. No. 39254

Seq. ID LIB3106-111-Q1-K1-C1

Method BLASTX
NCBI GI g2894567
BLAST score 300
E value 3.0e-27
Match length 100
% identity 57

NCBI Description (AL021890) hypothetical protein [Arabidopsis thaliana]

Seq. No. 39255

Seq. ID LIB3106-111-Q1-K1-D3

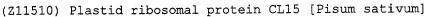
Method BLASTX
NCBI GI g400986
BLAST score 191
E value 3.0e-20
Match length 116
% identity 56

NCBI Description 50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)

>gi_81947_pir__S18001 ribosomal protein L15 precursor,

chloroplast - garden pea (fragment) >gi_20867_emb_CAA77595_





```
Seq. No.
                  LIB3106-111-Q1-K1-D5
Seq. ID
                  BLASTX
Method
                  g825756
NCBI GI
BLAST score
                  143
                  5.0e-09
E value
                  77
Match length
                  45
% identity
                  (U12391) beta-galactosidase alpha peptide [Cloning vector
NCBI Description
                  pSport2]
                  39257
Seq. No.
                  LIB3106-111-Q1-K1-D7
Seq. ID
Method
                  BLASTN
                  g18741
NCBI GI
BLAST score
                  60
                  4.0e-25
E value
Match length
                  124
                  87
% identity
                  Glycine max gene encoding ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase small subunit
Seq. No.
                  39258
                  LIB3106-111-Q1-K1-E8
Seq. ID
                  BLASTN
Method
                   a1055367
NCBI GI
BLAST score
                   329
                   0.0e + 00
E value
                   437
Match length
                   94
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   39259
Seq. No.
                   LIB3106-111-Q1-K1-F2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169897
                   296
BLAST score
                   1.0e-166
E value
                   436
Match length
% identity
                   92
NCBI Description G.max 28 kDa protein, complete cds
Seq. No.
                   39260
Seq. ID
                   LIB3106-111-Q1-K1-F3
Method
                   BLASTN
                   g1055367
NCBI GI
BLAST score
                   51
                   9.0e-20
E value
                   115
Match length
                   86
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
```

Seq. No. 39261



LIB3106-111-Q1-K1-G2 Seq. ID BLASTX Method q134145 NCBI GI 199 BLAST score 2.0e-15 E value 85 Match length 51 % identity STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE NCBI Description PROTEIN A) >gi_99886_pir__S08511 28K protein - soybean >qi 169898 (M37530) 28 kDa protein [Glycine max] >gi_169975 $(M7\overline{6}981)$ vegetative storage protein [Glycine max] >gi_226867_prf__1609232B 28kD glycoprotein [Glycine max] >gi_444325_prf__1906374A vegetative storage protein [Glycine max] 39262 Seq. No. LIB3106-112-Q1-K1-A11 Seq. ID BLASTX Method g2815292 NCBI GI 102 BLAST score 1.0e-09 E value 74 Match length 53 % identity (Y15962) Germin-like protein 1 [Hordeum vulgare] NCBI Description 39263 Seq. No. LIB3106-112-Q1-K1-B8 Seq. ID BLASTN Method q169974 NCBI GI 213 BLAST score 1.0e-116 E value 345 Match length 91 % identity NCBI Description Glycine max vspA gene, complete cds 39264 Seq. No. LIB3106-112-Q1-K1-D1 Seq. ID BLASTX Method q3047104 NCBI GI 172 BLAST score 2.0e-20 E value 121 Match length 57 % identity NCBI Description (AF058919) No definition line found [Arabidopsis thaliana] 39265 Seq. No. LIB3106-112-Q1-K1-E3 Seq. ID BLASTX Method NCBI GI g3738302 243 BLAST score E value 9.0e-21 97 Match length

% identity 54

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>gi_4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

```
Seq. No.
                  LIB3106-112-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  a22380
NCBI GI
                  280
BLAST score
                  5.0e-25
E value
                  90
Match length
                  63
% identity
                  (X59714) CAAT-box DNA binding protein subunit B (NF-YB)
NCBI Description
                  [Zea mays]
                  39267
Seq. No.
                  LIB3106-112-Q1-K1-F8
Seq. ID
Method
                  BLASTX
                  q508304
NCBI GI
                  258
BLAST score
                  2.0e-29
E value
                  113
Match length
                   64
% identity
                  (L22305) corC [Medicago sativa]
NCBI Description
                   39268
Seq. No.
                  LIB3106-112-Q1-K1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2809257
                   355
BLAST score
                   1.0e-33
E value
                   88
Match length
                   75
% identity
                  (AC002560) F21B7.26 [Arabidopsis thaliana]
NCBI Description
                   39269
Seq. No.
                   LIB3106-112-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   g2501189
NCBI GI
BLAST score
                   331
                   7.0e-31
E value
                   88
Match length
                   75
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
                   39270
Seq. No.
                   LIB3106-113-Q1-K1-A8
Seq. ID
                   BLASTN
Method
                   q984307
NCBI GI
BLAST score
                   86
```

Method BLASTN
NCBI GI g984307
BLAST score 86
E value 9.0e-41
Match length 201
% identity 88

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151

protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. ID

Method



```
39271
Seq. No.
                  LIB3106-113-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g1236961
NCBI GI
                  99
BLAST score
E value
                  1.0e-09
                  63
Match length
                  49
% identity
NCBI Description (U50201) prunasin hydrolase precursor [Prunus serotina]
                  39272
Seq. No.
                  LIB3106-113-Q1-K1-G5
Seq. ID
                  BLASTN
Method
                  q479144
NCBI GI
                  228
BLAST score
                  1.0e-125
E value
                  256
Match length
                  97
% identity
NCBI Description G.max mRNA for ATP synthase subunit
                   39273
Seq. No.
                  LIB3106-113-Q1-K1-G9
Seq. ID
                  BLASTN
Method
                   g1055367
NCBI GI
                   107
BLAST score
                   2.0e-53
E value
                   111
Match length
                   99
% identity
NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
                   39274
Seq. No.
                   LIB3106-114-Q1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q309673
BLAST score
                   301
E value
                   8.0e-28
                   81
Match length
                   81
% identity
NCBI Description (L19651) light harvesting protein [Pisum sativum]
Seq. No.
                   39275
                   LIB3106-114-Q1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2811014
BLAST score
                   189
                   3.0e-14
E value
Match length
                   91
                   41
 % identity
                   DYNEIN LIGHT CHAIN LC6, FLAGELLAR OUTER ARM
 NCBI Description
                   >gi_2208914_dbj BAA20525_ (AB004830) outer arm dynein LC6
                   [Anthocidaris crassispina]
                   39276
 Seq. No.
```

6106

LIB3106-114-Q1-K1-D10

BLASTX



```
q4580470
NCBI GI
BLAST score
                  97
                  8.0e-09
E value
Match length
                  85
                  41
% identity
                 (AC006081) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  39277
Seq. No.
                  LIB3106-114-Q1-K1-G3
Seq. ID
                  BLASTX
Method
                  g20729
NCBI GI
                  157
BLAST score
                  4.0e-11
E value
Match length
                  53
                  70
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
                  39278
Seq. No.
                  LIB3106-115-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g3913633
NCBI GI
                  199
BLAST score
                  2.0e-15
E value
Match length
                  85
% identity
                  51
NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown
                  protein [Arabidopsis thaliana]
                  39279
Seq. No.
                  LIB3106-115-Q1-K1-D12
Seq. ID
                  BLASTN
Method
                   q170065
NCBI GI
                   218
BLAST score
                   1.0e-119
E value
                   338
Match length
% identity
NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP2)
                   gene, complete cds
                   39280
Seq. No.
                   LIB3106-115-Q1-K1-D8
Seq. ID
                   BLASTN
Method
                   g287814
NCBI GI
                   123
BLAST score
                   1.0e-62
E value
                   315
Match length
                   85
% identity
NCBI Description P.sativum mRNA for H-protein of leaf mitochondria
                   39281
Seq. No.
                   LIB3106-115-Q1-K1-D9
Seq. ID
Method
                   BLASTX
                   g133247
NCBI GI
                   171
BLAST score
                   4.0e-12
E value
                   96
Match length
```

22

% identity





NCBI Description CHLOROPLAST 28 KD RIBONUCLEOPROTEIN (28RNP)

 Seq. No.
 39282

 Seq. ID
 LIB3106-115-Q1-K1-F11

 Method
 BLASTX

NCBI GI g3860333 BLAST score 198 E value 3.0e-15 Match length 108 % identity 46

NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No. 39283

Seq. ID LIB3106-115-Q1-K1-G12

Method BLASTN
NCBI GI g169934
BLAST score 102
E value 3.0e-50
Match length 262
% identity 86

NCBI Description G.max (soybean) atpH gene encoding CFO-ATPase subunit III, chloroplast gene encoding chloroplast protein, complete cds

Seq. No. 39284

Seq. ID LIB3106-115-Q1-K1-G9

Method BLASTX
NCBI GI g2827619
BLAST score 702
E value 2.0e-74
Match length 157
% identity 85

NCBI Description (AL021636) hypothetical protein [Arabidopsis thaliana]

Seq. No. 39285

Seq. ID LIB3106-115-Q1-K1-H12

Method BLASTN
NCBI GI g1277163
BLAST score 322
E value 0.0e+00
Match length 443
% identity 94

NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No. 39286

Seq. ID LIB3106-116-Q1-K1-B6

Method BLASTN
NCBI GI g1055367
BLAST score 240
E value 1.0e-132
Match length 395
% identity 90

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 39287

Seq. ID LIB3106-116-Q1-K1-B9

Method BLASTX



NCBI GI g120663 BLAST score 189 E value 2.0e-19 Match length 103 % identity 53

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

CHLOROPLAST >gi_66027_pir__DEPMNB

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi_309671 (M55147) glyceraldehyde-3-phosphate

dehydrogenase B subunit [Pisum sativum]

Seq. No. 39288

Seq. ID LIB3106-116-Q1-K1-C1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 49
% identity 51

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 39289

Seq. ID LIB3106-116-Q1-K1-D4

Method BLASTX
NCBI GI g2511590
BLAST score 367
E value 4.0e-35
Match length 94
% identity 74

NCBI Description (Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi 3421111

(AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis

thaliana]

Seq. No. 39290

Seq. ID LIB3106-116-Q1-K1-F1

Method BLASTN
NCBI GI g169974
BLAST score 210
E value 1.0e-114
Match length 394
% identity 89

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 39291

Seq. ID LIB3106-116-Q1-K1-F10

Method BLASTX
NCBI GI g2911067
BLAST score 410
E value 3.0e-40
Match length 97
% identity 77

NCBI Description (AL021960) UV-damaged DNA-binding protein-like

[Arabidopsis thaliana]

Seq. No. 39292



Seq. ID LIB3106-116-Q1-K1-F11

Method BLASTN
NCBI GI g1199562
BLAST score 211
E value 1.0e-115
Match length 263
% identity 95

NCBI Description Glycine max 34 kDa maturing seed vacuolar thiol protease

mRNA, complete cds

Seq. No. 39293

Seq. ID LIB3106-116-Q1-K1-F4

Method BLASTN
NCBI GI g170067
BLAST score 146
E value 2.0e-76
Match length 409
% identity 77

NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)

gene, complete cds

Seq. No. 39294

Seq. ID LIB3106-116-Q1-K1-F7

Method BLASTX
NCBI GI g2500098
BLAST score 355
E value 8.0e-34
Match length 116
% identity 62

NCBI Description DNA REPAIR PROTEIN RECA PRECURSOR >gi 289208 (L15229) DNA

repair protein [Arabidopsis thaliana] >gi_3152570

(AC002986) Match to nuclear-encoded chloroplast DNA repair protein (E. coli recA homolog) gb_L15229. [Arabidopsis

thaliana]

Seq. No. 39295

Seq. ID LIB3106-116-Q1-K1-G8

Method BLASTN
NCBI GI g170089
BLAST score 359
E value 0.0e+00
Match length 443
% identity 95

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 39296

Seq. ID LIB3106-116-Q1-K1-H10

Method BLASTX
NCBI GI g2191128
BLAST score 374
E value 3.0e-36
Match length 97
% identity 74

NCBI Description (AF007269) belongs to the L5P family of ribosomal proteins

[Arabidopsis thaliana]

Seq. No. 39297

6110



```
LIB3106-116-Q1-K1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q454178
BLAST score
                  34
                  7.0e-10
E value
                  122
Match length
% identity
NCBI Description Glycine max rubisco-associated protein mRNA, complete cds
                  39298
Seq. No.
Seq. ID
                  LIB3106-116-Q1-K1-H3
Method
                  BLASTN
NCBI GI
                  q1370143
                  135
BLAST score
                  7.0e-70
E value
                  307
Match length
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB11B
                  39299
Seq. No.
                  LIB3106-116-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3202028
BLAST score
                  381
                  6.0e-45
E value
                  119
Match length
% identity
                  78
                  (AF069317) cystathionine gamma-synthase [Mesembryanthemum
NCBI Description
                  crystallinum]
                   39300
Seq. No.
                   LIB3107-001-Q1-K1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                   q1055367
BLAST score
                   331
                   0.0e+00
E value
Match length
                   418
                   95
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   39301
Seq. No.
                   LIB3107-001-Q1-K1-D7
Seq. ID
Method
                   BLASTX
                   g2129889
NCBI GI
                   403
BLAST score
                   2.0e-39
E value
Match length
                   94
                   80
% identity
                  methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
NCBI Description
                   39302
Seq. No.
                   LIB3107-001-Q1-K1-F11
Seq. ID
```

Method BLASTN
NCBI GI g2792154
BLAST score 41
E value 6.0e-14



Match length 85 % identity 88

NCBI Description Sesbania rostrata mRNA for putative chalcone reductase

Seq. No. 39303

Seq. ID LIB3107-001-Q1-K1-G4

Method BLASTX
NCBI GI 94538939
BLAST score 140
E value 8.0e-19
Match length 89
% identity 58

NCBI Description (ALO49483) Col-O casein kinase I-like protein [Arabidopsis

thaliana]

Seq. No. 39304

Seq. ID LIB3107-001-Q1-K1-G6

Method BLASTX
NCBI GI g2132124
BLAST score 135
E value 1.0e-09
Match length 66
% identity 57

NCBI Description hypothetical protein YOR304w - yeast (Saccharomyces

cerevisiae) >gi_1420671_emb_CAA99622_ (Z75212) ORF YOR304w

[Saccharomyces cerevisiae]

Seq. No. 39305

Seq. ID LIB3107-001-Q1-K1-H2

Method BLASTX
NCBI GI g531829
BLAST score 138
E value 7.0e-09
Match length 51
% identity 49

NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector

pSport1]

Seq. No. 39306

Seq. ID LIB3107-002-Q1-K1-B7

Method BLASTX
NCBI GI g4557068
BLAST score 188
E value 2.0e-21
Match length 92
% identity 64

NCBI Description (AC007045) putative pol polyprotein [Arabidopsis thaliana]

Seq. No.

39307

Seq. ID LIB3107-002-Q1-K1-C1

Method BLASTN
NCBI GI g303900
BLAST score 235
E value 1.0e-129
Match length 250
% identity 26

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. ID

Method NCBI GI



```
Seq. No.
                  39308
                  LIB3107-002-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4115341
BLAST score
                  245
E value
                   6.0e-21
Match length
                   95
                   49
% identity
                  (U51100) chromaffin granule ATPase II [Bos taurus]
NCBI Description
Seq. No.
                   39309
Seq. ID
                  LIB3107-002-Q1-K1-F12
Method
                  BLASTN
NCBI GI
                   q2760171
                   38
BLAST score
                   6.0e-12
E value
Match length
                   86
% identity
                   86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPA24, complete sequence [Arabidopsis thaliana]
                   39310
Seq. No.
Seq. ID
                   LIB3107-002-Q1-K1-F5
Method
                   BLASTX
                   g3800881
NCBI GI
BLAST score
                   223
E value
                   3.0e-18
Match length
                   130
% identity
                   36
                  (AF098799) RanBP7/importin 7 [Homo sapiens]
NCBI Description
                   39311
Seq. No.
Seq. ID
                   LIB3107-002-Q1-K1-G4
Method
                   BLASTX
NCBI GI
                   q3822223
BLAST score
                   307
E value
                   4.0e-28
Match length
                   90
% identity
                   60
                   (AF077955) branched-chain alpha keto-acid dehydrogenase E1
NCBI Description
                   alpha subunit [Arabidopsis thaliana]
Seq. No.
                   39312
                   LIB3107-003-Q1-K1-C6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g725331
BLAST score
                   53
                   3.0e-21
E value
Match length
                   73
% identity
                   93
                  Glycine max mitochondrion polymorphic marker DNA sequence
NCBI Description
                   39313
Seq. No.
```

6113

LIB3107-003-Q1-K1-D4

BLASTN

g4206101



```
BLAST score
E value
                  1.0e-153
                  430
Match length
% identity
                  Glycine max retroelement diaspora gag-pol polyprotein
NCBI Description
                  (gag-pol) pseudogene, partial sequence
Seq. No.
                  39314
                  LIB3107-004-Q1-K1-B8
Seq. ID
Method
                  BLASTX
                  g3747111
NCBI GI
                  140
BLAST score
                  7.0e-09
E value
Match length
                  38
% identity
                  68
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                  39315
Seq. No.
                  LIB3107-004-Q1-K1-C1
Seq. ID
                  BLASTX
Method
                  g3122265
NCBI GI
                  579
BLAST score
                   5.0e-60
E value
                   120
Match length
% identity
                   85
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
NCBI Description
                   (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT)
                   (EIF-4F P26 SUBUNIT) >gi 2288883_emb_CAA71580_ (Y10548)
                   eIF4E protein [Arabidopsis thaliana]
                   39316
Seq. No.
                   LIB3107-004-Q1-K1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4206306
BLAST score
                   146
                   3.0e-09
E value
Match length
                   63
% identity
                   46
                  (AF049110) prpol [Zea mays]
NCBI Description
                   39317
Seq. No.
                   LIB3107-004-Q1-K1-F4
Seq. ID
Method
                   BLASTX
                   g3176686
NCBI GI
```

BLAST score 315 4.0e-29 E value 80 Match length 75 % identity

(AC003671) Similar to high affinity potassium transporter, NCBI Description

HAK1 protein gb_U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No.

39318

LIB3107-004-Q1-K1-F8 Seq. ID

BLASTX Method g2598589 NCBI GI BLAST score 448



```
1.0e-44
E value
Match length
                  115
% identity
                  65
NCBI Description (Y15367) MtN19 [Medicago truncatula]
Seq. No.
                  39319
                  LIB3107-005-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1899188
BLAST score
                  166
                  1.0e-11
E value
                  63
Match length
% identity
                  57
NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]
                  39320
Seq. No.
                  LIB3107-006-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g100488
NCBI GI
BLAST score
                  170
                  5.0e-12
E value
Match length
                  132
% identity
                  36
NCBI Description TNP2 protein - garden snapdragon
                  39321
Seq. No.
                  LIB3107-006-Q1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g541950
BLAST score
                  165
                  2.0e-11
E value
Match length
                  97
                  45
% identity
NCBI Description SPCP1 protein - soybean >gi 310576 (L12257) nodulin-26
                  [Glycine max]
Seq. No.
                  39322
                  LIB3107-006-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3688182
BLAST score
                  166
                  8.0e-17
E value
Match length
                  86
% identity
                  57
NCBI Description (AL031804) P-Protein - like protein [Arabidopsis thaliana]
Seq. No.
                  39323
Seq. ID
                  LIB3107-006-Q1-K1-C6
Method
                  BLASTN
NCBI GI
                  g1053044
BLAST score
                  38
                  2.0e-12
E value
```

Match length % identity

NCBI Description Glycine max histone H3 gene, partial cds, clone S1

Seq. No. 39324

42

98

```
LIB3107-006-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                  g1076583
NCBI GI
                  151
BLAST score
                  2.0e-10
E value
                  42
Match length
                  74
% identity
NCBI Description histone H3 variant H3.3 - tomato (fragment)
Seq. No.
                  39325
                  LIB3107-006-Q1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1217993
BLAST score
                  121
                  2.0e-61
E value
                  233
Match length
                  89
% identity
NCBI Description Glycine max dynamin-like protein SDL12A mRNA, complete cds
                  39326
Seq. No.
                  LIB3107-006-Q1-K1-E4
Seq. ID
Method
                  BLASTN
                  g170065
NCBI GI
BLAST score
                  122
E value
                  3.0e-62
Match length
                  254
                  59
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP2)
NCBI Description
                  gene, complete cds
                  39327
Seq. No.
                  LIB3107-006-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4558664
BLAST score
                   171
E value
                   3.0e-12
Match length
                   107
                   10
% identity
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]
                   39328
Seq. No.
                   LIB3107-006-Q1-K1-G6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g609224
BLAST score
                   132
E value
                   4.0e-68
Match length
                   348
                   84
% identity
                  P.sativum mRNA for SAMS-2 >gi 609558 gb_L36681 PEADENSYNB
```

39329 Seq. No.

NCBI Description

LIB3107-007-Q1-K1-B10 Seq. ID

cds

BLASTN Method NCBI GI q16508 55 BLAST score

Pisum sativum S-adenosylmethionine synthase mRNA, complete



3.0e-22 E value Match length 143 % identity 85 NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi 166871 gb M55077 ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds Seq. No. 39330 LIB3107-007-Q1-K1-E8 Seq. ID BLASTXMethod NCBI GI g2795806 BLAST score 560 E value 9.0e-58 Match length 134 % identity 82 NCBI Description (AC003674) unknown protein [Arabidopsis thaliana] 39331 Seq. No. LIB3107-007-Q1-K1-G8 Seq. ID Method BLASTX q4063760 NCBI GI 247 BLAST score E value 4.0e-28 Match length 111 % identity NCBI Description (AC005561) putative POL3 protein [Arabidopsis thaliana] Seq. No. 39332 LIB3107-007-Q1-K1-H12 Seq. ID BLASTX Method g2961389 NCBI GI 189 BLAST score E value 1.0e-14 68 Match length 54 % identity NCBI Description (AL022141) purple acid phosphatase like protein [Arabidopsis thaliana] >gi 4006925 emb CAB16853 (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana] Seq. No. 39333 Seq. ID LIB3107-008-Q1-K1-C1 Method BLASTN NCBI GI q2055227 BLAST score 46 1.0e-16 E value Match length 88 94 % identity NCBI Description Glycine max mRNA for SRC1, complete cds Seq. No. 39334 Seq. ID LIB3107-008-Q1-K1-D2

Method BLASTX q4105772 NCBI GI BLAST score 356 4.0e-34 E value Match length 79 % identity 43



NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 39335

Seq. ID LIB3107-008-Q1-K1-E4

Method BLASTN
NCBI GI g287810
BLAST score 85
E value 3.0e-40
Match length 189
% identity 86

NCBI Description M.sativa mRNA for phosphoprotein phosphatase type 2A

Seq. No. 39336

Seq. ID LIB3107-008-Q1-K1-F2

Method BLASTX
NCBI GI g3292829
BLAST score 298
E value 3.0e-27
Match length 97
% identity 58

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 39337

Seq. ID LIB3107-008-Q1-K1-F9

Method BLASTX
NCBI GI g3779218
BLAST score 125
E value 7.0e-14
Match length 59
% identity 75

NCBI Description (AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No.

39338

Seq. ID LIB3107-009-Q1-K1-A1

Method BLASTX
NCBI GI g2497752
BLAST score 169
E value 3.0e-12
Match length 88
% identity 42

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1)

>gi_1321911_emb_CAA65475_ (X96714) lipid transfer protein

[Prunus dulcis]

Seq. No. 39339

Seq. ID LIB3107-009-Q1-K1-C2

Method BLASTN
NCBI GI g3982595
BLAST score 283
E value 1.0e-158
Match length 405
% identity 92

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39340

Seq. ID

LIB3107-009-Q1-K1-C8

Method BLASTX

Seq. ID

Method NCBI GI



```
NCBI GI
                   q4545262
BLAST score
                   165
                   2.0e-11
E value
Match length
                   46
                   67
% identity
NCBI Description
                   (AF118230) metallothionein-like protein [Gossypium
                   hirsutum]
                   39341
Seq. No.
Seq. ID
                   LIB3107-009-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   g1805654
BLAST score
                   218
                   2.0e-35
E value
Match length
                   129
                   60
% identity
                   (X99972) calmodulin-stimulated calcium-ATPase [Brassica
NCBI Description
                   oleracea]
                   39342
Seq. No.
                   LIB3107-009-Q1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2055228
BLAST score
                   189
                   2.0e-14
E value
                   79
Match length
                   53
% identity
                   (AB000129) SRC1 [Glycine max]
NCBI Description
                   39343
Seq. No.
                   LIB3107-009-Q1-K1-H4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3413169
                   80
BLAST score
E value
                   5.0e-37
Match length
                   136
% identity
                   90
NCBI Description Cicer arietinum mRNA for 40S ribosomal protein S6, partial
                   39344
Seq. No.
                   LIB3107-010-Q1-K1-C6
Seq. ID
Method
                   BLASTX
                   g114657
NCBI GI
                   159
BLAST score
                   3.0e-15
E value
Match length
                   111
% identity
                   54
                   ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV)
NCBI Description
                   >gi 67926 pir LWRZ6 H+-transporting ATP synthase (EC
                   3.6.1.34) chain a - rice chloroplast
                   >gi_11975_emb_CAA33990_ (X15901) ATPase a subunit [Oryza
sativa] >gi_226693_prf__1603356U ATPase a [Oryza sativa]
                   39345
Seq. No.
```

6119

LIB3107-010-Q1-K1-F4

BLASTX

g2995405

BLAST score

Match length

% identity

E value

159 8.0e-11

89

46



```
BLAST score
                  5.0e-14
E value
                  121
Match length
                  35
% identity
                  (Y12432) polyprotein [Ananas comosus]
NCBI Description
Seq. No.
                  39346
                  LIB3107-010-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3747111
BLAST score
                  171
E value
                  5.0e-12
Match length
                  81
                  43
% identity
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  39347
Seq. ID
                  LIB3107-011-Q1-K1-C1
Method
                  BLASTN
                  q1778371
NCBI GI
                  113
BLAST score
                  9.0e-57
E value
Match length
                  249
% identity
                  86
                  Glycine max asparagine synthetase 1 (AS1) mRNA, complete
NCBI Description
                   39348
Seq. No.
Seq. ID
                  LIB3107-011-Q1-K1-C7
                  BLASTN
Method
NCBI GI
                   g4206101
BLAST score
                   60
                   5.0e-25
E value
Match length
                   172
% identity
                  Glycine max retroelement diaspora gag-pol polyprotein
NCBI Description
                   (gag-pol) pseudogene, partial sequence
Seq. No.
                   39349
                   LIB3107-011-Q1-K1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g256142
BLAST score
                   83
E value
                   9.0e-39
                   391
Match length
% identity
                   81
                   cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                   Prize, mRNA, 1450 nt]
                   39350
Seq. No.
                   LIB3107-011-Q1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2645699
```

6120



NCBI Description (AF031933) glycine-rich RNA-binding protein [Euphorbia esula]

Seq. No. 39351

Seq. ID LIB3107-011-Q1-K1-E6

Method BLASTN
NCBI GI g4206101
BLAST score 106
E value 2.0e-52
Match length 286
% identity 85

NCBI Description Glycine max retroelement diaspora gag-pol polyprotein

(gag-pol) pseudogene, partial sequence

Seq. No. 39352

Seq. ID LIB3107-011-Q1-K1-F5

Method BLASTX
NCBI GI g3172538
BLAST score 169
E value 7.0e-12
Match length 42
% identity 79

NCBI Description (AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]

Seq. No. 39353

Seq. ID LIB3107-011-Q1-K1-G11

Method BLASTX
NCBI GI g3176072
BLAST score 329
E value 1.0e-30
Match length 106
% identity 61

NCBI Description (AJ002485) protein phosphatase 1, catalytic beta subunit

[Medicago sativa]

Seq. No. 39354

Seq. ID LIB3107-012-Q1-K1-A9

Method BLASTX
NCBI GI g541943
BLAST score 148
E value 3.0e-11
Match length 69
% identity 57

NCBI Description metallothionein - soybean >gi 228682 prf_ 1808316A

metallothionein-like protein [Glycine max]

Seq. No. 39355

Seq. ID LIB3107-012-Q1-K1-D8

Method BLASTN
NCBI GI g3747131
BLAST score 36
E value 8.0e-11
Match length 48
% identity 94

NCBI Description Lycopersicon esculentum expansin (LeEXP2) mRNA, complete

cds



```
Seq. No.
                   39356
Seq. ID
                  LIB3107-012-Q1-K1-F8
Method
                  BLASTN
NCBI GI
                   q516853
BLAST score
                   65
E value
                   2.0e-28
Match length
                  148
% identity
                   45
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.
                   39357
                  LIB3107-012-Q1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3941448
BLAST score
                  298
E value
                   4.0e-27
Match length
                  80
                   70
% identity
NCBI Description
                  (AF062878) putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  39358
                  LIB3107-013-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g497417
BLAST score
                  197
E value
                  3.0e-15
Match length
                  80
% identity
                  51
NCBI Description
                 (U10111) dehydrin-like protein [Glycine max]
Seq. No.
                  39359
Seq. ID
                  LIB3107-013-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g629669
BLAST score
                  187
E value
                  3.0e-14
Match length
                  74
                  50
% identity
NCBI Description hypothetical protein - tomato
Seq. No.
                  39360
Seq. ID
                  LIB3107-013-Q1-K1-E11
Method
                  BLASTN
NCBI GI
                  g12245
BLAST score
                  200
E value
                  1.0e-108
Match length
                  369
% identity
NCBI Description Spinach chloroplast DNA inversion containing ORF
Seq. No.
                  39361
Seq. ID
```

LIB3107-013-Q1-K1-F2

Method BLASTN NCBI GI g1695795 BLAST score 40 E value 3.0e-13



```
Match length
% identity
                  81
NCBI Description Pisum sativum 18S small subunit nuclear ribosomal RNA gene
Seq. No.
                  39362
                  LIB3107-013-Q1-K1-F8
Seq. ID
Method
                  BLASTX
                  g3294467
NCBI GI
                  206
BLAST score
                  2.0e-16
E value
Match length
                  89
                  51
% identity
                  (U89341) phosphoglucomutase 1 [Zea mays]
NCBI Description
                  39363
Seq. No.
                  LIB3107-013-Q1-K1-G8
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4206101
BLAST score
                  98
                  9.0e-48
E value
                  227
Match length
                  86
% identity
NCBI Description Glycine max retroelement diaspora gag-pol polyprotein
                   (gag-pol) pseudogene, partial sequence
Seq. No.
                  39364
                  LIB3107-013-Q1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3183637
                  107
BLAST score
                   1.0e-10
E value
Match length
                   81
% identity
                   44
                   (AJ002234) polyprotein, cleavage products include viral
NCBI Description
                   coat protein and proteins with homology to an aspartic
                   protease, reverse transcriptase and RNase H [banana streak
                   virus]
                   39365
Seq. No.
Seq. ID
                   LIB3107-014-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   g4160280
BLAST score
                   121
E value
                   9.0e-09
Match length
                   82
                   41
% identity
                  (AJ006224) purple acid phosphatase [Ipomoea batatas]
NCBI Description
Seq. No.
                   39366
Seq. ID
                   LIB3107-014-Q1-K1-E7
Method
                   BLASTX
```

NCBI GI g1172762 BLAST score 163 2.0e-11 E value Match length 105 % identity 39

NCBI Description PUROMYCIN RESISTANCE PROTEIN PUR8 >gi_632205_pir__S43017



anulatus]

puromycin resistance protein pur8 - Streptomyces anulatus >gi 499330 emb CAA54186 (X76855) pur8 [Streptomyces

Seq. No. 39367

Seq. ID LIB3107-014-Q1-K1-F9

Method BLASTX
NCBI GI g2739376
BLAST score 161
E value 2.0e-11
Match length 74
% identity 53

NCBI Description (AC002505) putative permease [Arabidopsis thaliana]

Seq. No. 39368

Seq. ID LIB3107-014-Q1-K1-G3

Method BLASTN
NCBI GI g1236948
BLAST score 158
E value 1.0e-83
Match length 310
% identity 88

NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds

Seq. No. 39369

Seq. ID LIB3107-014-Q1-K1-H6

Method BLASTX
NCBI GI g3183088
BLAST score 239
E value 3.0e-20
Match length 76
% identity 55

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR

(LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034 emb_CAA56113 (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 39370

Seq. ID LIB3107-014-Q1-K1-H7

Method BLASTN
NCBI GI g3982595
BLAST score 334
E value 0.0e+00
Match length 382
% identity 97

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39371

Seq. ID LIB3107-015-Q1-K1-B5

Method BLASTN
NCBI GI g2264318
BLAST score 35
E value 4.0e-10
Match length 142
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUP24, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  39372
                  LIB3107-015-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4163997
BLAST score
                  617
E value
                  2.0e-64
                  122
Match length
                  89
% identity
                  (AF087483) alpha-xylosidase precursor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  39373
                  LIB3107-015-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1167523
                  153
BLAST score
E value
                  4.0e-10
                  115
Match length
% identity
                  38
NCBI Description (D83003) ORF(AA 1-1338) [Nicotiana tabacum]
                  39374
Seq. No.
Seq. ID
                  LIB3107-015-Q1-K1-F6
Method
                  BLASTN
NCBI GI
                  q456713
BLAST score
                  51
                  3.0e-20
E value
Match length
                  71
% identity
                  31
NCBI Description Glycine max gene for ubiquitin, complete cds
                  39375
Seq. No.
Seq. ID
                  LIB3107-016-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                  q170091
BLAST score
                   46
E value
                  7.0e-17
Match length
                   224
% identity
                   78
NCBI Description
                  Glycine max vegetative storage protein (vspB) gene,
                   complete cds
Seq. No.
                   39376
                   LIB3107-016-Q1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1619602
BLAST score
                  202
                  2.0e-16
E value
Match length
                   60
% identity
                  70
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
                   39377
Seq. No.
```

BLASTN NCBI GI g1163180

LIB3107-016-Q1-K1-E5

Seq. ID

Method

6125



BLAST score E value 1.0e-52 238 Match length 87 % identity

Glycine max arginine decarboxylase mRNA, complete cds NCBI Description

Seq. No.

LIB3107-016-Q1-K1-F4 Seq. ID

Method BLASTX q728880 NCBI GI BLAST score 222 E value 2.0e-18 Match length 69 % identity 62

N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG NCBI Description

>gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]

39379 Seq. No.

LIB3107-017-Q1-K1-B10 Seq. ID

Method BLASTX NCBI GI g2262116 BLAST score 319 2.0e-29 E value Match length 109 51 % identity

(AC002343) cellulose synthase isolog [Arabidopsis thaliana] NCBI Description

39380 Seq. No.

LIB3107-017-Q1-K1-C7 Seq. ID

Method BLASTN NCBI GI q984307 BLAST score 148 1.0e-77 E value Match length 416 % identity

Glycine max ribosomal protein S16 (rps16) gene, partial NCBI Description

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 39381

LIB3107-017-Q1-K1-E6 Seq. ID

Method BLASTN NCBI GI g170091 BLAST score 291 1.0e-163 E value Match length 410 % identity 93

Glycine max vegetative storage protein (vspB) gene, NCBI Description

complete cds

Seq. No. 39382

LIB3107-017-Q1-K1-F4 Seq. ID

BLASTX Method



g1346526 NCBI GI BLAST score 607 3.0e-63 E value 135 Match length 84 % identity

S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

> >gi 1076533 pir __S52218 methionine adenosyltransferase (EC 2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077) methionine adenosyltransferase [Pisum sativum] >gi_609559 (L36681) S-adenosylmethionine synthase [Pisum sativum]

39383 Seq. No.

LIB3107-017-Q1-K1-F7 Seq. ID

Method BLASTX g1346526 NCBI GI BLAST score 364 7.0e-35 E value Match length 111 68 % identity

S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>gi_1076533_pir__S52218 methionine adenosyltransferase (EC 2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077) methionine adenosyltransferase [Pisum sativum] >gi_609559 (L36681) S-adenosylmethionine synthase [Pisum sativum]

Ţ,

39384 Seq. No.

LIB3107-017-Q1-K1-F8 Seq. ID

Method BLASTX q4325351 NCBI GI 310 BLAST score 2.0e-28 E value Match length 111 % identity 57

(AF128394) similar to Antirrhinum majus (garden snapdragon) NCBI Description

TNP2 protein (GB:X57297) [Arabidopsis thaliana]

39385 Seq. No.

Seq. ID LIB3107-017-Q1-K1-G3 BLASTX

Method q1769887 NCBI GI 202 BLAST score 8.0e-16 E value Match length 101 % identity 54

(X95736) amino acid permease 6 [Arabidopsis thaliana] NCBI Description

Seq. No.

Seq. ID LIB3107-018-Q1-K1-C1

39386

Method BLASTN NCBI GI g170087 BLAST score 152 4.0e-80 E value Match length 296 % identity 87

NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)



Seq. No. 39387
Seq. ID LIB31

LIB3107-018-Q1-K1-C7

Method BLASTX
NCBI GI g133933
BLAST score 178
E value 5.0e-13
Match length 50
% identity 70

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3

>gi_1363605_pir__S58590 ribosomal protein S3 - maize
chloroplast >gi_12469_emb_CAA68427_ (Y00340) ribosomal
protein S3 [Zea mays] >gi_902260_emb_CAA60324_ (X86563)

ribosomal protein S3 [Zea mays]

Seq. No. 39388

Seq. ID LIB3107-018-Q1-K1-D4

Method BLASTX
NCBI GI g439493
BLAST score 173
E value 5.0e-13
Match length 92
% identity 60

NCBI Description (D26086) zinc-finger protein [Petunia x hybrida]

Seq. No. 39389

Seq. ID LIB3107-018-Q1-K1-E3

Method BLASTX
NCBI GI g3875304
BLAST score 358
E value 5.0e-34
Match length 97
% identity 65

NCBI Description (Z74030) predicted using Genefinder; cDNA EST EMBL:C07609

comes from this gene; cDNA EST EMBL:C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com

Seq. No. 39390

Seq. ID LIB3107-018-Q1-K1-G11

Method BLASTX
NCBI GI g1168609
BLAST score 264
E value 2.0e-31
Match length 97
% identity 76

NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir__S35071 auxin-resistance protein AXR1 - Arabidopsis thaliana

>gi_304104 (L13922) ubiquitin-activating enzyme E1
[Arabidopsis thaliana] >gi_2388579 (AC000098) Match to
Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana]
>gi_448755_prf__1917337A ubiquitin-activating enzyme E1

[Arabidopsis thaliana]

Seq. No. 39391

Seq. ID LIB3107-019-Q1-K1-E9

Method BLASTX



```
q4325363
NCBI GI
BLAST score
                  127
                  4.0e-11
E value
                  98
Match length
                  38
% identity
                  (AF128395) contains similarity to transposase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  39392
                  LIB3107-020-Q1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18764
BLAST score
                  165
                  5.0e-88
E value
                  209
Match length
                  95
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
Seq. No.
                  39393
                  LIB3107-020-Q1-K1-A5
Seq. ID
Method
                  BLASTN
                  g18764
NCBI GI
BLAST score
                  116
E value
                  9.0e-59
Match length
                  231
% identity
                  88
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                  39394
Seq. No.
                  LIB3107-020-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                  g541943
NCBI GI
                  173
BLAST score
E value
                  1.0e-12
                  44
Match length
% identity
                  73
NCBI Description metallothionein - soybean >gi_228682_prf__1808316A
                  metallothionein-like protein [Glycine max]
Seq. No.
                  39395
Seq. ID
                  LIB3107-020-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  q3914473
BLAST score
                  135
E value
                  2.0e-17
Match length
                  105
                  45
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 479684 pir S35151 photosystem I chain XI -
                  spinach >gi_396275_emb_CAA45775_ (X64445) subunit XI of
                  photosystem I reaction center [Spinacia oleracea]
```

Seq. No. 39396

LIB3107-020-Q1-K1-F5 Seq. ID

Method BLASTN NCBI GI g456713 83 BLAST score



E value 5.0e-39
Match length 183
% identity 35

NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 39397

Seq. ID LIB3107-021-Q1-K1-A3

Method BLASTX
NCBI GI g1170936
BLAST score 144
E value 3.0e-09
Match length 95
% identity 44

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_1084406_pir__S46538 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429104_emb_CAA80865_ (Z24741) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 39398

Seq. ID LIB3107-021-Q1-K1-B2

Method BLASTN
NCBI GI g3449321
BLAST score 34
E value 2.0e-09
Match length 58
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG10, complete sequence [Arabidopsis thaliana]

Seq. No. 39399

Seq. ID LIB3107-021-Q1-K1-D4

Method BLASTN
NCBI GI g4490324
BLAST score 37
E value 2.0e-11
Match length 53
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14

(ESSA project)

Seq. No. 39400

Seq. ID LIB3107-021-Q1-K1-D7

Method BLASTX
NCBI GI g542125
BLAST score 166
E value 1.0e-11
Match length 85
% identity 46

NCBI Description translation elongation factor eEF-1 alpha chain - barley

>gi 396134 emb CAA80666 (Z23130) protein synthesis

elongation factor-1 alpha [Hordeum vulgare]

Seq. No. 39401

Seq. ID LIB3107-021-Q1-K1-E2

Method BLASTX



```
q3860333
NCBI GI
BLAST score
                  157
                  2.0e-10
E value
                  58
Match length
                  59
% identity
                  (AJ012693) basic blue copper protein [Cicer arietinum]
NCBI Description
Seq. No.
                  39402
                  LIB3107-021-Q1-K1-E8
Seq. ID
Method
                  BLASTN
                  g1885374
NCBI GI
BLAST score
                  43
E value
                  2.0e-15
Match length
                  43
                  100
% identity
                  Glycine soja small subunit ribosomal RNA gene, partial
NCBI Description
                  sequence, internal transcribed spacer 1, 5.8S ribosomal RNA
                  gene and internal transcribed spacer 2, complete sequence,
                  and large subunit ribosomal RNA gene, partial se
                  39403
Seq. No.
                  LIB3107-021-Q1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2815245
BLAST score
                  86
E value
                  1.0e-40
                  242
Match length
                  84
% identity
NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:
                  CanMT-2)
                  39404
Seq. No.
                  LIB3107-021-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  q2129889
NCBI GI
BLAST score
                  169
E value
                  9.0e-22
                  82
Match length
% identity
NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
                  39405
Seq. No.
                  LIB3107-021-Q1-N1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q59591
BLAST score
                  250
E value
                  1.0e-138
Match length
                  286
% identity
                  97
NCBI Description Human cytomegalovirus strain AD169 complete genome
Seq. No.
                  39406
```

LIB3107-021-Q1-N1-A9 Seq. ID

Method BLASTN NCBI GI g202416 BLAST score 89 1.0e-42 E value



Match length 192 % identity 87

NCBI Description Mouse germline IgM chain gene, mu-delta region

Seq. No. 3940

Seq. ID LIB3107-021-Q1-N1-B11

Method BLASTN
NCBI GI g2501763
BLAST score 263
E value 1.0e-146
Match length 335

Match length 335 % identity 95

NCBI Description Glycine max calmodulin-like domain protein kinase isoenzyme

beta mRNA, complete cds

Seq. No. 39408

Seq. ID LIB3107-021-Q1-N1-C9

Method BLASTX
NCBI GI g3335337
BLAST score 293
E value 2.0e-26
Match length 117
% identity 56

NCBI Description (AC004512) Similar to acyl carrier protein, mitochondrial

precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330

come from this gene

Seq. No. 39409

Seq. ID LIB3107-021-Q1-N1-E10

Method BLASTX
NCBI GI g4138583
BLAST score 194
E value 4.0e-15
Match length 94
% identity 48

NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No. 39410

Seq. ID LIB3107-021-Q1-N1-F12

Method BLASTN
NCBI GI g3982595
BLAST score 82
E value 2.0e-38
Match length 162
% identity 90

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39411

Seq. ID LIB3107-021-Q1-N1-G9

Method BLASTN
NCBI GI g330624
BLAST score 40
E value 1.0e-13
Match length 60
% identity 92

6132



NCBI Description Human cytomegalovirus major immediate-early protein gene, 5' end

Seq. No. 39412

Seq. ID LIB3107-021-Q1-N1-H12

Method BLASTN
NCBI GI g59591
BLAST score 174
E value 3.0e-93
Match length 186
% identity 98

NCBI Description Human cytomegalovirus strain AD169 complete genome

Seq. No. 39413

Seq. ID LIB3107-022-Q1-K1-A3

Method BLASTX
NCBI GI g2129889
BLAST score 331
E value 5.0e-31
Match length 77
% identity 82

NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea

Seq. No. 39414

Seq. ID LIB3107-022-Q1-K1-B3

Method BLASTX
NCBI GI g4415931
BLAST score 165
E value 1.0e-11
Match length 83
% identity 46

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 39415

Seq. ID LIB3107-022-Q1-K1-E1

Method BLASTN
NCBI GI g984307
BLAST score 73
E value 5.0e-33
Match length 261
% identity 82

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 39416

Seq. ID LIB3107-022-Q1-K1-E12

Method BLASTX
NCBI GI g4538939
BLAST score 295
E value 1.0e-26
Match length 87
% identity 66



(AL049483) Col-O casein kinase I-like protein [Arabidopsis NCBI Description thaliana]

39417 Seq. No.

LIB3107-022-Q1-K1-F10 Seq. ID

Method BLASTX NCBI GI q3047065 218 BLAST score 1.0e-17 E value 65 Match length

% identity 63

(AF058825) contains similarity to human OS-9 precurosor NCBI Description

(GB:U41635) [Arabidopsis thaliana]

Seq. No. 39418

LIB3107-022-Q1-K1-F3 Seq. ID

Method BLASTX NCBI GI q131148 190 BLAST score 1.0e-14 E value 82 Match length 52 % identity

PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 NCBI Description

>gi_72674_pir__A2RZP7 photosystem I P700 apoprotein A2 rice chloroplast >gi_11981_emb_CAA33995_ (X15901) PSI P700 apoprotein A2 [Oryza sativa] >gi_226604_prf_1603356AA photosystem I P700 apoprotein A2 [Oryza sativa]

Seq. No. 39419

LIB3107-022-Q1-K1-H8 Seq. ID

Method BLASTX NCBI GI g3776027 BLAST score 484 E value 6.0e-49Match length 115 % identity 82

(AJ010475) RNA helicase [Arabidopsis thaliana] NCBI Description

Seq. No.

39420

LIB3107-023-Q1-K1-H5 Seq. ID

Method BLASTX g4539377 NCBI GI BLAST score 141 E value 1.0e-08 Match length 53 49 % identity

(ALO49525) acyl-CoA synthetase-like protein (fragment) NCBI Description

[Arabidopsis thaliana]

Seq. No. 39421

LIB3107-024-Q1-K1-A1 Seq. ID

BLASTN Method NCBI GI g3982595 BLAST score 274 1.0e-153 E value 354 Match length 94 % identity





```
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                  39422
Seq. No.
Seq. ID
                  LIB3107-024-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q2673906
BLAST score
                  145
                  2.0e-09
E value
Match length
                  45
                  62
% identity
NCBI Description
                  (AC002561) putative DNA polymerase delta small subunit
                  [Arabidopsis thaliana]
                  39423
Seq. No.
                  LIB3107-024-Q1-K1-B5
Seq. ID
Method
                  BLASTX
                  q2262105
NCBI GI
BLAST score
                  268
                  7.0e-36
E value
Match length
                  111
% identity
                  67
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                  39424
                  LIB3107-024-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  a4104974
NCBI GI
                  159
BLAST score
E value
                  6.0e-11
Match length
                  97
                  41
% identity
NCBI Description (AF043109) spermidine synthase 2 [Pisum sativum]
Seq. No.
                  39425
Seq. ID
                  LIB3107-024-Q1-K1-F1
Method
                  BLASTN
NCBI GI
                  g14311
BLAST score
                  220
E value
                  1.0e-120
                  292
Match length
% identity
                  94
NCBI Description G.max chloroplast gene rps19 and flanking regions
Seq. No.
                  39426
                  LIB3107-024-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402678
```

Method BLASTX
NCBI GI g3402678
BLAST score 221
E value 2.0e-18
Match length 72
% identity 61

NCBI Description (AC004697) putative adenylate kinase [Arabidopsis thaliana]

Seq. No. 39427

Seq. ID LIB3107-024-Q1-K1-F7

Method BLASTN NCBI GI g343648

6135



BLAST score E value 4.0e-11 Match length 80 86 % identity NCBI Description Vigna unquiculata chloroplast ribosomal protein (L16 and L14) genes, 3' and 5' end respectively 39428 Seq. No. LIB3107-024-Q1-K1-G7 Seq. ID

Method BLASTN g170091 NCBI GI BLAST score 271 E value 1.0e-151 423 Match length 91 % identity

Glycine max vegetative storage protein (vspB) gene, NCBI Description

complete cds

Seq. No. 39429

Seq. ID LIB3107-024-Q1-K1-H6 Method BLASTN

g2815245 NCBI GI BLAST score 68 E value 6.0e-30 Match length 236 % identity 82

C.arietinum mRNA for class I type 2 metallothionein (clone: NCBI Description

CanMT-2)

39430 Seq. No.

LIB3107-025-Q1-K1-E3 Seq. ID

Method BLASTN NCBI GI g2815245 BLAST score 75 E value 5.0e-34 Match length 223 % identity

C.arietinum mRNA for class I type 2 metallothionein (clone: NCBI Description

CanMT-2)

Seq. No.

39431

Seq. ID LIB3107-025-Q1-K1-E8

Method BLASTX NCBI GI g3600048 BLAST score 194 6.0e-15 E value Match length 100 % identity 47

(AF080120) similar to hypothetical proteins in NCBI Description

Schizosaccharomyces pombe (GB:Z98533) and C. elegans

(GB:Z48334 and Z78419) [Arabidopsis thaliana]

39432 Seq. No.

Seq. ID LIB3107-025-Q1-K1-F11

Method BLASTX g548770 NCBI GI 206 BLAST score



E value 2.0e-16
Match length 74
% identity 57

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 39433

Seq. ID LIB3107-025-Q1-K1-G5

Method BLASTX
NCBI GI g1703227
BLAST score 153
E value 6.0e-10
Match length 56
% identity 59

NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC

TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)

(ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC 2.6.1.2) - barley >gi_469148_emb_CAA81231_ (Z26322) alanine

aminotransferase [Hordeum vulgare]

Seq. No. 39434

Seq. ID LIB3107-025-Q1-K1-H4

Method BLASTX
NCBI GI g3204134
BLAST score 156
E value 6.0e-11
Match length 42
% identity 76

NCBI Description (AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No. 39435

Seq. ID LIB3107-025-Q1-K1-H8

Method BLASTN
NCBI GI g20755
BLAST score 54
E value 1.0e-21
Match length 198
% identity 82

NCBI Description P.sativum mRNA rab for ras-related GTP-binding protein

Seq. No. 39436

Seq. ID LIB3107-026-Q1-K1-G12

Method BLASTX
NCBI GI g3355477
BLAST score 316
E value 3.0e-29
Match length 100
% identity 63

NCBI Description (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis

thaliana]

Seq. No. 39437

Seq. ID LIB3107-027-Q1-K1-D3

Method BLASTN NCBI GI g609224 BLAST score 76



```
1.0e-34
E value
                  265
Match length
                  85
% identity
                  P.sativum mRNA for SAMS-2 >gi 609558_gb_L36681_PEADENSYNB
NCBI Description
                  Pisum sativum S-adenosylmethionine synthase mRNA, complete
Seq. No.
                  39438
Seq. ID
                  LIB3107-028-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2245136
                  192
BLAST score
                  9.0e-15
E value
                  79
Match length
% identity
                  54
                   (Z97344) trehalose-6-phosphate synthase homolog
NCBI Description
                   [Arabidopsis thaliana]
                  39439
Seq. No.
Seq. ID
                  LIB3107-028-Q1-K1-E6
Method
                  BLASTN
NCBI GI
                  g303900
BLAST score
                  55
                   3.0e-22
E value
Match length
                  207
% identity
                   44
NCBI Description Soybean gene for ubiquitin, complete cds
                   39440
Seq. No.
Seq. ID
                  LIB3107-028-Q1-K1-E7
Method
                  BLASTX
                  g4240120
NCBI GI
BLAST score
                  162
                   3.0e-11
E value
Match length
                  59
% identity
                   61
NCBI Description (AB007801) cytochrome b5 [Arabidopsis thaliana]
                   39441
Seq. No.
Seq. ID
                  LIB3107-029-Q1-K1-A3
Method
                  BLASTN
                   g505584
NCBI GI
BLAST score
                   326
                   0.0e+00
E value
                   338
Match length
                   99
% identity
NCBI Description G.max mRNA for Glyoxalase I
Seq. No.
                   39442
Seq. ID
                  LIB3107-029-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                   g3915037
```

NCBI GI g391503/ BLAST score 121 E value 4.0e-15

Match length 85 % identity 47

NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)



>gi_2570067_emb_CAA04512_ (AJ001071) second sucrose synthase [Pisum sativum]

Seq. No. 39443

Seq. ID LIB3107-029-Q1-K1-B1

Method BLASTN
NCBI GI g1438878
BLAST score 362
E value 0.0e+00
Match length 370
% identity 99

NCBI Description Glycine max choline kinase GmCK1p mRNA, complete cds

Seq. No. 39444

Seq. ID LIB3107-029-Q1-K1-E3

Method BLASTN
NCBI GI g456713
BLAST score 36
E value 7.0e-11
Match length 71
% identity 87

NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 39445

Seq. ID LIB3107-029-Q1-K1-E9

Method BLASTN
NCBI GI g3449312
BLAST score 47
E value 2.0e-17
Match length 71
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K16L22, complete sequence [Arabidopsis thaliana]

Seq. No. 39446

Seq. ID LIB3107-029-Q1-K1-G11

Method BLASTX
NCBI GI g4249380
BLAST score 184
E value 9.0e-14
Match length 95
% identity 42

NCBI Description (AC005966) ESTs gb Z37637, gb AA042498 and gb AA042269 come

from this gene. [Arabidopsis thaliana]

Seq. No. 39447

Seq. ID LIB3107-029-Q1-K1-G5

Method BLASTX
NCBI GI g728744
BLAST score 207
E value 9.0e-17
Match length 71
% identity 56

NCBI Description AUXIN-INDUCED PROTEIN PCNT115 >gi_100305_pir___\$16390

auxin-induced protein - common tobacco

>gi 19799 emb CAA39708 (X56267) auxin-induced protein

[Nicotiana tabacum]



```
Seq. No.
                    39448
 Seq. ID
                   LIB3107-029-Q1-K1-H6
 Method
                   BLASTX
 NCBI GI
                   q3747111
 BLAST score
                   227
 E value
                   1.0e-18
Match length
                   78
 % identity
                   56
NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]
 Seq. No.
                   39449
                   LIB3107-030-Q1-K1-A12
 Seq. ID
Method
                   BLASTX
NCBI GI
                   q3451075
BLAST score
                   281
E value
                   4.0e-32
Match length
                   125
% identity
                   55
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   39450
Seq. ID
                   LIB3107-030-Q1-K1-E7
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   368
E value
                   0.0e + 00
Match length
                   412
% identity
                   97
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                   complete cds
Seq. No.
                   39451
Seq. ID
                   LIB3107-031-Q1-K1-B4
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   327
E value
                   0.0e+00
Match length
                   413
% identity
                   95
NCBI Description
                   Glycine max vegetative storage protein (vspB) gene,
                   complete cds
Seq. No.
                   39452
Seq. ID
                   LIB3107-031-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   g2341033
BLAST score
                   340
E value
                   5.0e-32
Match length
                  89
% identity
                  80
NCBI Description
                  (AC000104) Similar to Babesia aldo-keto reductase
                   (gb_M93122). [Arabidopsis thaliana]
```

39453 Seq. ID LIB3107-031-Q1-K1-E10 BLASTX

Seq. No.

Method

6140

```
q2499611
NCBI GI
BLAST score
                    234
E value
                    1.0e-19
Match length
                    51
% identity
                    MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)
NCBI Description
                    (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
                    >qi 457406 dbj BAA04870_ (D21843) MAP kinase [Arabidopsis
                    thaliana]
                    39454
Seq. No.
Seq. ID
                    LIB3107-031-Q1-K1-F11
Method
                    BLASTN
                    g169974
NCBI GI
BLAST score
                    311
                    1.0e-175
E value
Match length
                    410
% identity
                    94
NCBI Description Glycine max vspA gene, complete cds
                    39455
Seq. No.
                    LIB3107-031-Q1-K1-H4
Seq. ID
Method
                    BLASTN
NCBI GI
                    g2924257
BLAST score
                    260
                    1.0e-144
E value
Match length
                    380
                    92
% identity
NCBI Description Tobacco chloroplast genome DNA
                    39456
Seq. No.
                    LIB3107-033-Q1-K1-C5
Seq. ID
Method
                    BLASTX
NCBI GI
                    q136057
BLAST score
                    394
E value
                    3.0e-38
                    106
Match length
% identity
                    TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                    >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
Coptis japonica >gi_556171 (J04121) triosephosphate
                    isomerase [Coptis japonica]
Seq. No.
                    39457
                    LIB3107-034-Q1-K1-A8
Seq. ID
Method
                    BLASTN
NCBI GI
                    g343348
BLAST score
                    51
                    8.0e-20
E value
Match length
                    67
% identity
                    94
```

39458 Seq. No.

NCBI Description

LIB3107-034-Q1-K1-D6 Seq. ID

initiation motif

Glycine max mitochondrial DNA sequence, transcription



```
Method
NCBI GI
                  q2809233
                  179
BLAST score
                  3.0e-13
E value
                  54
Match length
                  61
% identity
                  (AC002560) F21B7.2 [Arabidopsis thaliana]
NCBI Description
                  39459
Seq. No.
                  LIB3107-034-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                  g4512663
NCBI GI
BLAST score
                  261
E value
                  9.0e-23
                  88
Match length
                  57
% identity
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4544470_gb_AAD22377.1 AC006580 9 (AC006580)
                  hypothetical protein [Arabidopsis thaliana]
                   39460
Seq. No.
                  LIB3107-034-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   g3650035
NCBI GI
BLAST score
                   157
                   2.0e-10
E value
Match length
                   75
                   52
% identity
                   (AC005396) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
                   39461
Seq. No.
                   LIB3107-034-Q1-K1-E8
Seq. ID
Method
                   BLASTX
                   g3135263
NCBI GI
BLAST score
                   408
E value
                   6.0e-40
                   135
Match length
                   39
% identity
NCBI Description
                   (AC003058) hypothetical protein [Arabidopsis thaliana]
                   39462
Seq. No.
                   LIB3107-035-Q1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q541943
                   275
BLAST score
                   2.0e-24
E value
                   55
Match length
% identity
                   91
                  metallothionein - soybean >gi 228682 prf 1808316A
NCBI Description
                   metallothionein-like protein [Glycine max]
```

39463

Seq. No. LIB3107-035-Q1-K1-C4 Seq. ID

Method BLASTX NCBI GI g3128209 BLAST score 143



```
E value
                  4.0e-09
Match length
                  53
% identity
                  55
                  (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  39464
                  LIB3107-035-Q1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18683
BLAST score
                  44
E value
                  2.0e-15
Match length
                  64
% identity
NCBI Description G.max N-20t gene
                  39465
Seq. No.
Seq. ID
                  LIB3107-035-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  q4417288
                  203
BLAST score
                  6.0e-16
E value
Match length
                  61
% identity
                  64
NCBI Description
                  (AC007019) unknown protein [Arabidopsis thaliana]
                  39466
Seq. No.
Seq. ID
                  LIB3107-035-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  q484656
BLAST score
                  301
E value
                  2.0e-27
Match length
                  102
% identity
                  monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
NCBI Description
                  cucumber >gi_452165 dbj_BAA05408 (D26392)
                  monodehydroascorbate reductase [Cucumis sativus]
Seq. No.
                  39467
Seq. ID
                  LIB3107-035-Q1-K1-H7
Method
                  BLASTN
NCBI GI
                  g2995831
BLAST score
                  50
                  2.0e-19
E value
Match length
                  54
% identity
                  98
                  Trifolium michelianum 18S ribosomal RNA gene, partial
NCBI Description
                  sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
                  gene and internal transcribed spacer 2, complete sequence;
                  and 26S ribosomal RNA gene, partial sequence
                  39468
Seq. No.
Seq. ID
                  LIB3107-036-Q1-K1-C12
```

 Seq. No.
 39468

 Seq. ID
 LIB3107-036-Q1-K1-C12

 Method
 BLASTX

 NCBI GI
 g2462929

 BLAST score
 200

9.0e-16

Match length 76

E value



% identity

NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.

39469

Seq. ID

LIB3107-036-Q1-K1-E11

Method NCBI GI BLASTX g4567304

BLAST score

211

E value Match length % identity

7.0e-17 66

59

NCBI Description

(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.

39470

Seq. ID

LIB3107-036-Q1-K1-F10

Method NCBI GI BLAST score BLASTX g3402678 182

E value Match length

5.0e-14 53 66

% identity NCBI Description

(AC004697) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.

39471

Seq. ID

LIB3107-036-Q1-K1-F12

Method BLASTN g3850955 NCBI GI BLAST score 60 2.0e-25 E value Match length 196

% identity 83

NCBI Description

Xylomelum scottianum ATP synthase beta subunit (atpB) gene, chloroplast gene encoding chloroplast protein, partial cds

Seq. No.

39472

Seq. ID

LIB3107-036-Q1-K1-G3

Method BLASTN NCBI GI q2815245 BLAST score 70 E value 5.0e-31 Match length 242 % identity 82

NCBI Description

C.arietinum mRNA for class I type 2 metallothionein (clone:

CanMT-2)

Seq. No.

39473

Seq. ID

LIB3107-037-Q1-K1-C5

Method BLASTX NCBI GI q4467147 BLAST score 144 E value 4.0e-09 Match length 74 % identity

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No.

39474

Seq. ID

LIB3107-037-Q1-K1-C9

Seq. ID

Method

NCBI GI

BLAST score

```
Method
NCBI GI
                  q541943
                  197
BLAST score
                  4.0e-15
E value
Match length
                  55
                  64
% identity
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                  39475
Seq. No.
                  LIB3107-037-Q1-K1-E5
Seq. ID
Method
                  BLASTN
                  g343344
NCBI GI
                  39
BLAST score
                  1.0e-12
E value
Match length
                  107
                  85
% identity
                  Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end),
NCBI Description
                  Ile-tRNA, and Ala-tRNA genes
                  39476
Seq. No.
                  LIB3107-037-Q1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3738299
BLAST score
                   363
E value
                   1.0e-34
                   93
Match length
                   77
% identity
                   (AC005309) putative glutaredoxin [Arabidopsis thaliana]
NCBI Description
                   >gi 4249395 (AC006072) putative glutaredoxin [Arabidopsis
                   thaliana]
                   39477
Seq. No.
Seq. ID
                   LIB3107-037-Q1-K1-F6
Method
                   BLASTN
                   q169974
NCBI GI
BLAST score
                   44
                   1.0e-15
E value
                   100
Match length
% identity
                   86
                  Glycine max vspA gene, complete cds
NCBI Description
Seq. No.
                   39478
Seq. ID
                   LIB3107-037-Q1-K1-H9
Method
                   BLASTN
NCBI GI
                   g3097320
BLAST score
                   43
E value
                   7.0e-15
Match length
                   135
                   84
% identity
NCBI Description Glycine max gene for Bd 30K, complete cds
                   39479
Seq. No.
```

6145

LIB3107-038-Q1-K1-D1

BLASTN g3982595



```
E value
                    2.0e-50
 Match length
                   134
 % identity
 NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
 Seq. No.
                   39480
 Seq. ID
                   LIB3107-038-Q1-K1-G3
 Method
                   BLASTN
 NCBI GI
                   g169974
 BLAST score
                   32
 E value
                   1.0e-08
Match length
                   48
 % identity
                   92
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   39481
Seq. ID
                   LIB3107-038-Q1-K1-H3
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   187
E value
                   1.0e-101
Match length
                   279
                   92
% identity
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                   39482
Seq. ID
                   LIB3107-039-Q1-K1-A6
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   77
E value
                   3.0e-35
Match length
                   183
% identity
                   47
NCBI Description Tobacco chloroplast genome DNA
                   39483
Seq. No.
                   LIB3107-039-Q1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2623295
BLAST score
                   112
E value
                   5.0e-11
Match length
                   78
% identity
                   53
NCBI Description
                  (AC002409) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   39484
Seq. ID
                   LIB3107-039-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   g4559342
BLAST score
                   362
E value
                   8.0e-35
Match length
                  97
% identity
                  70
NCBI Description
                   (AC007087) putative copper methylamine oxidase [Arabidopsis
                  thaliana]
```

No. 39485

Seq. No.

```
LIB3107-039-01-K1-E2
Seq. ID
                   BLASTX
Method
                   g2501850
NCBI GI
                   374
BLAST score
                   5.0e-36
E value
                   102
Match length
                   74
% identity
                   (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
-NCBI Description
                   39486
Seq. No.
                   LIB3107-039-Q1-K1-G2
Seq. ID
                   BLASTX
Method
                   g3980254
NCBI GI
BLAST score
                   292
                   3.0e-26
E value
                   78
Match length
                   72
 % identity
                   (AJ006053) peroxisomal membrane protein [Arabidopsis
NCBI Description
                   thaliana]
                   39487
 Seq. No.
                   LIB3107-040-Q1-K1-C2
 Seq. ID
                   BLASTN
Method
                   g4218188
NCBI GI
 BLAST score
                   41
                   1.0e-13
 E value
                   122
Match length
                   89
 % identity
                   Glycine max cytosolic glutamine synthetase (gs15) gene
 NCBI Description
                   promoter
                   39488
 Seq. No.
                   LIB3107-040-Q1-K1-C3
 Seq. ID
                   BLASTX
 Method
                   q4454482
 NCBI GI
 BLAST score
                   180
                   2.0e-13
 E value
 Match length
                   77
                   45
 % identity
                   (AC006234) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   39489
 Seq. No.
                   LIB3107-040-Q1-K1-E5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q3449378
                   168
 BLAST score
                   7.0e-15
 E value
                   89
 Match length
 % identity
                    46
```

NCBI Description (AF039681) plant resistance protein [Lycopersicon

esculentum]

Seq. No. 39490

Seq. ID LIB3107-040-Q1-K1-G4

Method BLASTN NCBI GI g169897 BLAST score 231

```
E value
Match length
                  379
                  90
% identity
NCBI Description G.max 28 kDa protein, complete cds
                  39491
Seq. No.
                  LIB3107-041-Q1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2815245
BLAST score
                  86
                  1.0e-40
E value
                  242
Match length
% identity
                  84
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                  CanMT-2)
                  39492
Seq. No.
                  LIB3107-041-Q1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170091
BLAST score
                  257
                  1.0e-142
E value
                  321
Match length
% identity
                  95
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                  complete cds
                  39493
Seq. No.
                  LIB3107-041-Q1-K1-F12
Seq. ID
Method
                  BLASTN
                  g3982595
NCBI GI
                  179
BLAST score
```

4.0e-96 E value Match length 323 % identity

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. Seq. ID LIB3107-041-Q1-K1-G12 Method BLASTX NCBI GI q3023945 BLAST score 419 E value 1.0e-41 Match length 91 % identity 82

HISTONE DEACETYLASE (HD) >gi 2318131 (AF014824) histone NCBI Description

deacetylase [Arabidopsis thaliana]

Seq. No. 39495

Seq. ID LIB3107-041-Q1-K1-G6

39494

Method BLASTX g1086252 NCBI GI 123 BLAST score 4.0e-12 E value Match length 94 47 % identity

NCBI Description sucrose cleavage protein - Potato >gi_707001_bbs_157931

% identity

NCBI Description



(S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No. 39496 Seq. ID LIB3107-042-Q1-K1-A7 Method BLASTN NCBI GI q176000 BLAST score 40 E value 4.0e-13 Match length 80 % identity 88 NCBI Description Spinach chloroplast Leu-tRNA-3 39497 Seq. No. Seq. ID LIB3107-042-Q1-K1-B5 Method BLASTX NCBI GI q3150415 BLAST score 180 2.0e-13 E value Match length 56 % identity 68 NCBI Description (ACOO4165) sec13-related protein [Arabidopsis thaliana] >gi 3420046 (AC004680) sec13-related protein [Arabidopsis thaliana] 39498 Seq. No. Seq. ID LIB3107-042-Q1-K1-B8 Method BLASTN NCBI GI q11576 BLAST score 60 E value 2.0e-25 Match length 116 % identity 88 NCBI Description Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NADH dehydrogenase and ORF Seq. No. 39499 Seq. ID LIB3107-042-Q1-K1-D12 Method BLASTX NCBI GI q4432835 BLAST score 142 9.0e-09 E value Match length 64 % identity 48 (AC006283) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 39500 Seq. ID LIB3107-042-Q1-K1-E12 Method BLASTN NCBI GI q170091 BLAST score 38 3.0e-12 E value Match length 126 83

complete cds

Glycine max vegetative storage protein (vspB) gene,

Seq. No.

Seq. ID

39506

LIB3107-044-Q1-K1-E10



```
Seq. No.
                  39501
Seq. ID
                  LIB3107-044-Q1-K1-B11
Method
                  BLASTN
NCBI GI
                  g343026
BLAST score
                  40
                  2.0e-13
E value
Match length
                  153
                  85
% identity
                  Pea Chloroplast 4.5S, 5S, 16S and 23S mRNA
NCBI Description
Seq. No.
                  39502
                  LIB3107-044-Q1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3176689
BLAST score
                  218
E value
                  7.0e-28
Match length
                  98
                  67
% identity
NCBI Description
                  (AC003671) Contains similarity to ubiquitin
                  carboxyl-terminal hydrolase 14 gb Z35927 from S.
                  cerevisiae. [Arabidopsis thaliana]
Seq. No.
                  39503
Seq. ID
                  LIB3107-044-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q2388710
BLAST score
                  168
E value
                  7.0e-12
Match length
                  76
                  47
% identity
                   (AF017150) betaine aldehyde dehydrogenase [Amaranthus
NCBI Description
                  hypochondriacus]
Seq. No.
                  39504
Seq. ID
                  LIB3107-044-Q1-K1-D2
Method
                  BLASTN
                  q11303
NCBI GI
BLAST score
                  101
                  2.0e-49
E value
                  229
Match length
% identity
                  86
NCBI Description G.max chloroplast mRNA for ndhK polypeptide and orf 158/159
                  39505
Seq. No.
                  LIB3107-044-Q1-K1-D9
Seq. ID
Method
                  BLASTX
                  q3786005
NCBI GI
BLAST score
                  187
                  8.0e-20
E value
                  100
Match length
                  41
% identity
                  (AC005499) putative phosphoethanolamine
NCBI Description
```

6150

cytidylyltransferase [Arabidopsis thaliana]

```
Method
NCBI GI
                  q4567311
BLAST score
                  219
E value
                   6.0e-18
Match length
                  64
                  66
% identity
NCBI Description
                  (AC005956) putative protein kinase [Arabidopsis thaliana]
                  39507
Seq. No.
Seq. ID
                  LIB3107-044-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g4545262
BLAST score
                  165
E value
                  2.0e-11
Match length
                  64
% identity
                   48
NCBI Description
                  (AF118230) metallothionein-like protein [Gossypium
                  hirsutum]
                  39508
Seq. No.
                  LIB3107-044-Q1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170050
BLAST score
                  288
                  1.0e-161
E value
                   348
Match length
% identity
                   96
NCBI Description Soybean pyruvate kinase mRNA, complete cds
                   39509
Seq. No.
                  LIB3107-047-Q1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2815245
BLAST score
                   82
E value
                   3.0e-38
Match length
                   242
% identity
                   83
NCBI Description
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
                  CanMT-2)
Seq. No.
                   39510
Seq. ID
                   LIB3107-048-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                   g3834388
BLAST score
                   147
                   3.0e-09
E value
Match length
                   68
                   43
```

% identity NCBI Description

(AF038547) beta-1,4-mannanase [Bacillus stearothermophilus]

Seq. No.

39511

LIB3107-048-Q1-K1-C12 Seq. ID

BLASTX Method NCBI GI g3298540 BLAST score **1**59 1.0e-10 E value 87 Match length



```
% identity
                  (AC004681) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  39512
Seq. ID
                  LIB3107-049-Q1-K1-B5
                  BLASTX
Method
NCBI GI
                  g3928097
BLAST score
                  178
E value
                  2.0e-15
Match length
                  111
% identity
                  42
NCBI Description
                  (AC005770) unknown protein, 5' partial [Arabidopsis
                  thaliana]
Seq. No.
                  39513
Seq. ID
                  LIB3107-049-Q1-K1-D5
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  51
E value
                  1.0e-19
Match length
                  143
% identity
                  85
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                  39514
Seq. ID
                  LIB3107-049-Q1-K1-D8
Method
                  BLASTN
NCBI GI
                  g516102
BLAST score
                  215
E value
                  1.0e-117
Match length
                  315
% identity
                  92
NCBI Description
                  Soybean phytochrome B (phyB) gene exons 1-5, complete cds
Seq. No.
                  39515
Seq. ID
                  LIB3107-049-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2632252
BLAST score
                  171
E value
                  4.0e-12
Match length
                  48
% identity
                  77
NCBI Description
                  (Y12464) serine/threonine kinase [Sorghum bicolor]
Seq. No.
                  39516
Seq. ID
                  LIB3107-049-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  q541943
BLAST score
                  194
E value
                  4.0e-20
                  73
Match length
% identity
                  68
NCBI Description
                  metallothionein - soybean >qi 228682 prf 1808316A
```

Seq. No. 39517

Seq. ID LIB3107-049-Q1-K1-F9

metallothionein-like protein [Glycine max]

Seq. No.

Seq. ID Method

39522

BLASTX

LIB3107-050-Q1-K1-D10



```
Method
NCBI GI
                  q114623
                  288
BLAST score
                  7.0e-26
E value
                  137
Match length
                  53
% identity
NCBI Description
                  ATP SYNTHASE B CHAIN (SUBUNIT I) >gi_67933_pir__PWPM1
                  H+-transporting ATP synthase (EC 3.6.1.34) chain I - garden
                  pea chloroplast >gi_311715_emb_CAA29351_ (X05917) atpF
                  protein [Pisum sativum]
                  39518
Seq. No.
                  LIB3107-050-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2462746
BLAST score
                  446
                  2.0e-58
E value
                  148
Match length
                  70
% identity
                  (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
                  39519
Seq. No.
                  LIB3107-050-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462746
BLAST score
                  454
                  2.0e-45
E value
Match length
                  127
% identity
                  71
                  (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
                  39520
Seq. No.
                  LIB3107-050-Q1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170091
                  90
BLAST score
                  4.0e-43
E value
Match length
                  267
% identity
                  84
NCBI Description Glycine max vegetative storage protein (vspB) gene,
                  complete cds
Seq. No.
                   39521
                  LIB3107-050-Q1-K1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g231660
BLAST score
                  182
                  2.0e-13
E value
Match length
                  114
                   42
% identity
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
```



```
NCÉI GI
                  q2506276
BLAST score
                  481
E value
                  1.0e-48
Match length
                  107
                  92
% identity
NCBI Description
                  RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
                  KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)
                  >gi 2129561 pir S71235 chaperonin-60 alpha chain -
                  Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60
                  alpha subunit [Arabidopsis thaliana]
                  >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco
                  binding protein alpha subunit [Arabidopsis thaliana]
Seq. No.
                  39523
Seq. ID
                  LIB3107-050-Q1-K1-D11
Method
                  BLASTX
                  g3298542
NCBI GI
BLAST score
                  151
E value
                  7.0e-10
Match length
                  48
% identity
                  56
NCBI Description
                  (AC004681) putative cellulose synthase [Arabidopsis
                  thaliana]
Seq. No.
                  39524
                  LIB3107-050-Q1-K1-D2
```

Seq. ID Method BLASTN g14311 NCBI GI BLAST score 91 9.0e-44 E value

Match length 267 % identity 84

NCBI Description G.max chloroplast gene rps19 and flanking regions

Seq. No. 39525

Seq. ID LIB3107-050-Q1-K1-D9

Method BLASTX NCBI GI q3021357 BLAST score 495 E value 4.0e-50 Match length 120 % identity 79

NCBI Description (AJ005082) UDP-galactose 4-epimerase [Cyamopsis

tetragonoloba]

Seq. No. 39526

Seq. ID LIB3107-050-Q1-K1-E9

Method BLASTX NCBI GI g2244792 BLAST score 649 E value 3.0e-74Match length 148 % identity

(Z97336) ankyrin homolog [Arabidopsis thaliana] NCBI Description

Seq. No. 39527

Seq. ID LIB3107-050-Q1-K1-F10

Match length

NCBI Description

% identity

148 72

[Arabidopsis thaliana]



```
BLASTX
Method
NCBI GI
                   q1172556
BLAST score
                   221
                   4.0e-18
E value
                   88
Match length
% identity
                   49
                   36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
NCBI Description
                   (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato
                   mitochondrion >gi 515360 emb CAA56600 (X80387) 36kDA porin
                   II [Solanum tuberosum]
                   39528
Seq. No.
Seq. ID
                   LIB3107-050-Q1-K1-F11
Method
                   BLASTX
NCBI GI
                   g1173027
BLAST score
                   418
E value
                   4.0e-41
Match length
                   120
                   72
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
                   protein L31 [Nicotiana glutinosa]
Seq. No.
                   39529
Seq. ID
                   LIB3107-050-Q1-K1-F2
Method
                   BLASTN
NCBI GI
                   g609224
BLAST score
                   98
                   1.0e-47
E value
                   306
Match length
                   83
% identity
                   P.sativum mRNA for SAMS-2 >gi 609558 gb L36681 PEADENSYNB
NCBI Description
                   Pisum sativum S-adenosylmethionine synthase mRNA, complete
                   cds
                   39530
Seq. No.
Seq. ID
                   LIB3107-050-Q1-K1-F7
Method
                   BLASTX
                   g2827082
NCBI GI
BLAST score
                   190
                   5.0e-15
E value
Match length
                   72
% identity
                   61
                  (AF020272) malate dehydrogenase [Medicago sativa]
NCBI Description
                   39531
Seq. No.
Seq. ID
                   LIB3107-050-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   g4406780
BLAST score
                   552
                   1.0e-56
E value
```

(AC006532) putative multispanning membrane protein

```
39532
Seq. No.
                  LIB3107-050-Q1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1928981
BLAST score
                   480
```

2.0e-48

107 Match length 85 % identity (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica NCBI Description

oleracea var. botrytis]

39533 Seq. No. LIB3107-050-Q1-K1-H11 Seq. ID Method BLASTX NCBI GI g2244977 BLAST score 298

5.0e-27 E value Match length 119 % identity

E value

NCBI Description (Z97340) cysteine proteinase [Arabidopsis thaliana]

39534 Seq. No. LIB3107-050-Q1-K1-H12 Seq. ID Method BLASTX g3170525 NCBI GI BLAST score 148 1.0e-09 E value Match length 51 61 % identity

NCBI Description

(AF054615) cellulase [Fragaria x ananassa]

39535 Seq. No. LIB3107-050-Q1-K1-H9 Seq. ID BLASTN Method g2150129 NCBI GI 151 BLAST score 2.0e-79

E value 395 Match length 85 % identity

Arabidopsis thaliana cytoplasmic ribosomal protein S15a NCBI Description

mRNA, complete cds

39536 Seq. No.

LIB3107-052-Q1-K1-B2 Seq. ID

BLASTX Method g629693 NCBI GI 265 BLAST score 2.0e-23 E value 85 Match length 54 % identity

probable integrase - common tobacco (fragment) NCBI Description

>gi_530742_emb_CAA56791_ (X80830) integrase [Nicotiana

tabacum]

Seq. No.

39537

LIB3107-052-Q1-K1-F2 Seq. ID

BLASTX Method

6156

Ne. -



```
NCBI GI
                    q3068705
BLAST score
                    177
                    6.0e-13
E value
Match length
                    67
% identity
                    49
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                    39538
                    LIB3107-052-Q1-K1-G9
Seq. ID
Method
                    BLASTN
NCBI GI
                    q3982595
BLAST score
                    296
E value
                    1.0e-166
                    356
Match length
% identity
                    96
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                    39539
Seq. No.
Seq. ID
                    LIB3107-052-Q1-K1-H6
Method
                    BLASTN
                    g169974
NCBI GI
BLAST score
                    100
E value
                    5.0e-49
Match length
                    280
% identity
                    86
NCBI Description Glycine max vspA gene, complete cds
                    39540
Seq. No.
Seq. ID
                    LIB3107-053-Q1-K1-B4
Method
                    BLASTX
NCBI GI
                    g3420982
BLAST score
                    176
E value
                    1.0e-12
Match length
                    81
% identity
                    42
NCBI Description
                    (Z97628) Similarity to Brugia peptidylprolyl isomerase
                    (TR:G984562) [Caenorhabditis elegans]
                    >gi_3876969_emb_CAB03088_ (Z81080) Similarity to Brugia
peptidylproTyl isomerase (TR:G984562) [Caenorhabditis
                    elegans]
Seq. No.
                    39541
Seq. ID
                    LIB3107-053-Q1-K1-C11
Method
                    BLASTX
NCBI GI
                    g4337175
BLAST score
                    345
E value
                    2.0e-32
Match length
                    98
% identity
NCBI Description
                    (AC006416) ESTs gb_T20589, gb T04648, gb AA597906,
                    gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                    gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
```

Seq. No.

39542

Seq. ID

LIB3107-053-Q1-K1-C6

Method

BLASTX

% identity



```
g3482975
NCBI GI
                  254
BLAST score
                  8.0e-22
E value
Match length
                  116
% identity
                  48
                  (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                  39543
Seq. No.
                  LIB3107-053-Q1-K1-D2
Seq. ID
                  BLASTX
Method
                  g3212877
NCBI GI
                  453
BLAST score
                  3.0e-45
E value
                  118
Match length
% identity
                  74
                  (AC004005) Lea-like protein [Arabidopsis thaliana]
NCBI Description
                  39544
Seq. No.
                  LIB3107-053-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  163
                  2.0e-11
E value
Match length
                  46
% identity
                  67
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
Seq. No.
                  39545
                  LIB3107-053-Q1-K1-G3
Seq. ID
                  BLASTN
Method
                  q2815245
NCBI GI
BLAST score
                  62
                  3.0e-26
E value
                  182
Match length
                  84
% identity
NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:
                  CanMT-2)
                  39546
Seq. No.
                  LIB3107-054-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g2792188
NCBI GI
                  Ī71
BLAST score
                   4.0e-12
E value
                  136
Match length
% identity
                   26
                  (AJ002236) Hcr9-9E [Lycopersicon pimpinellifolium]
NCBI Description
                   39547
Seq. No.
                  LIB3107-054-Q1-K1-B5
Seq. ID
Method
                   BLASTX
                   q3183088
NCBI GI
BLAST score
                   245
                   8.0e-21
E value
Match length
                   96
                   52
```



PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR NCBI Description

(LTP) >gi_629658_pir__S47084 lipid transfer like protein cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 39548

LIB3107-054-Q1-K1-C12 Seq. ID

Method BLASTX g2618699 NCBI GI BLAST score 306 E value 6.0e-28 Match length 82 % identity 74

(AC002510) unknown protein [Arabidopsis thaliana] NCBI Description

39549 Seq. No.

LIB3107-054-Q1-K1-C9 Seq. ID

Method BLASTN NCBI GI q170023 BLAST score 109 1.0e-54 E value 221 Match length % identity 88

NCBI Description Glycine max maturation-associated protein (MAT9) mRNA,

complete cds

39550 Seq. No.

LIB3107-054-Q1-K1-E3 Seq. ID

Method BLASTN g169897 NCBI GI BLAST score 41 E value 6.0e-14 Match length 189

% identity 80

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 39551

LIB3107-054-Q1-K1-G2 Seq. ID

Method BLASTX g1903034 NCBI GI BLAST score 117 E value 5.0e-09 Match length 78 % identity 44

NCBI Description (X94625) amp-binding protein [Brassica napus]

Seq. No.

39552

LIB3107-054-Q1-K1-H1 Seq. ID

Method BLASTX NCBI GI q2894610 BLAST score 308 E value 3.0e-28 Match length 72 % identity 76

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 39553



```
Seq. ID
                  LIB3107-054-Q1-K1-H4
                  BLASTN
Method
                  q2258103
NCBI GI
BLAST score
                  72
                  3.0e-32
E value
Match length
                  80
% identity
                  97
                  Arabidopsis thaliana chloroplast genes for trnC and rpoB,
NCBI Description
                  partial cds
Seq. No.
                  39554
Seq. ID
                  LIB3107-055-Q1-K1-A5
Method
                  BLASTN
NCBI GI
                  q169897
BLAST score
                  140
E value
                  8.0e-73
                  277
Match length
% identity
                  87
NCBI Description G.max 28 kDa protein, complete cds
                  39555
Seq. No.
Seq. ID
                  LIB3107-055-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q2792297
BLAST score
                  216
E value
                  2.0e-17
                  66
Match length
                  59
% identity
NCBI Description
                  (AF039183) GAST-like gene product [Fragaria x ananassa]
Seq. No.
                  39556
Seq. ID
                  LIB3107-055-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3033395
BLAST score
                  241
                  2.0e-20
E value
Match length
                  100
% identity
                   47
NCBI Description
                   (AC004238) putative zinc-finger protein [Arabidopsis
                   thaliana]
Seq. No.
                  39557
Seq. ID
                  LIB3107-055-Q1-K1-D12
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                   45
                  3.0e-16
E value
Match length
                  81
                  89
% identity
                  Cloning vector pSport1, complete cds
NCBI Description
Seq. No.
                  39558
```

Seq. ID LIB3107-055-Q1-K1-D3

Method BLASTX NCBI GI g2244816 BLAST score 154 E value 4.0e-10



```
Match length 97
% identity 46
NCBI Description (Z97
```

CBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 39559

Seq. ID LIB3107-055-Q1-K1-F2

Method BLASTX
NCBI GI g3122785
BLAST score 203
E value 5.0e-16
Match length 60
% identity 70

NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi_2565340 (AF026079) ribosomal

protein S14 [Lupinus luteus]

Seq. No. 39560

Seq. ID LIB3107-055-Q1-K1-F7

Method BLASTN
NCBI GI g170089
BLAST score 52
E value 2.0e-20
Match length 180
% identity 83

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 39561

Seq. ID LIB3107-055-Q1-K1-G11

Method BLASTX
NCBI GI g477280
BLAST score 209
E value 1.0e-16
Match length 121
% identity 45

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) 55K

protein precursor - potato >gi_410633_bbs_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

534 aa]

Seq. No. 39562

Seq. ID LIB3107-055-Q1-K1-H3

Method BLASTX
NCBI GI g1170508
BLAST score 147
E value 2.0e-09
Match length 78
% identity 46

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)

>gi 2119931 pir S60244 translation initiation factor

eIF-4A.8, anther-specific - common tobacco

>gi_475219_emb_CAA55639_ (X79004) translation initiation

factor (eIF-4A) [Nicotiana tabacum]

>gi 475221 emb CAA55640 (X79005) translation initiation

factor (eIF-4A) [Nicotiana tabacum]

Seq. No. 39563

Seq. ID LIB3107-055-Q1-K1-H4



```
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  219
E value
                  1.0e-120
                  387
Match length
                  89
% identity
NCBI Description
                  Glycine max vspA gene, complete cds
                  39564
Seq. No.
Seq. ID
                  LIB3107-055-Q1-K1-H6
Method
                  BLASTN
NCBI GI
                  q4204762
BLAST score
                  83
E value
                  7.0e-39
                  159
Match length
                  88
% identity
NCBI Description Glycine max peroxidase (sEPb1) mRNA, partial cds
                  39565
Seq. No.
Seq. ID
                  LIB3107-056-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  q2661412
BLAST score
                  156
E value
                  1.0e-10
Match length
                  86
% identity
                  43
                  (AJ000728) MAP kinase kinase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  39566
Seq. ID
                  LIB3107-056-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3242789
BLAST score
                  196
                   3.0e-15
E value
Match length
                   52
% identity
                   69
                   (AF055357) respiratory burst oxidase protein D [Arabidopsis
NCBI Description
                  thaliana]
                   39567
Seq. No.
Seq. ID
                  LIB3107-057-Q1-K1-A6
Method
                  BLASTX
                  g4127988
NCBI GI
BLAST score
                  222
                   3.0e-18
E value
                  80
Match length
% identity
                   (AJ005940) GTP-binding protein [Homo sapiens] >gi 4218945
NCBI Description
                   (AF078103) developmentally regulated GTP-binding protein
                   [Homo sapiens]
                  39568
Seq. No.
Seq. ID
                  LIB3107-057-Q1-K1-A9
```

Method BLASTN NCBI GI g577414 BLAST score 35 E value 4.0e-10



Match length 47 % identity 94

NCBI Description Human G protein-coupled receptor (GPR2) gene, partial cds

Seq. No. 39569

Seq. ID LIB3107-057-Q1-K1-B5

Method BLASTN
NCBI GI g984307
BLAST score 78
E value 1.0e-35
Match length 276
% identity 83

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 39570

Seq. ID LIB3107-057-Q1-K1-B8

Method BLASTX
NCBI GI g4006827
BLAST score 370
E value 2.0e-35
Match length 121
% identity 58

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 39571

Seq. ID LIB3107-057-Q1-K1-C1

Method BLASTX
NCBI GI g4538967
BLAST score 157
E value 2.0e-10
Match length 60
% identity 53

NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis

thaliana]

Seq. No. 39572

Seq. ID LIB3107-057-Q1-K1-C6

Method BLASTN
NCBI GI g516102
BLAST score 92
E value 2.0e-44
Match length 148
% identity 91

NCBI Description Soybean phytochrome B (phyB) gene exons 1-5, complete cds

Seq. No. 39573

Seq. ID LIB3107-057-Q1-K1-D1

Method BLASTX
NCBI GI g2642165
BLAST score 264
E value 5.0e-23
Match length 98
% identity 53



(AC003000) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 39574 LIB3107-057-Q1-K1-D9 Seq. ID Method BLASTN g537459 NCBI GI BLAST score 37 2.0e-11 E value Match length 61 90 % identity NCBI Description Cloning vector pSG930, HIS4-based plasmid, complete sequence Seq. No. 39575 LIB3107-057-Q1-K1-E11 Seq. ID Method BLASTX q4107099 NCBI GI BLAST score 179 3.0e-13 E value Match length 88 38 % identity NCBI Description (AB015141) AHP1 [Arabidopsis thaliana] >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis thaliana] Seq. No. 39576 LIB3107-057-Q1-K1-E5 Seq. ID Method BLASTN NCBI GI q313143 48 BLAST score 6.0e-18 E value Match length 112 % identity 86 NCBI Description A.medicago MSK-1 mRNA for protein kinase Seq. No. 39577 Seq. ID LIB3107-057-Q1-K1-F8 Method BLASTX NCBI GI q128838 BLAST score 530 E value 3.0e-54Match length 114 % identity NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE 49 KD SUBUNIT, CHLOROPLAST (ORF 393) >gi_82215_pir__A05216 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 393 - common tobacco chloroplast >gi_1223674_emb_CAA77398_ (Z00044) NADH dehydrogenase 49kD subunit [Nicotiana tabacum] >gi 225262 prf 1211235CX ORF 393 [Nicotiana tabacum] 39578 Seq. No.

Seq. ID LIB3107-057-Q1-K1-H5 BLASTX Method

NCBI GI g541943 BLAST score 150 7.0e-17 E value 79 Match length

% identity metallothionein - soybean >gi 228682 prf 1808316A NCBI Description metallothionein-like protein [Glycine max] 39579 Seq. No. Seq. ID LIB3107-057-Q1-K1-H6 Method BLASTX NCBI GI q4467151 BLAST score 392 E value 5.0e-38 Match length 146 % identity 55 (AL035540) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 39580 LIB3107-057-Q1-K1-H9 Seq. ID BLASTN

Method BLASTN
NCBI GI g2815245
BLAST score 62
E value 2.0e-26
Match length 242
% identity 81

NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:

CanMT-2)

Seq. No. 39581

Seq. ID LIB3107-058-Q1-K1-A5

Method BLASTX
NCBI GI g600855
BLAST score 173
E value 1.0e-12
Match length 69
% identity 54

NCBI Description (U17887) bZIP protein [Arabidopsis thaliana]

Seq. No. 39582

Seq. ID LIB3107-058-Q1-K1-A6

Method BLASTN
NCBI GI g470890
BLAST score 32
E value 9.0e-09
Match length 60
% identity 92

NCBI Description Cycas revoluta 28S ribosomal RNA (28S rRNA), ca. bp 738 to

938 in mature rRNA

Seq. No. 39583

Seq. ID LIB3107-058-Q1-K1-C11

Method BLASTN
NCBI GI g343344
BLAST score 51
E value 2.0e-20
Match length 59
% identity 97

NCBI Description Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end),

Ile-tRNA, and Ala-tRNA genes



```
Seq. No.
                   39584
                  LIB3107-058-Q1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3850583
BLAST score
                   154
E value
                   4.0e-10
Match length
                   41
                   73
% identity
                   (AC005278) Contains similarity to transcription initiation
NCBI Description
                   factor IIE, alpha subunit gb X63468 from Homo sapiens.
                   [Arabidopsis thaliana]
Seq. No.
                   39585
                   LIB3107-058-Q1-K1-C6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q531828
BLAST score
                   48
E value
                   4.0e-18
Match length
                   80
                   90
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                   39586
Seq. ID
                   LIB3107-058-Q1-K1-D8
Method
                   BLASTN
NCBI GI
                   q3511284
BLAST score
                   32
E value
                   7.0e-09
Match length
                   52
                   90
% identity
                  Populus alba x Populus tremula cellulose synthase (cell)
NCBI Description
                   mRNA, complete cds
                   39587
Seq. No.
                   LIB3107-058-Q1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2982303
BLAST score
                   211
                   3.0e-17
E value
                   72
Match length
% identity
                   61
                   (AF051236) hypothetical protein [Picea mariana]
NCBI Description
                   39588
Seq. No.
Seq. ID
                   LIB3107-058-Q1-K1-E5
                   BLASTX
Method
                   q4579913
NCBI GI
BLAST score
                   158
E value
                   1.0e-10
                   43
Match length
% identity
                   (AB023423) sulfate transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   39589
```

Seq. ID BLASTX Method

NCBI GI

g3093294

LIB3107-058-Q1-K1-E6

```
BLAST score
E value
                  1.0e-09
                  34
Match length
% identity
                  76
                  (Y12782) putative villin [Arabidopsis thaliana]
NCBI Description
                  39590
Seq. No.
                  LIB3107-058-Q1-K1-E8
Seq. ID
Method
                  BLASTN
                  g2924257
NCBI GI
BLAST score
                  56
E value
                  1.0e-22
Match length
                  201
% identity
                  86
NCBI Description Tobacco chloroplast genome DNA
                  39591
Seq. No.
                  LIB3107-059-Q1-K1-E10
Seq. ID
Method
                  BLASTX
                  g1171577
NCBI GI
BLAST score
                  162
                  5.0e-11
E value
Match length
                  90
% identity
                  40
NCBI Description
```

(X95343) hypersensitivity-related gene [Nicotiana tabacum]

39592 Seq. No. LIB3107-060-Q1-K1-A12 Seq. ID Method BLASTX q4510348 NCBI GI BLAST score 145 3.0e-09 E value

58 Match length % identity 48

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 39593

Seq. ID LIB3107-060-Q1-K1-B10

Method BLASTN NCBI GI q1326160 BLAST score 59 E value 2.0e-24 Match length 161 96 % identity

NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No. 39594

Seq. ID LIB3107-060-Q1-K1-B9

Method BLASTX NCBI GI g1619602 BLAST score 192 1.0e-14 E value 58 Match length % identity 62

(Y08726) MtN3 [Medicago truncatula] NCBI Description

39595 Seq. No.



```
Seq. ID
                  LIB3107-060-Q1-K1-C5
Method
                  BLASTX
                  q2129709
NCBI GI
BLAST score
                  176
                  1.0e-12
E value
                  118
Match length
% identity
                  reverse transcriptase - Arabidopsis thaliana
NCBI Description
                  retrotransposon Tall-1 >gi 976278 (L47193) reverse
                  transcriptase [Arabidopsis thaliana]
Seq. No.
                  39596
Seq. ID
                  LIB3107-060-Q1-K1-C7
Method
                  BLASTN
NCBI GI
                  q516853
                  108
BLAST score
                  7.0e-54
E value
Match length
                  192
% identity
                  32
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
                  39597
Seq. No.
Seq. ID
                  LIB3107-060-Q1-K1-E10
Method
                  BLASTN
                  g609224
NCBI GI
                  174
BLAST score
                   4.0e-93
E value
                  306
Match length
% identity
                  89
                  P.sativum mRNA for SAMS-2 >gi 609558 gb L36681_PEADENSYNB
NCBI Description
                  Pisum sativum S-adenosylmethionine synthase mRNA, complete
Seq. No.
                   39598
Seq. ID
                  LIB3107-060-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                   g3702343
BLAST score
                   380
E value
                   1.0e-36
Match length
                   121
% identity
                   (AC005397) putative homeotic gene regulator [Arabidopsis
NCBI Description
                   thaliana]
                   39599
Seq. No.
                   LIB3107-060-Q1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244916
                   148
BLAST score
                   2.0e-09
E value
                   107
Match length
% identity
                   29
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
```

NCBI Description

39600

Seq. No. Seq. ID LIB3107-060-Q1-K1-G4

BLASTX Method



```
q4512617
NCBI GI
                  167
BLAST score
                  1.0e-11
E value
                  120
Match length
% identity
                  43
                  (AC004793) F28K20.16 [Arabidopsis thaliana]
NCBI Description
                  39601
Seq. No.
                  LIB3107-060-Q1-K1-H11
Seq. ID
                  BLASTX
Method
                  g4263711
NCBI GI
BLAST score
                  285
                  2.0e-25
E value
                   64
Match length
% identity
                   83
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   39602
Seq. No.
                  LIB3107-060-Q1-K1-H8
Seq. ID
                  BLASTN
Method
                   g170091
NCBI GI
                   306
BLAST score
                   1.0e-172
E value
                   386
Match length
                   95
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   39603
Seq. No.
                   LIB3107-061-Q1-K1-B10
Seq. ID
                   BLASTX
Method
                   g1657855
NCBI GI
BLAST score
                   278
                   1.0e-24
E value
                   68
Match length
                   72
% identity
                   (U73216) cold acclimation protein WCOR413 [Triticum
NCBI Description
                   aestivum]
Seq. No.
                   39604
                   LIB3107-061-Q1-K1-C3
Seq. ID
                   BLASTN
Method
                   g255576
NCBI GI
BLAST score
                   377
                   0.0e + 00
E value
                   395
Match length
                   99
% identity
                   small auxin up RNA gene cluster: orf 6B [Glycine
NCBI Description
                   max=soybeans, cv. Wayne, Genomic, 665 nt]
                   39605
Seq. No.
                   LIB3107-061-Q1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567295
BLAST score
                   404
```

2.0e-39

E value

BLAST score

Match length

% identity

E value

48

120

85

3.0e-18



```
Match length
% identity
                  58
                  (AC006918) putative pol polyprotein [Arabidopsis thaliana]
NCBI Description
                  39606
Seq. No.
                  LIB3107-061-Q1-K1-D12
Seq. ID
Method
                  BLASTN
                  g166379
NCBI GI
BLAST score
                  67
                  2.0e-29
E value
                  195
Match length
                  84
% identity
NCBI Description Alfalfa glucose-regulated endoplasmic reticular protein
                  mRNA, complete cds
                  39607
Seq. No.
                  LIB3107-061-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q541943
                  166
BLAST score
                  9.0e-14
E value
                  74
Match length
                  65
% identity
NCBI Description
                  metallothionein - soybean >gi 228682 prf_1808316A
                  metallothionein-like protein [Glycine max]
                  39608
Seq. No.
                  LIB3107-061-Q1-K1-E7
Seq. ID
Method
                  BLASTX
                  g123587
NCBI GI
BLAST score
                  145
                  1.0e-09
E value
Match length
                   61
% identity
                   49
                  HEAT SHOCK 70 KD PROTEIN >gi_81239_pir__JQ1515 heat-shock
NCBI Description
                  protein HSP70 - Chlamydomonas reinhardtii >gi 167421
                   (M76725) 70 kDa heat shock protein [Chlamydomonas
                   reinhardtii]
Seq. No.
                   39609
                   LIB3107-061-Q1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4262180
BLAST score
                   101
                   2.0e-10
E value
Match length
                   53
% identity
                   66
NCBI Description
                   (AC005508) 29621 [Arabidopsis thaliana]
Seq. No.
                   39610
                   LIB3107-061-Q1-K1-G11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18729
```



93

complete cds

% identity

NCBI Description

```
NCBI Description Soybean (Glycine max) 18S ribosomal RNA
                    39611
Seq. No.
                    LIB3107-061-Q1-K1-G2
Seq. ID
                    BLASTX
Method
                    g3367574
NCBI GI
BLAST score
                    283
                    2.0e-25
E value
                    103
Match length
                    54
% identity
                    (AL031135) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    39612
Seq. No.
                    LIB3107-062-Q1-K1-A11
Seq. ID
                    BLASTX
Method
                    q1173187
NCBI GI
                    275
BLAST score
                    1.0e-24
E value
                    64
Match length
                    81
% identity
                    40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden
NCBI Description
                    strawberry >gi_643074 (U19940) putative 40S ribosomal
                    protein s12 [Fragaria x ananassa]
                    39613
Seq. No.
                    LIB3107-062-Q1-K1-A8
Seq. ID
                    BLASTN
Method
                    g18761
NCBI GI
BLAST score
                    66
                    6.0e-29
E value
                    174
Match length
                    85
% identity
                    Soybean stem mRNA for 31 kD glycoprotein
NCBI Description
                    39614
Seq. No.
                    LIB3107-062-Q1-K1-B5
Seq. ID
Method
                    BLASTX
                    q541943
NCBI GI
BLAST score
                    170
                     4.0e-12
E value
                     65
Match length
                     52
% identity
                    metallothionein - soybean >gi_228682_prf__1808316A
metallothionein-like protein [Glycine max]
NCBI Description
                     39615
Seq. No.
                     LIB3107-062-Q1-K1-B8
Seq. ID
Method
                     BLASTN
NCBI GI
                     g555615
BLAST score
                     218
                     1.0e-119
E value
                     306
Match length
```

Glycine max Mandarin cytokinin induced message (cim1) mRNA,

```
Seq. No.
                  LIB3107-062-Q1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4126473
BLAST score
                   157
E value
                   9.0e-11
Match length
                   96
                   38
% identity
                   (AB014884) adenylyl cyclase associated protein [Gossypium
NCBI Description
Seq. No.
                   39617
Seq. ID
                  LIB3107-062-Q1-K1-H2
Method
                  BLASTN
NCBI GI
                  a984307
BLAST score
                   147
                   6.0e-77
E value
Match length
                   176
```

% identity 95
NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 39618

Seq. ID LIB3107-063-Q1-K1-A10

Method BLASTN
NCBI GI g170091
BLAST score 359
E value 0.0e+00
Match length 407
% identity 97

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 39619

Seq. ID LIB3107-063-Q1-K1-B5

Method BLASTN
NCBI GI g303900
BLAST score 220
E value 1.0e-120
Match length 314
% identity 29

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No.

39620

39621

Seq. ID LIB3107-063-Q1-K1-B8

Method BLASTX
NCBI GI g3063460
BLAST score 576
E value 1:0e-59
Match length 136
% identity 85

NCBI Description (AC003981) F22013.22 [Arabidopsis thaliana]

Seq. No.

BLAST score

E value

267

2.0e-23



```
LIB3107-063-Q1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4325285
BLAST score
                  36
                  1.0e-10
E value
Match length
                   68
% identity
                  88
                  Arabidopsis thaliana NAC domain protein NAM mRNA, complete
NCBI Description
Seq. No.
                   39622
Seq. ID
                  LIB3107-063-Q1-K1-C7
Method
                  BLASTX
NCBI GI
                  q541943
BLAST score
                   329
E value
                   8.0e-31
                   79
Match length
% identity
                  77
                  metallothionein - soybean >gi 228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                   39623
Seq. No.
Seq. ID
                   LIB3107-063-Q1-K1-E10
Method
                  BLASTN
                   q4138388
NCBI GI
BLAST score
                   97
                   3.0e-47
E value
                   214
Match length
% identity
                   89
NCBI Description Pisum sativum chloroplast ndhK gene
Seq. No.
                   39624
Seq. ID
                   LIB3107-064-Q1-K1-B10
Method
                   BLASTX
NCBI GI
                   g1817526
BLAST score
                   280
                   6.0e-25
E value
Match length
                   136
% identity
                  (D63884) intermediate chain 1 [Anthocidaris crassispina]
NCBI Description
                   39625
Seq. No.
Seq. ID
                   LIB3107-064-Q1-K1-D5
Method
                   BLASTN
                   g836895
NCBI GI
                   37
BLAST score
                   1.0e-11
E value
Match length
                   65
                   89
% identity
NCBI Description Saccharomyces cerevisiae CSP2 gene, complete cds
                   39626
Seq. No.
Seq. ID
                   LIB3107-064-Q1-K1-D9
Method
                   BLASTX
                   g282994
NCBI GI
```



Match length 76
% identity 67
NCBI Description Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No. 39627

Seq. ID LIB3107-064-Q1-K1-E7

Method BLASTN
NCBI GI g18655
BLAST score 89
E value 2.0e-42
Match length 261
% identity 84

NCBI Description Soybean heat-shock gene hs6871 sequence

Seq. No. 39628

Seq. ID LIB3107-064-Q1-K1-F11

Method BLASTN
NCBI GI g296444
BLAST score 270
E value 1.0e-150
Match length 374
% identity 93

NCBI Description G.max ADR6 mRNA

Seq. No. 39629

Seq. ID LIB3107-064-Q1-K1-F3

Method BLASTX
NCBI GI g1946690
BLAST score 357
E value 6.0e-34
Match length 84
% identity 77

NCBI Description (U94495) glutathione peroxidase [Arabidopsis thaliana]

Seq. No. 39630

Seq. ID LIB3107-064-Q1-K1-F5

Method BLASTX
NCBI GI g3377797
BLAST score 288
E value 7.0e-26
Match length 117
% identity 57

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 39631

Seq. ID LIB3107-064-Q1-K1-F6

Method BLASTN
NCBI GI g296442
BLAST score 49
E value 2.0e-18
Match length 129
% identity 85



NCBI Description G.max ADR11 mRNA

```
39632
Seq. No.
                  LIB3107-064-Q1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18729
BLAST score
                   64
E value
                  9.0e-28
Match length
                  140
                   91
% identity
NCBI Description Soybean (Glycine max) 18S ribosomal RNA
Seq. No.
                   39633
Seq. ID
                  LIB3107-064-Q1-K1-G6
Method
                  BLASTN
NCBI GI
                   a4204764
BLAST score
                   135
E value
                   7.0e-70
                  335
Match length
% identity
                   85
NCBI Description Glycine max peroxidase (sEPb2) mRNA, partial cds
Seq. No.
                   39634
Seq. ID
                  LIB3107-064-Q1-K1-H12
Method
                  BLASTN
                   g3982595
NCBI GI
BLAST score
                   342
E value
                   0.0e + 00
Match length
                   410
                   96
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                   39635
Seq. ID
                   LIB3107-064-Q1-K1-H3
Method
                   BLASTX
NCBI GI
                   q1350969
BLAST score
                   213
                   1.0e-17
E value
Match length
                   55
% identity
                   76
                   40S RIBOSOMAL PROTEIN S26 (S31) >gi 971284 dbj BAA07208
NCBI Description
                   (D38011) ribosomal protein S31 [Oryza sativa]
Seq. No.
                   39636
Seq. ID
                   LIB3107-065-Q1-K1-A8
                   BLASTX
Method
NCBI GI
                   g2511693
BLAST score
                   164
                   1.0e-11
E value
                   95
Match length
                   43
% identity
```

Seq. No. 39637

NCBI Description

Seq. ID LIB3107-065-Q1-K1-C11

Method BLASTN NCBI GI g1431738

(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

% identity



```
BLAST score
 E value
                   2.0e-33
Match length
                   197
 % identity
                   90
NCBI Description
                   Soybean (Glycine max) low MW heat shock protein gene
                   (Gmhsp17.5-M)
Seq. No.
                   39638
Seq. ID
                   LIB3107-065-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   g3421391
BLAST score
                   217
E value
                   2.0e-17
Match length
                   47
% identity
                   87
NCBI Description
                   (AF082158) putative cysteine synthase [Arabidopsis
                   thaliana]
                   39639
Seq. No.
Seq. ID
                   LIB3107-065-Q1-K1-D7
Method
                   BLASTN
NCBI GI
                   g296446
BLAST score
                   65
E value
                   2.0e-28
Match length
                   209
% identity
                   83
NCBI Description
                  G.max AmyB mRNA
Seq. No.
                   39640
Seq. ID
                   LIB3107-065-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   q3023752
BLAST score
                   178
E value
                   4.0e-13
Match length
                   67
% identity
                   51
NCBI Description
                   FERREDOXIN I PRECURSOR >gi 1418982 emb CAA99756 (Z75520)
                   ferredoxin-I [Lycopersicon esculentum]
Seq. No.
                   39641
Seq. ID
                   LIB3107-065-Q1-K1-F7
Method
                  BLASTN
NCBI GI
                   q403326
BLAST score
                   55
E value
                   3.0e-22
Match length
                  150
% identity
                  87
NCBI Description
                  T.repens TrMT1A mRNA for metallothionein-like protein
Seq. No.
                  39642
Seq. ID
                  LIB3107-066-Q1-K1-A7
                  BLASTN
Method
NCBI GI
                  q403326
BLAST score
                  51
E value
                  7.0e-20
Match length
                  171
```



NCBI Description T.repens TrMT1A mRNA for metallothionein-like protein

Seq. No. 39643

Seq. ID LIB3107-066-Q1-K1-B4

Method BLASTX
NCBI GI g2160189
BLAST score 217
E value 1.0e-17
Match length 108
% identity 10

NCBI Description (AC000132) Similar to A. thaliana receptor-like protein

kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come

from this gene. [Arabidopsis thaliana]

Seq. No. 39644

Seq. ID LIB3107-066-Q1-K1-C11

Method BLASTN
NCBI GI g474002
BLAST score 44
E value 2.0e-15
Match length 82
% identity 89

NCBI Description Rice mRNA, partial homologous to ribosomal protein L39 gene

Seq. No. 39645

Seq. ID LIB3107-066-Q1-K1-D2

Method BLASTX
NCBI GI g2281090
BLAST score 292
E value 2.0e-26
Match length 111
% identity 61

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 39646

Seq. ID LIB3107-066-Q1-K1-E3

Method BLASTX
NCBI GI g3660471
BLAST score 269
E value 7.0e-24
Match length 92
% identity 59

NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha

subunit [Arabidopsis thaliana]

Seq. No. 39647

Seq. ID LIB3107-066-Q1-K1-F11

Method BLASTX
NCBI GI g731651
BLAST score 145
E value 4.0e-09
Match length 44
% identity 55

NCBI Description HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN

PUT2-SRB2 INTERGENIC REGION >gi_626608_pir__S46746 hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) >gi_488180 (U00062) Yhr039cp [Saccharomyces



cerevisiae]

```
39648
Seq. No.
                   LIB3107-066-Q1-K1-F5
Seq. ID
                   BLASTX
Method
                   q544250
NCBI GI
BLAST score
                   183
E value
                   2.0e-13
                   36
Match length
                   89
% identity
                   ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR)
NCBI Description
                   >gi_541860_pir__A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana
                   39649
Seq. No.
                   LIB3107-066-Q1-K1-H4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539357
                   146
BLAST score
                   3.0e-09
E value
                   126
Match length
% identity
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]
                   39650
Seq. No.
                   LIB3107-067-Q1-K1-A6
Seq. ID
                   BLASTX
Method
                   q1170878
NCBI GI
BLAST score
                   204
                   1.0e-16
E value
                   66
Match length
% identity
                   67
                   MALATE SYNTHASE, GLYOXYSOMAL (MS) >gi 170026 (L01629)
NCBI Description
                   malate synthase [Glycine max]
Seq. No.
                   39651
                   LIB3107-067-Q1-K1-B12
Seq. ID
                   BLASTX
Method
                   g3688170
NCBI GI
BLAST score
                   287
                   8.0e-26
E value
Match length
                   87
% identity
                   (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   39652
Seq. No.
                   LIB3107-067-Q1-K1-D6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g170087
                    95
BLAST score
                    5.0e-46
E value
                   215
Match length
                    86
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
```

39653

LIB3107-067-Q1-K1-D8

Seq. No.

Seq. ID

Match length



```
BLASTN
Method
                   q169897
NCBI GI
                   121
BLAST score
                   1.0e-61
E value
                   221
Match length
                   89
% identity
NCBI Description G.max 28 kDa protein, complete cds
                   39654
Seq. No.
                   LIB3107-067-Q1-K1-E11
Seq. ID
                   BLASTN
Method
                   q1673362
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
                   150
Match length
                   89
% identity
NCBI Description A.fungosa plastid rps16 gene (intron)
                   39655
Seq. No.
                   LIB3107-067-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   q4415924
NCBI GI
                   227
BLAST score
                   5.0e-19
E value
                   89
Match length
                   48
% identity
                   (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   39656
Seq. No.
                   LIB3107-067-Q1-K1-E3
Seq. ID
                   BLASTX
Method
                   g3928150
NCBI GI
BLAST score
                   153
                   1.0e-10
E value
                   54
Match length
                    61
 % identity
                   (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                    39657
Seq. No.
                   LIB3107-067-Q1-K1-H2
 Seq. ID
                   BLASTX
Method
                    g1865677
 NCBI GI
                    157
BLAST score
                    2.0e-10
 E value
                    34
 Match length
 % identity
                    (Y08568) trehalose-6-phosphate synthase [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    39658
                    LIB3107-068-Q1-K1-C1
 Seq. ID
 Method
                    BLASTN
                    g12137
 NCBI GI
 BLAST score
                    186
                    1.0e-100
 E value
                    324
```

```
% identity
                  Pea chloroplast DNA (4.7 kb) 5' to ATP-synthase a subunit
NCBI Description
                  gene
                  39659
Seq. No.
                  LIB3107-068-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3158476
                  173
BLAST score
                  1.0e-12
E value
                  61
Match length
                  57
% identity
                  (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
                  39660
Seq. No.
                  LIB3107-068-Q1-K1-F11
Seq. ID
                  BLASTX
Method
                  q136057
NCBI GI
                   200
BLAST score
                   1.0e-15
E value
                   75
Match length
                   55
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                   Coptis japonica >gi_556171 (J04121) triosephosphate
                   isomerase [Coptis japonica]
                   39661
Seq. No.
                   LIB3107-069-Q1-K1-A5
Seq. ID
Method
                   BLASTN
                   g1480927
NCBI GI
                   144
BLAST score
                   3.0e-75
E value
                   228
Match length
% identity
                   Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed
NCBI Description
                   pseudogene
                   39662
Seq. No.
Seq. ID
                   LIB3107-069-Q1-K1-D12
                   BLASTX
Method
                   g1184121
NCBI GI
                   156
BLAST score
E value
                   2.0e-10
Match length
                   71
                   48
% identity
                   (U20808) auxin-induced protein [Vigna radiata]
NCBI Description
                   39663
 Seq. No.
                   LIB3107-069-Q1-K1-D5
 Seq. ID
Method
                   BLASTN
                   g2668739
 NCBI GI
                   39
 BLAST score
```

NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA,

1.0e-12

83

87

E value

Match length % identity

NCBI Description

39669

LIB3107-070-Q1-K1-F2

Seq. No.

Seq. ID



```
39664
Seq. No.
                  LIB3107-069-Q1-K1-F1
Seq. ID
                  BLASTN
Method
                  g2815245
NCBI GI
BLAST score
                  73
                  8.0e-33
E value
                  177
Match length
                  85
% identity
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                   CanMT-2)
                   39665
Seq. No.
                   LIB3107-069-Q1-K1-H2
Seq. ID
Method
                   BLASTX
                   g3164136
NCBI GI
BLAST score
                   160
                   6.0e-11
E value
Match length
                   70
% identity
                   (D78603) cytochrome P450 monooxygenase [Arabidopsis
NCBI Description
                   thaliana]
                   39666
Seq. No.
                   LIB3107-070-Q1-K1-B9
Seq. ID
                   BLASTN
Method
                   q456713
NCBI GI
BLAST score
                   130
E value
                   4.0e-67
                   185
Match length
                   28
% identity
                   Glycine max gene for ubiquitin, complete cds
NCBI Description
                   39667
Seq. No.
                   LIB3107-070-Q1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g12269
BLAST score
                   192
                   1.0e-104
E value
                   304
Match length
                   91
% identity
                   Spinach plastid genes psaA, psaB and rps14 for p700
NCBI Description
                   chlorophyll a apoproteins and ribosomal protein S14
                   39668
Seq. No.
                   LIB3107-070-Q1-K1-F1
 Seq. ID
Method
                   BLASTX
                   g3641863
 NCBI GI
 BLAST score
                   107
                    3.0e-12
 E value
                    44
 Match length
                    80
 % identity
                   (AJ005042) beta-galactosidase [Cicer arietinum]
```



```
Method
                   BLASTX
NCBI GI
                   g3046815
BLAST score
                   336
E value
                   6.0e-32
Match length
                   79
% identity
                   82
NCBI Description
                   (AL021687) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   39670
Seq. ID
                   LIB3107-070-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   q4416302
BLAST score
                   428
E value
                   2.0e-42
Match length
                   113
% identity
                   72
NCBI Description
                   (AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.
                   39671
Seq. ID
                   LIB3107-070-Q1-K1-H1
Method
                   BLASTN
NCBI GI
                   g516853
BLAST score
                   152
E value
                   4.0e-80
Match length
                   199
% identity
                   32
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.
                   39672
Seq. ID
                   LIB3107-071-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2062475
BLAST score
                   184
E value
                   4.0e-14
Match length
                   76
% identity
                   53
NCBI Description
                  (U83903) TNF-stimulated gene 6 protein [Mus musculus]
Seq. No.
                   39673
Seq. ID
                   LIB3107-071-Q1-K1-E10
Method
                   BLASTX
NCBI GI
                  q3461835
BLAST score
                   164
                   6.0e-12
E value
Match length
                   54
% identity
                   61
                   (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  >gi_3927840 (AC005727) putative protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  39674
Seq. ID
                  LIB3107-071-Q1-K1-E7
Method
                  BLASTN
NCBI GI
                  g2815245
BLAST score
                  37
E value
```

2.0e-11

101

Match length

```
% identity
                  C.arietinum mRNA for class I type 2 metallothionein (clone:
NCBI Description
                  CanMT-2)
Seq. No.
                  39675
Seq. ID
                  LIB3107-072-Q1-K1-B12
Method
                  BLASTN
NCBI GI
                  g14311
BLAST score
                  112
E value
                  3.0e-56
Match length
                  291
% identity
                  85
NCBI Description G.max chloroplast gene rps19 and flanking regions
                  39676
Seq. No.
Seq. ID
                  LIB3107-072-Q1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1616628
BLAST score
                  145
E value
                   3.0e-09
Match length
                  94
                   39
% identity
NCBI Description
                  (X80472) sts15 [Solanum tuberosum]
                   39677
Seq. No.
Seq. ID
                  LIB3107-072-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2492506
BLAST score
                   220
E value
                   3.0e-18
Match length
                   64
% identity
                   64
NCBI Description
                  PEROXISOME ASSEMBLY FACTOR-2 (PAF-2) (PEROXISOMAL-TYPE
                  ATPASE 1) (PEROXIN-6) >gi_2135899 pir__S71090 peroxisome
                   biogenesis disorder group 4 protein PXAAA1 - human
                   >gi_1354753 (U56602) Pxaaalp [Homo sapiens]
                   39678
Seq. No.
Seq. ID
                   LIB3107-074-Q1-K1-A6
Method
                  BLASTN
                   g19395
NCBI GI
                   35
BLAST score
                   4.0e-10
E value
Match length
                   55
```

% identity 91

Tomato U6 small nuclear RNA gene NCBI Description

Seq. No. 39679

Seq. ID LIB3107-074-Q1-K1-C12

Method BLASTX NCBI GI g4567251 151 BLAST score E value 6.0e-10 Match length 50 54 % identity

(AC007070) unknown protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
Seq. ID
                  LIB3107-074-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1709804
BLAST score
                  205
                  5.0e-16
E value
Match length
                  56
                  68
% identity
                  26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED
NCBI Description
                  ATPASE DOMAIN PROTEIN 44) >gi 1045497 (U36395) conserved
                  ATPase domain protein 44 [Spermophilus tridecemlineatus]
                  >gi 2213932 (AF006305) 26S proteasome regulatory subunit
                  [Homo sapiens]
                  39681
Seq. No.
                  LIB3107-074-01-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2119719
                  119
BLAST score
                  4.0e-15
E value
                  73
Match length
                  59
% identity
NCBI Description heat-shock cognate protein 70-3 - tomato >gi 762844
                  (L41253) Hsc70 [Lycopersicon esculentum]
                  39682
Seq. No.
                  LIB3107-075-Q1-K1-A9
Seq. ID
Method
                  BLASTX
                  g541943
NCBI GI
BLAST score
                  189
                  2.0e-14
E value
                  62
Match length
                  58
% identity
NCBI Description
                  metallothionein - soybean >gi 228682 prf 1808316A
                  metallothionein-like protein [Glycine max]
Seq. No.
                  39683
Seq. ID
                  LIB3107-075-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1946360
BLAST score
                  179
                  3.0e-15
E value
Match length
                  107
% identity
                  47
                  (U93215) elicitor response element binding protein WRKY3
NCBI Description
                  isolog [Arabidopsis thaliana]
Seq. No.
                  39684
```

Seq. ID LIB3107-075-Q1-K1-C10

Method BLASTX q3560143 NCBI GI 150 BLAST score 8.0e-10 E value Match length 71 % identity

(AL031534) putative vacuolar protein sorting-associated NCBI Description

protein [Schizosaccharomyces pombe]

NCBI GI

BLAST score



```
39685
Seq. No.
                  LIB3107-075-Q1-K1-C4
Seq. ID
                  BLASTN
Method
                  q1142700
NCBI GI
                  34
BLAST score
                  1.0e-09
E value
                  107
Match length
                  90
% identity
NCBI Description Glycine max satellite STR120-A.2
                  39686
Seq. No.
                  LIB3107-075-Q1-K1-C8
Seq. ID
Method
                  BLASTN
                  q166411
NCBI GI
                  162
BLAST score
                   6.0e-86
E value
                              , γ
                   326
Match length
                   87
% identity
NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds
                   39687
Seq. No.
                  LIB3107-075-Q1-K1-D1
Seq. ID
                  BLASTX
Method
                   g4467156
NCBI GI
                   323
BLAST score
                   3.0e-30
E value
                   100
Match length
% identity
                   62
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                   39688
Seq. No.
                   LIB3107-075-Q1-K1-D3
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1906414
                   149
BLAST score
                   3.0e-78
E value
Match length
                   313
% identity
                   Nepenthes alata ORF2280 gene homolog, chloroplast gene
NCBI Description
                   encoding chloroplast protein, partial cds
                   39689
Seq. No.
                   LIB3107-075-Q1-K1-G1
Seq. ID
Method
                   BLASTX
                   q3747111
NCBI GI
                   255
BLAST score
                   5.0e-22
E value
Match length
                   72
                   65
% identity
NCBI Description (AF095641) MTN3 homolog [Arabidopsis thaliana]
                   39690
Seq. No.
                   LIB3107-076-Q1-K1-B4
Seq. ID
Method
                   BLASTX
```

g3747111

```
E value
Match length
                  69
% identity
NCBI Description
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
                  39691
Seq. No.
Seq. ID
                  LIB3107-076-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  q4559351
BLAST score
                  185
E value
                  8.0e-14
Match length
                  108
% identity
NCBI Description
                  (AC006585) hypothetical protein [Arabidopsis thaliana]
                  39692
Seq. No.
                  LIB3107-076-Q1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076534
BLAST score
                  182
                  1.0e-13
E value
                  63
Match length
% identity
                  59
NCBI Description
                  monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden
                  pea >gi_497120 (U06461) monodehydroascorbate reductase
                  [Pisum sativum]
                  39693
Seq. No.
Seq. ID
                  LIB3107-077-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  q3980417
BLAST score
                  277
E value
                  1.0e-24
Match length
                  60
% identity
NCBI Description
                  (AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.
                  39694
Seq. ID
                  LIB3107-077-Q1-K1-E8
Method
                  BLASTN
NCBI GI
                  q169974
BLAST score
                  59
                  7.0e-25
E value
Match length
                  86
% identity
                  93
NCBI Description
                  Glycine max vspA gene, complete cds
```

Seq. No. 39695

Seq. ID LIB3107-078-Q1-K1-A4

Method BLASTN
NCBI GI g3176694
BLAST score 35
E value 3.0e-10

Match length 87 % identity 85

NCBI Description Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]



```
Seq. No.
                  39696
Seq. ID
                  LIB3107-078-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q2055228
BLAST score
                  130
E value
                  4.0e-09
Match length
                   64
                  58
% identity
NCBI Description
                  (AB000129) SRC1 [Glycine max]
Seq. No.
                   39697
Seq. ID
                  LIB3107-078-Q1-K1-E4
Method
                  BLASTX
                  q2654870
NCBI GI
                  158
BLAST score
                   1.0e-10
E value
Match length
                  30
                   90
% identity
                  (AF015302) RbohAOsp [Oryza sativa]
NCBI Description
                   39698
Seq. No.
Seq. ID
                  LIB3107-078-Q1-K1-E7
Method
                  BLASTX
                  g4490728
NCBI GI
                  205
BLAST score
                   4.0e-16
E value
Match length
                   77
% identity
                   51
NCBI Description
                  (AL035709) putative protein [Arabidopsis thaliana]
Seq. No.
                   39699
Seq. ID
                   LIB3107-078-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                   g629733
BLAST score
                   341
E value
                   4.0e-32
Match length
                   118
% identity
                   61
                   sulfate adenylyltransferase (EC 2.7.7.4) met3-2 - potato
NCBI Description
                   >gi_2130000_pir__S67498 sulfate adenylyltransferase (EC
                   2.7.7.4) (clone StMet3-2) - potato >gi 479090 emb CAA55655
                   (X79053) sulfate adenylyltransferase [Solanum tuberosum]
                   39700
Seq. No.
Seq. ID
                   LIB3107-078-Q1-K1-F5
Method
                   BLASTN
                   q1053046
NCBI GI
BLAST score
                   55
                   4.0e-22
E value
                   169
Match length
                   86
% identity
NCBI Description Glycine max histone H3 gene, partial cds, clone S2
```

od BLASTX

39701

LIB3107-078-Q1-K1-G5

Seq. No. Seq. ID

Method



```
NCBI GI
                  g2245109
BLAST score
                  149
E value
                  4.0e-11
Match length
                  114
% identity
                  (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  39702
                  LIB3107-078-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2507421
BLAST score
                  264
E value
                  2.0e-23
Match length
                  61
                  82
% identity
NCBI Description
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >qi 1800277
                  (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi 4490709 emb CAB38843.1 (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
Seq. No.
                  39703
Seq. ID
                  LIB3107-078-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2735764
BLAST score
                  209
E value
                  1.0e-16
Match length
                  49
% identity
                  88
NCBI Description
                  (AF008651) MADS transcriptional factor; STMADS16 [Solanum
                  tuberosum]
                  39704
Seq. No.
Seq. ID
                  LIB3107-079-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3775987
BLAST score
                  391
E value
                  5.0e-38
Match length
                  123
                  72
% identity
NCBI Description
                  (AJ010457) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  39705
Seq. ID
                  LIB3107-079-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g2995380
BLAST score
                  183
                  9.0e-14
E value
Match length
                  80
% identity
                  46
NCBI Description
                  (AJ001903) thioredoxin H [Triticum durum]
Seq. No.
                  39706
Seq. ID
                  LIB3107-079-Q1-K1-D10
Method
```

6188

BLASTX

170

g3810596

NCBI GI

BLAST score



76

% identity

NCBI Description

```
E value
Match length
                   106
% identity
                   (AC005398) reverse-transcriptase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   39707
Seq. No.
                   LIB3107-079-Q1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1619602
BLAST score
                   297
E value
                   6.0e-27
Match length
                   82
% identity
                   65
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                   39708
Seq. No.
                   LIB3107-079-Q1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g130080
BLAST score
                   162
                   4.0e-11
E value
Match length
                   100
% identity
                   25
NCBI Description PHLB PROTEIN PRECURSOR >gi 79140 pir C31390 phlB protein -
                   Serratia liquefaciens
                   39709
Seq. No.
Seq. ID
                   LIB3107-079-Q1-K1-H3
Method
                   BLASTN
                   g1420935
NCBI GI
BLAST score
                   172
                   6.0e-92
E value
Match length
                   275
                   91
% identity
NCBI Description Vigna unguiculata aspartic proteinase mRNA, complete cds
Seq. No.
                   39710
Seq. ID
                   LIB3107-080-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   q4206196
BLAST score
                   172
                   2.0e-12
E value
Match length
                   96
% identity
                   44
NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   39711
Seq. ID
                   LIB3107-080-Q1-K1-B8
Method
                   BLASTX
                   g1173055
NCBI GI
BLAST score
                   181
                   1.0e-24
E value
Match length
                   88
```

60S RIBOSOMAL PROTEIN L11 (L5) >gi 541961 pir__S42497

ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819

Seq. No.

39717





RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_ (X78284) RL5 ribosomal protein [Medicago sativa]

```
39712
Seq. No.
Seq. ID
                  LIB3107-080-Q1-K1-C9
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  290
                   4.0e-26
E value
Match length
                  73
% identity
                  77
                  metallothionein - soybean >gi 228682 prf 1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                   39713
Seq. No.
Seq. ID
                  LIB3107-080-Q1-K1-F2
Method
                  BLASTN
NCBI GI
                   q11575
BLAST score
                   257
                   1.0e-142
E value
                   273
Match length
                   99
% identity
NCBI Description G.max chloroplast DNA for tRNA (Arg)
                   39714
Seq. No.
                   LIB3107-080-Q1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4454471
BLAST score
                   141
E value
                   1.0e-17
Match length
                   86
                   55
% identity
NCBI Description
                   (AC006234) putative G protein coupled receptor [Arabidopsis
                   thaliana]
                   39715
Seq. No.
                   LIB3107-080-Q1-K1-H4
Seq. ID
Method
                   BLASTX
                   g285741
NCBI GI
                   177
BLAST score
                   7.0e-13
E value
Match length
                   80
% identity
                   41
NCBI Description
                  (D14550) EDGP precursor [Daucus carota]
                   39716
Seq. No.
Seq. ID
                   LIB3107-080-Q1-K1-H9
Method
                   BLASTN
                   q4218188
NCBI GI
BLAST score
                   66
                   1.0e-28
E value
                  102
Match length
% identity
                  Glycine max cytosolic glutamine synthetase (gs15) gene
NCBI Description
                   promoter
```

NCBI GI

BLAST score



```
LIB3107-081-Q1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1703478
BLAST score
                  210
                  4.0e-17
E value
Match length
                  81
% identity
                  (U40566) ubiquitin activating enzyme 2 [Arabidopsis
NCBI Description
                  thaliana]
                  39718
Seq. No.
                  LIB3107-082-Q1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543650
BLAST score
                  146
                  2.0e-09
E value
Match length
                  42
                  57
% identity
NCBI Description P48h-10 protein precursor - Zinnia elegans (cv. Envy)
                  39719
Seq. No.
                  LIB3107-082-Q1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169980
BLAST score
                  124
                  2.0e-63
E value
Match length
                  256
% identity
                  88
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                  39720
Seq. No.
                  LIB3107-082-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  234
E value
                  8.0e-20
Match length
                  67
% identity
                  70
                  metallothionein - soybean >gi 228682 prf 1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
Seq. No.
                   39721
                  LIB3107-082-Q1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2444415
                  239
BLAST score
E value
                   1.0e-132
Match length
                   307
% identity
                   94
                  Gleditsia fera NADH dehydrogenase-like protein (ndhF) gene,
NCBI Description
                   chloroplast gene encoding chloroplast protein, partial cds
Seq. No.
                   39722
Seq. ID
                   LIB3107-082-Q1-K1-G11
Method
                   BLASTX
```

6191

g4006891

```
E value 6.0e-10
Match length 56
% identity 55
```

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 39723

Seq. ID LIB3107-082-Q1-K1-G12

Method BLASTN
NCBI GI g1142699
BLAST score 146
E value 2.0e-76
Match length 297
% identity 34

NCBI Description Glycine max satellite STR120-A.1

Seq. No. 39724

Seq. ID LIB3109-001-Q1-K1-C1

Method BLASTN
NCBI GI g3982595
BLAST score 308
E value 1.0e-173
Match length 380
% identity 95

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39725

Seq. ID LIB3109-001-Q1-K1-C2

Method BLASTX
NCBI GI g2245378
BLAST score 555
E value 4.0e-57
Match length 134
% identity 77

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No. 39726

Seq. ID LIB3109-001-Q1-K1-C5

Method BLASTX
NCBI GI g4056506
BLAST score 214
E value 3.0e-17
Match length 116
% identity 43

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 39727

Seq. ID LIB3109-001-Q1-K1-E10

Method BLASTN
NCBI GI g2204063
BLAST score 48
E value 3.0e-18

Match length 72 % identity 92

NCBI Description Pisum sativum mRNA for F1 ATPase, complete cds

Seq. No. 39728

Seq. ID LIB3109-001-Q1-K1-F1

NCBI GI

BLAST score

g340933



```
RLASTX
Method
                  g4027897
NCBI GI
                  155
BLAST score
                  7.0e-11
E value
                  54
Match length
                  57
% identity
                 (AF049353) alpha-expansin precursor [Nicotiana tabacum]
NCBI Description
                  39729
Seq. No.
                  LIB3109-001-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g2665890
NCBI GI
                  265
BLAST score
                  3.0e-23
E value
Match length
                  87
% identity
                  63
                  (AF035944) calcium-dependent protein kinase [Fragaria x
NCBI Description
                  ananassa]
                  39730
Seq. No.
                  LIB3109-001-Q1-K1-G6
Seq. ID
                  BLASTX
Method
                  g3461836
NCBI GI
                  133
BLAST score
                   2.0e-11
E value
Match length
                  79
                   49
% identity
                   (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi 3927841 (AC005727) putative protein kinase [Arabidopsis
                   thaliana]
                   39731
Seq. No.
                   LIB3109-001-Q1-K1-G7
Seq. ID
                   BLASTX
Method
                   g3641837
NCBI GI
                   246
BLAST score
                   4.0e-21
E value
                   86
Match length
% identity
                   56
                   (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   39732
Seq. No.
                   LIB3109-002-Q1-K1-D11
Seq. ID
                   BLASTN
Method
                   g3982595
NCBI GI
                   69
BLAST score
                   2.0e-30
E value
                   253
Match length
                   82
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   39733
Seq. No.
                   LIB3109-002-Q1-K1-E11
Seq. ID
                   BLASTN
Method
```



```
E value
                   1.0e-16
Match length
                  62
% identity
                  94
NCBI Description Zea mays 10-kDa zein gene, complete cds
Seq. No.
                  39734
                  LIB3109-002-Q1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1762148
BLAST score
                  270
E value
                  5.0e-24
Match length
                  77
% identity
                  68
NCBI Description
                  (U48695) glutamate dehydrogenase [Solanum lycopersicum]
Seq. No.
                  39735
                  LIB3109-002-Q1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q939779
BLAST score
                  318
                  2.0e-29
E value
Match length
                  116
% identity
                  59
NCBI Description
                  (L46397) MADS box protein [Zea mays]
Seq. No.
                  39736
                  LIB3109-002-Q1-K1-F12
Seq. ID
Method
                  BLASTN
                  g3982595
NCBI GI
BLAST score
                  319
E value
                  1.0e-179
Match length
                  391
% identity
                  95
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  39737
Seq. ID
                  LIB3109-002-Q1-K1-G10
                  BLASTX
Method
NCBI GI
                  g2961385
BLAST score
                  160
E value
                  7.0e-11
                  70
Match length
% identity
                  49
                  (AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  39738
Seq. ID
                  LIB3109-002-Q1-K2-E1
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  273
                  4.0e-24
E value
                  93
Match length
                  59
% identity
NCBI Description
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
```

5-methyltetrahydropteroyltriglutamate--homocysteine

>gi 2129919 pir S65957



S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

39739 Seq. No.

LIB3109-002-Q1-K2-F6 Seq. ID

Method BLASTX NCBI GI g1931647 255 BLAST score E value 3.0e-22 Match length 93 61 % identity

NCBI Description (U95973) endomembrane protein EMP70 precusor isolog

[Arabidopsis thaliana]

39740 Seq. No.

LIB3109-002-Q1-K3-D1 Seq. ID

Method BLASTN g3982595 NCBI GI BLAST score 279 E value 1.0e-156 Match length 303 98 % identity

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39741

LIB3109-002-Q1-K3-D9 Seq. ID

Method BLASTX NCBI GI q134145 BLAST score 177 1.0e-16 E value 99 Match length % identity 52

STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE NCBI Description

PROTEIN A) >gi_99886_pir__S08511 28K protein - soybean >gi_169898 (M37530) 28 kDa protein [Glycine max] >gi_169975

(M76981) vegetative storage protein [Glycine max]

>gi_226867_prf__1609232B 28kD glycoprotein [Glycine max]
>gi_444325_prf__1906374A vegetative storage protein

[Glycine max]

Seq. No. 39742

Seq. ID LIB3109-002-Q1-K3-E1

Method BLASTX NCBI GI q1814403 BLAST score 197 E value 4.0e-17 Match length 81 % identity 64

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No.

LIB3109-002-Q1-K3-E5 Seq. ID

39743

Method BLASTX g2706450 NCBI GI 194 BLAST score



E value 5.0e-15 Match length 67 % identity 64

NCBI Description (AJ225172) magnesium dependent soluble inorganic

pyrophosphatase [Solanum tuberosum]

Seq. No. 39744

Seq. ID LIB3109-003-Q1-K1-A11

Method BLASTN
NCBI GI g187444
BLAST score 400
E value 0.0e+00
Match length 424
% identity 99

NCBI Description Human pseudo-chlordecone reductase mRNA, complete cds

Seq. No. 39745

Seq. ID LIB3109-003-Q1-K1-B2

Method BLASTN
NCBI GI g12134
BLAST score 51
E value 5.0e-20
Match length 87
% identity 90

NCBI Description Pisum sativum chloroplast psaA1 and psaA2 genes for P700

chlorophyll a-apoproteins (84 and 82 kD polypeptides)

Seq. No. 39746

Seq. ID LIB3109-003-Q1-K1-C3

Method BLASTX
NCBI GI g1709804
BLAST score 239
E value 4.0e-20
Match length 128
% identity 43

NCBI Description 26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED

ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi_2213932 (AF006305) 26S proteasome regulatory subunit

[Homo sapiens]

Seq. No. 39747

Seq. ID LIB3109-005-Q1-K1-A2

Method BLASTN
NCBI GI g3982595
BLAST score 133
E value 1.0e-68
Match length 333
% identity 85

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39748

Seq. ID LIB3109-005-Q1-K1-A4

Method BLASTN
NCBI GI g1778371
BLAST score 96
E value 1.0e-46

E value

Match length

NCBI Description

% identity



```
Match length
% identity
                  83
                  Glycine max asparagine synthetase 1 (AS1) mRNA, complete
NCBI Description
Seq. No.
                  39749
Seq. ID
                  LIB3109-005-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  q4389443
BLAST score
                  165
E value
                  2.0e-11
Match length
                  62
% identity
                  60
                  (AE001574) SPC 21-kDa-like [Drosophila melanogaster]
NCBI Description
                  39750
Seq. No.
                  LIB3109-005-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  334
                  3.0e-31
E value
Match length
                  79
% identity
                  73
NCBI Description
                  metallothionein - soybean >gi_228682_prf__1808316A
                  metallothionein-like protein [Glycine max]
Seq. No.
                  39751
                  LIB3109-005-Q1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1262439
BLAST score
                  150
                  6.0e-79
E value
Match length
                  266
% identity
                  89
NCBI Description Glycine max lipoxygenase (vlxC) mRNA, complete cds
Seq. No.
                  39752
Seq. ID
                  LIB3109-005-Q1-K1-C5
Method
                  BLASTX
                  g1498053
NCBI GI
BLAST score
                  121
E value
                  1.0e-09
Match length
                  60
% identity
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                  39753
Seq. ID
                  LIB3109-005-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  q3776581
BLAST score
                  340
```

6.0e-32

89

74

6197

(AC005388) Similar to Beta integral membrane protein homolog gb U43629 from A. thaliana. [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                   LIB3109-005-Q1-K1-H12
                   BLASTX
Method
NCBI GI
                   q3386596
BLAST score
                   231
E value
                   2.0e-19
                   78
Match length
% identity
                   56
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3702346 (AC005397) unknown protein [Arabidopsis
                   thaliana]
                   39755
Seq. No.
Seq. ID
                   LIB3109-005-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   q4406775
BLAST score
                   161
E value
                   6.0e-11
Match length
                   93
% identity
                   34
NCBI Description
                   (AC006836) unknown protein [Arabidopsis thaliana]
Seq. No.
                   39756
Seq. ID
                   LIB3109-006-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   g1617274
BLAST score
                   204
E value
                   5.0e-25
Match length
                   95
% identity
                   62
NCBI Description
                   (Z72152) AMP-binding protein [Brassica napus]
Seq. No.
                   39757
Seq. ID
                   LIB3109-006-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g2342727
BLAST score
                   145
                                    4
E value
                   3.0e-09
                   40
Match length
                   68
% identity
                   (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   39758
Seq. ID
                   LIB3109-006-Q1-K1-C6
Method
                   BLASTX
NCBI GI
                   g4204793
BLAST score
                   368
E value
                   2.0e-35
Match length
                   117
% identity
                   32
                  (U52079) P-glycoprotein [Solanum tuberosum]
NCBI Description
```

Seq. No. 39759

Seq. ID LIB3109-006-Q1-K1-D9

Method BLASTN NCBI GI g3982595 BLAST score 312



E value 1.0e-175
Match length 356
% identity 97

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39760

Seq. ID LIB3109-006-Q1-K1-F10

Method BLASTN
NCBI GI g166379
BLAST score 37
E value 1.0e-11
Match length 79
% identity 94

NCBI Description Alfalfa glucose-regulated endoplasmic reticular protein

mRNA, complete cds

Seq. No. 39761

Seq. ID LIB3109-006-Q1-K1-F9

Method BLASTX
NCBI GI g3341697
BLAST score 378
E value 2.0e-36
Match length 118
% identity 66

NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No. 39762

Seq. ID LIB3109-007-Q1-K1-A10

Method BLASTN
NCBI GI g35271
BLAST score 205
E value 1.0e-112
Match length 256
% identity 95

NCBI Description Human mRNA for endothelial plasminogen activator inhibitor

(PAI)

Seq. No. 39763

Seq. ID LIB3109-007-Q1-K1-A9

Method BLASTN
NCBI GI g2780413
BLAST score 323
E value 0.0e+00
Match length 335
% identity 99

NCBI Description Homo sapiens mRNA for brain acyl-CoA hydrolase, complete

cds

Seq. No. 39764

Seq. ID LIB3109-007-Q1-K1-C12

Method BLASTN
NCBI GI g1944124
RLAST score 166

BLAST score 166
E value 1.0e-88
Match length 170
% identity 99

NCBI Description Homo sapiens mRNA for Qip1, complete cds



>gi_4504900_ref_NM_002268.1_KPNA4_ Homo sapiens karyopherin alpha 4 (importin alpha 3) (KPNA4) mRNA

Seq. No. 39765 Seq. ID LIB3109-007-Q1-K1-D11 Method BLASTN NCBI GI g1296606 BLAST score 176 E value 2.0e-94 Match length 299 90 % identity NCBI Description H.sapiens mRNS for clathrin-associated protein Seq. No. 39766 Seq. ID LIB3109-007-Q1-K1-E11 Method BLASTN NCBI GI g2280483 BLAST score 351 E value 0.0e + 00Match length 359 % identity 99 NCBI Description Human mRNA for KIAA0372 gene, complete cds Seq. No. 39767 Seq. ID LIB3109-007-Q1-K1-E12 Method BLASTN NCBI GI g34391 BLAST score 182 E value 5.0e-98 Match length 286 % identity 92 NCBI Description Human mRNA for LLRep3 >gi 4506718 ref NM 002952.1 RPS2 Homo sapiens ribosomal protein S2 (RPS2) mRNA Seq. No. 39768 Seq. ID LIB3109-007-Q1-K1-F10 Method BLASTN NCBI GI g33853 BLAST score 103 E value 8.0e-51 Match length 111 % identity 98 NCBI Description Human mRNA for transcription factor ILF Seq. No. 39769 Seq. ID LIB3109-007-Q1-K1-F6 Method BLASTN NCBI GI g3982595 BLAST score 319 E value 1.0e-179 Match length 391 % identity 95 NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds Seq. No.

6200

39770

BLASTN

LIB3109-007-Q1-K1-F9

Seq. ID

Method

BLAST score

E value

278 7.0e-25



```
NCBI GI
                   q401844
BLAST score
                   306
E value
                   1.0e-172
Match length
                   312
                   99
% identity
NCBI Description
                  Homo sapiens ribosomal protein L18a mRNA, complete cds
Seq. No.
                   39771
Seq. ID
                  LIB3109-007-Q1-K1-G10
Method
                  BLASTN
NCBI GI
                   q4309945
BLAST score
                   206
E value
                   1.0e-112
                   214
Match length
% identity
                   99
                  Homo sapiens chromosome 17, clone hRPK.692 E 18, complete
NCBI Description
                   sequence [Homo sapiens]
Seq. No.
                   39772
Seq. ID
                  LIB3109-007-Q1-K1-G11
Method
                  BLASTN
NCBI GI
                  g187109
BLAST score
                   237
E value
                  1.0e-131
Match length
                  260
% identity
                   98
NCBI Description
                  Human 14 kd lectin mRNA, complete cds.
                  >gi_4504980_ref_NM_002305.1_LGALS1_ Homo sapiens lectin,
                   galactoside-binding, soluble, 1 (galectin 1) (LGALS1) mRNA
                  >gi_589939_gb_I07803_ Sequence 5 from Patent EP
Seq. No.
                   39773
Seq. ID
                  LIB3109-007-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                  q1653966
BLAST score
                  148
E value
                   1.0e-09
Match length
                   55
% identity
                  56
NCBI Description
                  (D90917) 47 kD protein [Synechocystis sp.]
Seq. No.
                  39774
Seq. ID
                  LIB3109-007-Q1-K1-H9
Method
                  BLASTN
NCBI GI
                  g777400
BLAST score
                  85
E value
                  5.0e-40
Match length
                  160
                  100
% identity
NCBI Description Human clone mcaq11 chromosome 1 CAG repeat region
Seq. No.
                  39775
Seq. ID
                  LIB3109-009-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g4415917
```



Match length 101 % identity 54

NCBI Description (AC006282) putative protein containing zinc finger domain

[Arabidopsis thaliana]

Seq. No. 39776

Seq. ID LIB3109-009-Q1-K1-D8

Method BLASTX
NCBI GI g3047082
BLAST score 433
E value 2.0e-45
Match length 117
% identity 75

NCBI Description (AF058914) similar to Vigna radiata pectinacetylesterase

precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No. 39777

Seq. ID LIB3109-009-Q1-K1-E4

Method BLASTX
NCBI GI g1743354
BLAST score 291
E value 2.0e-26
Match length 108
% identity 52

NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.

Seq. ID LIB3109-009-Q1-K1-F8

39778

Method BLASTN
NCBI GI g3982595
BLAST score 356
E value 0.0e+00
Match length 379
% identity 99

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.

39779

-Seq. ID LIB3109-009-Q1-K1-H5

Method BLASTX
NCBI GI g2736186
BLAST score 277
E value 9.0e-25
Match length 67
% identity 84

NCBI Description (AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No.

39780

Seq. ID LIB3109-009-Q1-K1-H7

Method BLASTN
NCBI GI g1694899
BLAST score 122
E value 4.0e-62
Match length 240
% identity 94

NCBI Description P.sativum mRNA for Cop1 protein

Seq. No.

```
Seq. ID
                   LIB3109-010-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g2947059
                   <u>1</u>72
BLAST score
E value
                   2.0e-12
Match length
                   110
% identity
                   45
NCBI Description
                   (AC002521) similar to myb transforming protein [Arabidopsis
                   thaliana]
                   39782
Seq. No.
Seq. ID
                   LIB3109-010-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   q4559330
BLAST score
                   216
E value
                   1.0e-17
Match length
                   84
% identity
                   50
NCBI Description
                  (AC007087) unknown protein [Arabidopsis thaliana]
Seq. No.
                   39783
Seq. ID
                   LIB3109-010-Q1-K1-H2
Method
                   BLASTX
NCBI GI
                   g2252868
BLAST score
                   286
E value
                   1.0e-25
Match length
                   88
% identity
                   67
NCBI Description
                   (AF013294) No definition line found [Arabidopsis thaliana]
Seq. No.
                   39784
Seq. ID
                   LIB3109-010-Q1-K1-H4
Method
                   BLASTN
NCBI GI
                   g4204762
BLAST score
                   288
E value
                   1.0e-161
Match length
                   386
% identity
                   98
NCBI Description
                  Glycine max peroxidase (sEPb1) mRNA, partial cds
Seq. No.
                  39785
Seq. ID
                  LIB3109-011-Q1-K1-A8
Method
                  BLASTX
```

غد .

NCBI GI g2529670
BLAST score 146
E value 3.0e-09
Match length 59
% identity 58

NCBI Description (AC002535) ribosomal protein L18-like [Arabidopsis

thaliana]

Seq. No. 39786

Seq. ID LIB3109-011-Q1-K1-B12

Method BLASTN
NCBI GI g4204764
BLAST score 33
E value 2.0e-09



Match length % identity 85

NCBI Description Glycine max peroxidase (sEPb2) mRNA, partial cds

Seq. No. 39787

Seq. ID LIB3109-011-Q1-K1-C11

Method BLASTN NCBI GI q310575 BLAST score 154 E value 3.0e-81 Match length 294 % identity 90

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 39788

Seq. ID LIB3109-011-Q1-K1-G5

Method BLASTN NCBI GI g3378649 BLAST score 133 E value 1.0e-68 Match length 341 % identity 85

NCBI Description M.sativa mRNA translated from abscisic activated gene

Seq. No. 39789

Seq. ID LIB3109-011-Q1-K1-G7

Method BLASTX NCBI GI g134145 BLAST score 142 E value 4.0e-09 Match length 65 % identity 51

NCBI Description STEM 28 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE

PROTEIN A) >gi_99886_pir__S08511 28K protein - soybean

>gi 169898 (M3 $\overline{7}$ 530) $\overline{28}$ k \overline{Da} protein [Glycine max] $\overline{>}$ gi_169975

(M76981) vegetative storage protein [Glycine max]

>gi_226867_prf__1609232B 28kD glycoprotein [Glycine max]
>gi_444325_prf__1906374A vegetative storage protein

[Glycine max]

Seq. No. 39790

Seq. ID LIB3109-011-Q1-K1-H6 Method

BLASTN NCBI GI g169974 BLAST score 354 E value 0.0e + 00Match length 414 % identity 96

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 39791

Seq. ID LIB3109-012-Q1-K1-A1

Method BLASTX NCBI GI g541943 BLAST score 150 E value 2.0e-12 Match length 70



% identity NCBI Description metallothionein - soybean >gi_228682 prf 1808316A metallothionein-like protein [Glycine max] Seq. No. 39792 Seq. ID LIB3109-012-Q1-K1-A4 Method

BLASTX NCBI GI g3831456 BLAST score 420 E value 2.0e-41 Match length 134 % identity 60

(AC005700) putative ion channel protein [Arabidopsis NCBI Description

thaliana]

39793 Seq. No.

Seq. ID LIB3109-012-Q1-K1-B11

Method BLASTN NCBI GI g186803 BLAST score 165 E value 6.0e-88 Match length 257 % identity

NCBI Description Human tumor antigen (L6) mRNA, complete cds.

>gi_1825088_gb_I34297_I34297 Sequence 1 from patent US

Seq. No. 39794

Seq. ID LIB3109-012-Q1-K1-C11

Method BLASTN NCBI GI g562073 BLAST score 62 E value 2.0e-26 Match length 126 % identity 87

NCBI Description Human ribosomal protein L35 mRNA, complete cds

Seq. No. 39795

Seq. ID LIB3109-012-Q1-K1-E5

Method BLASTX NCBI GI g3510253 BLAST score 181 E value 2.0e-13 Match length 59 % identity 53

NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.

39796 Seq. ID LIB3109-012-Q1-K1-F10

Method BLASTN NCBI GI g455418 BLAST score 140 E value 4.0e-73 Match length 200 % identity 93

NCBI Description H.sapiens PR264 gene

Seq. No. 39797



```
Seq. ID
                   LIB3109-012-Q1-K1-F11
 Method
                   BLASTN
 NCBI GI
                   g36512
BLAST score
                   342
 E value
                   0.0e+00
Match length
                   342
 % identity
                   100
NCBI Description H.sapiens RNA for snRNP protein B
Seq. No.
                   39798
Seq. ID
                   LIB3109-012-Q1-K1-F3
Method
                   BLASTN
NCBI GI
                   q169974
BLAST score
                   204
E value
                   1.0e-111
Match length
                   320
% identity
                   91
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   39799
Seq. ID
                   LIB3109-012-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g585775
BLAST score
                   173
E value
                   2.0e-12
Match length
                   91
% identity
                   42
NCBI Description
                   RAB PROTEINS GERANYLGERANYLTRANSFERASE COMPONENT A 1 (RAB
                   ESCORT PROTEIN 1) (REP-1) >gi_476796_pir__A40686 Rab
                   geranylgeranyl transferase component A, Rab escort protein,
                   REP - rat >gi_347439 (L13722) RAB geranylgeranyl
                   transferase component A [Rattus norvegicus]
Seq. No.
                   39800
Seq. ID
                  LIB3109-012-Q1-K1-H11
Method
                  BLASTN
NCBI GI
                  g36145
BLAST score
                  283
E value
                  1.0e-158
Match length
                  311
% identity
NCBI Description
                  Human mRNA for ribosomal protein S12
                  >gi_4506682_ref_NM_001016.1_RPS12_ Homo sapiens ribosomal
                  protein S12 (RPS12) mRNA
Seq. No.
                  39801
Seq. ID
                  LIB3109-012-Q1-K1-H9
Method
                  BLASTN
NCBI GI
                  q32336
BLAST score
                  72
E value
                  1.0e-32
Match length
                  120
% identity
NCBI Description Human hmgI mRNA for high mobility group protein I
```

Seq. No. 39802

Seq. ID LIB3109-013-Q1-K1-A3

% identity



```
Method
 NCBI GI
                    g1839188
 BLAST score
                    279
 E value
                    2.0e-25
 Match length
                    66
 % identity
                    79
 NCBI Description
                   (U86081) root hair defective 3 [Arabidopsis thaliana]
 Seq. No.
                   39803
 Seq. ID
                   LIB3109-013-Q1-K1-C11
Method
                   BLASTN
NCBI GI
                   q1872159
BLAST score
                   121
 E value
                   2.0e-61
Match length
                   233
 % identity
                   88
NCBI Description Z.mays plastid mRNA for ORF170
                   39804
Seq. No.
Seq. ID
                   LIB3109-013-Q1-K1-G1
Method
                   {\tt BLASTX}
NCBI GI
                   g4539330
BLAST score
                   359
E value
                   2.0e-34
Match length
                   106
% identity
                   65
NCBI Description
                   (AL035679) putative receptor-like protein kinase (fragment)
                   [Arabidopsis thaliana]
Seq. No.
                   39805
Seq. ID
                   LIB3109-013-Q1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3452497
BLAST score
                   290
E value
                   2.0e-26
Match length
                   84
% identity
                   73
NCBI Description
                   (Y17796) ketol-acid reductoisomerase [Pisum sativum]
Seq. No.
                   39806
Seq. ID
                   LIB3109-014-Q1-K1-D1
Method
                   BLASTN
NCBI GI
                   g310575
BLAST score
                   230
E value
                   1.0e-126
Match length
                   391
% identity
                   92
NCBI Description Glycine max nodulin-26 mRNA, complete cds
Seq. No.
                   39807
Seq. ID
                   LIB3109-014-Q1-K1-D6
Method
                   BLASTX
NCBI GI
                   g4539369
BLAST score
                   190
E value
                   2.0e-14
Match length
                   93
```

```
NCBI Description
                  (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                  39808
Seq. ID
                  LIB3109-014-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  167
E value
                  1.0e-11
Match length
                  61
% identity
                  51
                  metallothionein - soybean >gi 228682 prf 1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
Seq. No.
                  39809
Seq. ID
                  LIB3109-014-Q1-K1-H4
Method
                  BLASTN
NCBI GI
                  g21952
BLAST score
                  83
E value
                  8.0e-39
Match length
                  215
```

% identity 85
NCBI Description T.repens mRNA for cyanogenic beta-glucosidase (linamarase)

Seq. No. 39810

Seq. ID LIB3109-014-Q1-K1-H8

Method BLASTN
NCBI GI g558628
BLAST score 49
E value 1.0e-18
Match length 167
% identity 89

NCBI Description P.vulgaris mRNA for RNP1 chloroplast RNA binding protein

Seq. No. 39811

Seq. ID LIB3109-015-Q1-K1-A10

Method BLASTX
NCBI GI g4220527
BLAST score 212
E value 4.0e-17
Match length 92
% identity 52

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 39812

Seq. ID LIB3109-015-Q1-K1-A8

Method BLASTX
NCBI GI g3540184
BLAST score 360
E value 2.0e-34
Match length 116
% identity 29

NCBI Description (AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No. 39813

Seq. ID LIB3109-015-Q1-K1-C12

Method BLASTX NCBI GI g4164408

Seq. No.

39819



```
BLAST score
  E valué
                    5.0e-49
  Match length
                    112
  % identity
                    79
 NCBI Description
                    (AJ132228) amino acid carrier [Ricinus communis]
                    39814
 Seq. No.
 Seq. ID
                    LIB3109-015-Q1-K1-G11
 Method
                    BLASTX
 NCBI GI
                    g2576255
 BLAST score
                    199
 E value
                    2.0e-17
 Match length
                    85
 % identity
                    60
 NCBI Description
                    (AJ001729) TH65 protein [Arabidopsis thaliana]
 Seq. No.
                    39815
 Seq. ID
                    LIB3109-015-Q1-K1-G4
 Method
                    BLASTN
 NCBI GI
                    g4204764
 BLAST score
                    93
 E value
                    6.0e-45
 Match length
                    173
 % identity
                    92
 NCBI Description
                   Glycine max peroxidase (sEPb2) mRNA, partial cds
 Seq. No.
                    39816
 Seq. ID
                    LIB3109-016-Q1-K1-C11
 Method
                    BLASTX
 NCBI GI
                    g3128209
 BLAST score
                    173
 E value
                    2.0e-12
 Match length
                    113
                    44
 % identity
 NCBI Description
                   (AC004077) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    39817
 Seq. ID
                    LIB3109-016-Q1-K1-D4
 Method
                   BLASTX
 NCBI GI
                    g4432844
 BLAST score
                    369
 E value
                    2.0e-35
 Match length
                    87
 % identity
                    76
 NCBI Description
                   (AC006283) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   39818
 Seq. ID
                   LIB3109-016-Q1-K1-F11
Method
                   BLASTX
NCBI GI
                   g2894378
BLAST score
                   316
E value
                   2.0e-29
Match length
                   84
% identity
NCBI Description
                   (Y14573) putative ribophorin I homologue [Hordeum vulgare]
```



Seq. ID LIB3109-016-Q1-K1-G12

Method BLASTX
NCBI GI g124202
BLAST score 263
E value 5.0e-23
Match length 83
% identity 65

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT

(EIF-2-ALPHA) >gi_92416_pir__A26711 translation initiation factor eIF-2 alpha chain - rat >gi_108753_pir__S18461 translation initiation factor eIF-2 alpha chain - bovine >gi_325_emb_CAA37728_ (X53689) initiation factor 2 alpha [Bos taurus] >gi_204002 (J02646) translational initiation factor eIF-2 alpha exhautter eIF-2 alpha eXha

factor eIF-2, alpha subunit [Rattus norvegicus]

Seq. No. 39820

Seq. ID LIB3109-016-Q1-K3-E3

Method BLASTX
NCBI GI g729442
BLAST score 251
E value 1.0e-21
Match length 103
% identity 33

NCBI Description PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR

>gi_166380 (M80235) glucose-regulated endoplasmic reticular

protein precursor [Medicago sativa]

Seq. No. 39821

Seq. ID LIB3109-016-Q1-K3-F5

Method BLASTX
NCBI GI g3183088
BLAST score 154
E value 4.0e-10
Match length 74
% identity 49

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR

(LTP) >gi_629658_pir__S47084 lipid transfer like protein -cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 39822

Seq. ID LIB3109-017-Q1-K1-A1

Method BLASTN
NCBI GI g169974
BLAST score 130
E value 4.0e-67
Match length 206
% identity 91

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 39823

Seq. ID LIB3109-017-Q1-K1-C6

Method BLASTX
NCBI GI g3639089
BLAST score 142
E value 9.0e-09
Match length 101



% identity

NCBI Description (AF090445) phospholipase D1 [Brassica oleracea]

>gi_4324969_gb_AAD17208_ (AF113918) phospholipase D1
[Brassica oleracea var. capitata]

Seq. No. 39824

Seq. ID LIB3109-017-Q1-K1-G6

Method BLASTX NCBI GI q416829 BLAST score 173 E value 5.0e-13 Match length 55 % identity 60

NCBI Description CYTOCHROME C OXIDASE POLYPEPTIDE II PRECURSOR

>gi_320102_pir__S28027 cytochrome-c oxidase (EC 1.9.3.1)

chain II precursor - soybean (fragment)

>gi_18570_emb_CAA78032_ (Z11980) cytochrome oxidase

subunit 2 [Glycine max]

Seq. No. 39825

Seq. ID LIB3109-017-Q1-K2-H5

Method BLASTN NCBI GI q3982595 BLAST score 115 E value 5.0e-58 Match length 178 % identity

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39826

Seq. ID LIB3109-018-Q1-K1-B1

Method BLASTX NCBI GI g2702281 BLAST score 276 2.0e-24 E value Match length 96 % identity 33

NCBI Description (AC003033) putative protein disulfide isomerase precursor

[Arabidopsis thaliana]

Seq. No.

39827

Seq. ID LIB3109-018-Q1-K1-B10 Method

BLASTN NCBI GI g1150683 BLAST score 38 E value 3.0e-12 Match length 103 % identity 90

NCBI Description V.radiata atpB, rbcL and trnK genes

Seq. No.

39828

Seq. ID LIB3109-018-Q1-K1-B11

Method BLASTN NCBI GI g3176695 BLAST score 34 E value 5.0e-10 Match length 54



% identity NCBI Description Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana] Seq. No. 39829 Seq. ID LIB3109-018-Q1-K1-C1 Method BLASTX NCBI GI g3510538 BLAST score 178 4.0e-13 E value Match length 75 % identity 44 NCBI Description (U93167) expansin [Prunus armeniaca] Seq. No. 39830 Seq. ID LIB3109-018-Q1-K1-C10 Method BLASTX NCBI GI q1123105 BLAST score 144 E value 4.0e-09 Match length 111 % identity 31 NCBI Description (U42438) similar to S. cerevisiae longevity-assurance protein 1 (SP:P38703) [Caenorhabditis elegans] Seq. No. 39831 Seq. ID LIB3109-018-01-K1-E5 Method BLASTN NCBI GI g14026 BLAST score 53 2.0e-21 E value Match length 108 % identity 87 NCBI Description O.berteriana mitochondrial gene for protein involved in cytochrome c biogenesis Seq. No. 39832 Seq. ID LIB3109-018-Q1-K1-E7 Method BLASTX NCBI GI g1171979 BLAST score 337 E value 8.0e-32

Match length 104 % identity 17

POLYADENYLATE-BINDING PROTEIN 5 (POLY(A) BINDING PROTEIN 5) NCBI Description

(PABP 5) $>gi_166786$ (M97657) poly(A)-binding protein

[Arabidopsis thaliana]

Seq. No. 39833

Seq. ID LIB3109-018-Q1-K1-E8

Method BLASTX NCBI GI g3128209 BLAST score 182 E value 2.0e-22 Match length 95 % identity 65

```
NCBI Description
                  (AC004077) unknown protein [Arabidopsis thaliana]
Seq. No.
                   39834
Seq. ID
                   LIB3109-018-Q1-K1-H2
Method
                   BLASTN
NCBI GI
                   g2738999
BLAST score
                   189
E value
                   1.0e-102
Match length
                   321
% identity
                   90
NCBI Description
                   Glycine max cytochrome P450 monooxygenase CYP71D10p
                   (CYP71D10) mRNA, complete cds
Seq. No.
                   39835
Seq. ID
                   LIB3109-019-Q1-K1-A1
Method
                   BLASTX
NCBI GI
                   g4191789
BLAST score
                   533
E value
                   1.0e-54
Match length
                   142
% identity
                   79
NCBI Description
                   (AC005917) putative transmembrane transport protein
                   [Arabidopsis thaliana]
Seq. No.
                   39836
Seq. ID
                   LIB3109-019-Q1-K1-B9
Method
                  BLASTN
NCBI GI
                   g3982595
BLAST score
                   80
E value
                  3.0e-37
Match length
                  118
                  96
% identity
NCBI Description
                  Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  39837
Seq. ID
                  LIB3109-019-Q1-K1-C5
Method
                  BLASTN
                  g170089
                  62
```

NCBI GI BLAST score E value 3.0e-26 Match length 239 % identity 85

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No.

39838

Seq. ID

LIB3109-019-Q1-K1-H7

Method BLASTX NCBI GI q416829 BLAST score 113 E value 6.0e-09 Match length 105 % identity 36

NCBI Description CYTOCHROME C OXIDASE POLYPEPTIDE II PRECURSOR

>gi_320102_pir__S28027 cytochrome-c oxidase (EC 1.9.3.1)

chain II precursor - soybean (fragment)

>gi_18570_emb_CAA78032_ (Z11980) cytochrome oxidase

subunit 2 [Glycine max]



```
Seq. No.
                   39839
Seq. ID
                   LIB3109-020-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   g4455787
BLAST score
                   161
E value
                   5.0e-11
Match length
                   97
% identity
                   34
NCBI Description
                   (AL035536) putative DNA polymerase accessory protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   39840
Seq. ID
                   LIB3109-020-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   q4056506
BLAST score
                   186
E value
                   6.0e-14
Match length
                   131
% identity
                   34
                  (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   39841
Seq. ID
                   LIB3109-020-Q1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2505870
BLAST score
                   202
E value
                   9.0e-16
Match length
                   54
% identity
                  70
NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  39842
Seq. ID
                  LIB3109-020-Q1-K1-D2
Method
                  BLASTN
NCBI GI
                  g3982595
BLAST score
                  374
E value
                  0.0e+00
Match length
                  392
% identity
                  99
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  39843
Seq. ID
                  LIB3109-020-Q1-K1-D9
Method
                  BLASTN
NCBI GI
                  g3982595
BLAST score
                  225
E value
                  1.0e-123
Match length
                  336
% identity
                  93
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  39844
```

Seq. ID LIB3109-020-Q1-K1-E10

Method BLASTX NCBI GI g140474 BLAST score 168



E value 8.0e-12 Match length 70 % identity 44

NCBI Description HYPOTHETICAL 69.2 KD PROTEIN IN HSP30-PMP1 INTERGENIC REGION >gi_83212 pir S19434 probable transport protein

YCR023c - yeast (Saccharomyces cerevisiae)

>gi_1907167_emb_CAA42315_ (X59720) YCR023c, len:611

[Saccharomyces cerevisiae]

Seq. No. 39845

Seq. ID LIB3109-020-Q1-K1-E7

Method BLASTX
NCBI GI g2072986
BLAST score 207
E value 1.0e-29
Match length 89

% identity 75

NCBI Description (U95142) putative G-protein-coupled receptor [Arabidopsis

thaliana] >gi_2072988 (U95143) putative G-protein-coupled

receptor [Arabidopsis thaliana]

Seq. No. 39846

Seq. ID LIB3109-020-Q1-K1-F9

Method BLASTN
NCBI GI g2815245
BLAST score 86
E value 1.0e-40
Match length 242
% identity 84

NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:

CanMT-2)

Seq. No. 39847

Seq. ID LIB3109-020-Q1-K1-G11

Method BLASTN
NCBI GI 94204762
BLAST score 155
E value 1.0e-81
Match length 229
% identity 95

NCBI Description Glycine max peroxidase (sEPb1) mRNA, partial cds

Seq. No. 39848

Seq. ID LIB3109-021-Q1-K1-A3

Method BLASTN
NCBI GI g170089
BLAST score 317
E value 1.0e-178
Match length 353
% identity 98

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 39849

Seq. ID LIB3109-021-Q1-K1-C10

Method BLASTN NCBI GI g3982595 BLAST score 139

E value

Match length

% identity



E value 3.0e-72 Match length 195 % identity 93 NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds Seq. No. 39850 Seq. ID LIB3109-021-Q1-K1-D10 Method BLASTX NCBI GI q1946265 BLAST score 158 E value 9.0e-18 Match length 85 % identity 58 NCBI Description (Y11414) myb [Oryza sativa] Seq. No. 39851 Seq. ID LIB3109-021-Q1-K1-F2 Method BLASTX NCBI GI g3877368 BLAST score 140 E value 1.0e-08 Match length 63 % identity 48 NCBI Description (Z68227) cDNA EST EMBL:T01259 comes from this gene; cDNA EST EMBL: D71316 comes from this gene; cDNA EST EMBL: D73984 comes from this gene; cDNA EST EMBL:C07316 comes from this gene; cDNA EST EMBL: C08642 comes from this gene; cDN Seq. No. 39852 Seq. ID LIB3109-021-Q1-K1-G7 Method BLASTX NCBI GI g4164408 BLAST score 166 E value 1.0e-11 Match length 72 % identity 53 NCBI Description (AJ132228) amino acid carrier [Ricinus communis] Seq. No. 39853 Seq. ID LIB3109-021-Q1-K2-B5 Method BLASTX NCBI GI g3559805 BLAST score 172 E value 1.0e-12 Match length 63 % identity 56 NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana] Seq. No. 39854 Seq. ID LIB3109-021-Q1-K2-C6 Method BLASTN NCBI GI g3982595 BLAST score 296

6216

1.0e-166

402

93

NCBI Description

thaliana]





```
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
 Seq. No.
                   39855
 Seq. ID
                   LIB3109-021-Q1-K2-C9
 Method
                   BLASTN
 NCBI GI
                   g3982595
BLAST score
                   267
E value
                   1.0e-148
Match length
                   391
 % identity
                   92
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                   39856
Seq. ID
                   LIB3109-021-Q1-K3-A9
Method
                   BLASTX
NCBI GI
                   g3096949
BLAST score
                   260
E value
                   8.0e-23
Match length
                   98
% identity
                   54
NCBI Description
                   (Y16328) putative cyclic nucleotide-regulated ion channel
                   [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
Seq. No.
                   39857
Seq. ID
                   LIB3109-021-Q1-K3-C9
Method
                   BLASTN
NCBI GI
                   g3982595
BLAST score
                   246
E value
                   1.0e-136
Match length
                  306
% identity
                   95
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                   39858
Seq. ID
                  LIB3109-021-Q1-K3-F11
Method
                  BLASTX
                                                           .,54.
NCBI GI
                  g118490
BLAST score
                  162
                  2.0e-11
E value
Match length
                  66
% identity
                   48
NCBI Description
                  BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)
                  >gi_99517_pir__S19135 betaine-aldehyde dehydrogenase (EC
                  1.2.1.8) precursor - beet >gi_17934_emb_CAA41377_ (X58463)
                  betaine aldehyd dehydrogenase [Beta vulgaris]
Seq. No.
                  39859
                  LIB3109-022-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3236241
BLAST score
                  335
E value
                  2.0e-31
Match length
                  76
% identity
```

(AC004684) putative zinc finger protein [Arabidopsis



```
Seq. No.
                    39860
Seq. ID
                    LIB3109-022-Q1-K1-B5
Method
                    BLASTN
NCBI GI
                    q3982595
BLAST score
                    282
                    1.0e-157
E value
                     404
Match length
% identity
                     92
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                     39861
Seq. No.
Seq. ID
                    LIB3109-022-Q1-K1-B7
Method
                    BLASTX
NCBI GI
                    g1827635
                    144
BLAST score
                     2.0e-09
E value
Match length
                     76
% identity
                     43
NCBI Description
                    Chain A, Kidney Bean Purple Acid Phosphatase
                    >gi_1827636_pdb_1KBP_B Chain B, Kidney Bean Purple Acid
Phosphatase >gi_1827637_pdb_1KBP_C Chain C, Kidney Bean
Purple Acid Phosphatase >gi_1827638_pdb_1KBP_D Chain D,
Kidney Bean Purple Acid Phosphatase >gi_1942856_pdb_3KBP_A
                     Chain A, Kidney Bean Purple Acid Phosphatase
                     >gi_1942857_pdb_3KBP_B Chain B, Kidney Bean Purple Acid
                     Phosphatase >gi_1942858_pdb_3KBP_C Chain C, Kidney Bean
                     Purple Acid Phosphatase >gi_1942859_pdb_3KBP_D Chain D,
                     Kidney Bean Purple Acid Phosphatase >gi 1942864 pdb 4KBP A
                     Chain A, Kidney Bean Purple Acid Phosphatase
                     >gi_1942865 pdb 4KBP_B Chain B, Kidney Bean Purple Acid
                     Phosphatase >gi_1942866_pdb_4KBP_C Chain C, Kidney Bean
                     Purple Acid Phosphatase >gi_1942867_pdb_4KBP_D Chain D,
                     Kidney Bean Purple Acid Phosphatase
Seq. No.
                     39862
                    LIB3109-022-Q1-K1-D4
Seq. ID
Method
                     BLASTX
NCBI GI
                     g3832528
BLAST score
                    161
E value
                     1.0e-11
                    65
Match length
% identity
                     55
NCBI Description (AF100167) unknown [Glycine max]
Seq. No.
                     39863
                    LIB3109-022-Q1-K1-F3
Seq. ID
```

Method BLASTN
NCBI GI g170041
BLAST score 138
E value 1.0e-71
Match length 285
% identity 93

NCBI Description Glycine max cv Prize protein kinase mRNA

Seq. No. 39864

Seq. ID LIB3109-022-Q1-K1-G1

E value

Match length

% identity

1.0e-18

NCBI Description hypothetical protein - tomato

118

39



```
Method
                    BLASTX
 NCBI GI
                    g1708236
 BLAST score
                    173
 E value
                    2.0e-12
 Match length
                    99
 % identity
                    41
 NCBI Description
                   HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
                    (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase
                    (EC 4.1.3.5) - Arabidopsis thaliana
                   >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                   >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA
                   synthase [Arabidopsis thaliana]
Seq. No.
                   39865
Seq. ID
                   LIB3109-022-Q1-K1-H1
Method
                   BLASTN
NCBI GI
                   g166379
BLAST score
                   46
E value
                   9.0e-17
Match length
                   94
% identity
                   87
NCBI Description
                   Alfalfa glucose-regulated endoplasmic reticular protein
                   mRNA, complete cds
Seq. No.
                   39866
Seq. ID
                   LIB3109-022-Q1-K1-H4
Method
                   BLASTX
NCBI GI
                   g541943
BLAST score
                   283
E value
                   3.0e-25
Match length
                   72
% identity
                   69
NCBI Description
                   metallothionein - soybean >gi_228682 prf _1808316A
                   metallothionein-like protein [Glycine max]
Seq. No.
                   39867
Seq. ID
                   LIB3109-022-Q1-K1-H6
Method
                   BLASTX
NCBI GI
                   g2459420
BLAST score
                   605
E value
                   5.0e-63
Match length
                   117
% identity
NCBI Description
                   (AC002332) putative ribosomal protein L17 [Arabidopsis
                   thaliana]
Seq. No.
                   39868
Seq. ID
                  LIB3109-022-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g629669
BLAST score
                  227
```



```
Seq. No.
                    39869
 Seq. ID
                   LIB3109-027-Q1-K1-C9
 Method
                   BLASTN
 NCBI GI
                   g3982595
 BLAST score
                   273
 E value
                   1.0e-152
 Match length
                   313
 % identity
                   97
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
 Seq. No.
                   39870
 Seq. ID
                   LIB3109-027-Q1-K1-D7
Method
                   BLASTX
NCBI GI
                   g3402722
BLAST score
                   454
E value
                   1.0e-45
Match length
                   101
% identity
                   83
NCBI Description
                   (AC004261) CPDK-related protein [Arabidopsis thaliana]
Seq. No.
                   39871
Seq. ID
                   LIB3109-027-Q1-K1-E8
Method
                   BLASTN
NCBI GI
                   g169974
BLAST score
                   148
E value
                   9.0e-78
Match length
                   220
% identity
                   92
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   39872
Seq. ID
                   LIB3109-027-Q1-K1-F3
Method
                   BLASTN
NCBI GI
                   g547507
BLAST score
                   117
E value
                   4.0e-59
Match length
                   137
% identity
                   97
NCBI Description G.max mRNA for glutamine synthetase
Seq. No.
                   39873
                   LIB3109-028-Q1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4468979
BLAST score
                   264
E value
                   4.0e-23
Match length
                   65
% identity
                  75
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                  39874
Seq. ID
                  LIB3109-028-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3687654
BLAST score
```

179

1.0e-13

E value



```
Match length
% identity
                   52
NCBI Description
                   thaliana]
Seq. No.
```

(AF047975) putative ethylene receptor; ETR2 [Arabidopsis

39875

LIB3109-028-Q1-K1-C8 Seq. ID Method BLASTX NCBI GI q1778378

BLAST score 197 E value 5.0e-17 Match length 84 % identity 56

NCBI Description (U81289) NAP1Ps [Pisum sativum]

Seq. No. 39876

Seq. ID LIB3109-028-Q1-K1-E10

Method BLASTX NCBI GI g3914472 BLAST score 253 E value 9.0e-22 Match length 62 % identity 79

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

>gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No.

39877

Seq. ID LIB3109-028-Q1-K1-E9

Method BLASTN NCBI GI g4063535 BLAST score 78 E value 9.0e-36 Match length 121 % identity 91

NCBI Description Capparis spinosa ATP synthase beta subunit (atpB) gene, chloroplast gene encoding chloroplast protein, partial cds

Seq. No.

39878

Seq. ID

LIB3109-028-Q1-K1-G9

Method BLASTX NCBI GI g2961378 BLAST score 219 E value 5.0e-18 Match length 97 % identity

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No.

39879

Seq. ID

LIB3109-028-Q1-K1-H1

Method BLASTX NCBI GI q4185507 BLAST score 310 E value 2.0e-28 Match length 121 % identity 53



NCBI Description (AF100163) EZA1 [Arabidopsis thaliana]

Seq. No. 39880

Seq. ID LIB3109-028-Q1-K1-H2

Method BLASTX
NCBI GI 9462138
BLAST score 177
E value 2.0e-13
Match length 63
% identity 62

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi_169091 (L07500) glyceraldehyde-3-phosphate

dehydrogenase [Pisum sativum] >gi_1345567_emb_CAA51675_

(X73150) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Pisum sativum]

Seq. No. 39881

Seq. ID LIB3109-029-Q1-K1-F3

Method BLASTN
NCBI GI g3982595
BLAST score 35
E value 3.0e-10
Match length 75
% identity 87

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39882

Seq. ID LIB3109-030-Q1-K1-A9

Method BLASTX
NCBI GI g2342683
BLAST score 201
E value 5.0e-16
Match length 87

% identity 53

NCBI Description (AC000106) Contains similarity to Bos beta-mannosidase

(gb_U46067). [Arabidopsis thaliana]

Seq. No. 39883

Seq. ID LIB3109-030-Q1-K1-B9

Method BLASTX
NCBI GI g3982596
BLAST score 178
E value 1.0e-13
Match length 63
% identity 67

NCBI Description (AF039027) cationic peroxidase 2 [Glycine max]

Seq. No. 39884

Seq. ID LIB3109-030-Q1-K1-C11

Method BLASTX
NCBI GI g1616659
BLAST score 205
E value 1.0e-16
Match length 58
% identity 69

NCBI Description (U49387) adenylosuccinate synthetase [Triticum aestivum]

Seq. No.

Seq. ID

Method

39890

BLASTN

LIB3109-031-Q1-K1-C12



```
Seq. No.
Seq. ID
                   LIB3109-030-Q1-K1-H11
Method
                   BLASTN
NCBI GI
                   g4204764
BLAST score
                   38
E value
                   2.0e-12
Match length
                   70
% identity
                   89
NCBI Description Glycine max peroxidase (sEPb2) mRNA, partial cds
                   39886
Seq. No.
Seq. ID
                   LIB3109-031-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   g1352345
BLAST score
                   213
E value
                   3.0e-17
Match length
                   109
                   47
% identity
NCBI Description
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                   >gi_18765_emb_CAA40182_ (X56856) eEF-1a [Glycine max]
Seq. No.
                   39887
Seq. ID
                   LIB3109-031-Q1-K1-A7
Method
                   BLASTN
NCBI GI
                   g16508
BLAST score
                   98
E value
                   7.0e-48
Match length
                   214
% identity
                   86
NCBI Description
                  A.thaliana DNA for S-adenosylmethionine synthetase gene
                   sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana
                   S-adenosylmethionine synthetase gene, complete cds
Seq. No.
                   39888
Seq. ID
                  LIB3109-031-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                  g541943
BLAST score
                   161
E value
                   6.0e-11
Match length
                   37
% identity
NCBI Description
                  metallothionein - soybean >gi_228682_prf_ 1808316A
                  metallothionein-like protein [Glycine max]
Seq. No.
                  39889
Seq. ID
                  LIB3109-031-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g3688162
BLAST score
                  267
E value
                  2.0e-23
Match length
                  77
% identity
                  42
NCBI Description
                  (AJ009672) centrin [Arabidopsis thaliana]
```

6223



```
q170053
NCBI GI
BLAST score
                  191
                  1.0e-103
E value
Match length
                   231
% identity
                   96
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
Seq. No.
                  39891
Seq. ID
                  LIB3109-031-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q2462925
BLAST score
                  444
E value
                  3.0e-44
Match length
                  140
% identity
                   63
NCBI Description
                   (AJ000053) GTP cyclohydrolase II /
                   3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                   thaliana]
Seq. No.
                  39892
Seq. ID
                  LIB3109-031-Q1-K1-F1
Method
                  BLASTN
NCBI GI
                  g2979540
BLAST score
                  57
E value
                  3.0e-23
Match length
                  161
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17K2 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  39893
Seq. ID
                  LIB3109-031-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3451068
BLAST score
                  336
                  2.0e-31
E value
Match length
                  97
                  69
% identity
NCBI Description
                  (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                  39894
Seq. ID
                  LIB3109-031-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g4038043
BLAST score
                  171
E value
                  4.0e-12
Match length
                  110
% identity
                  32
                   (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  39895
Seq. No.
```

Seq. ID LIB3109-031-Q1-K1-H6

Method BLASTN
NCBI GI g170091
BLAST score 51
E value 7.0e-20



Match length 87 % identity 90

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 39896

Seq. ID LIB3109-032-Q1-K1-B12

Method BLASTX
NCBI GI g2217970
BLAST score 143
E value 3.0e-09
Match length 81
% identity 14

NCBI Description (Z97074) p40 [Homo sapiens]

Seq. No. 39897

Seq. ID LIB3109-032-Q1-K1-E10

Method BLASTN
NCBI GI g170050
BLAST score 98
E value 1.0e-47
Match length 138
% identity 95

NCBI Description Soybean pyruvate kinase mRNA, complete cds

Seq. No. 39898

Seq. ID LIB3109-032-Q1-K1-H6

Method BLASTX
NCBI GI g3914002
BLAST score 146
E value 8.0e-10
Match length 50
% identity 62

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279

(AF033862) Lon protease [Arabidopsis thaliana]

Seq. No. 39899

Seq. ID LIB3109-033-Q1-K1-A2

Method BLASTX
NCBI GI 94490756
BLAST score 211
E value 1.0e-30
Match length 118
% identity 60

NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]

Seq. No.

39900

Seq. ID LIB3109-033-Q1-K1-A7

Method BLASTX
NCBI GI g1326161
BLAST score 203
E value 7.0e-16
Match length 59
% identity 78

NCBI Description (U54703) dehydrin [Phaseolus vulgaris]

Seq. No.

39901



Seq. ID LIB3109-033-Q1-K1-B1

Method BLASTX
NCBI GI g1174448
BLAST score 164
E value 2.0e-11
Match length 82
% identity 48

NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR

(TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative

[Arabidopsis thaliana]

Seq. No. 39902

Seq. ID LIB3109-033-Q1-K1-B4

Method BLASTX
NCBI GI g927577
BLAST score 212
E value 4.0e-23
Match length 121
% identity 65

NCBI Description (U12927) alpha-galactosidase [Phaseolus vulgaris]

Seq. No. 39903

Seq. ID LIB3109-033-Q1-K1-C6

Method BLASTX
NCBİ GI g3599491
BLAST score 253
E value 3.0e-24
Match length 110
% identity 57

NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No.

Seq. ID LIB3109-033-Q1-K1-D6

39904

Method BLASTX
NCBI GI g3511285
BLAST score 327
E value 1.0e-34
Match length 128
% identity 59

NCBI Description (AF081534) cellulose synthase [Populus alba x Populus

tremula]

Seq. No. 39905

Seq. ID LIB3109-033-Q1-K1-D8

Method BLASTX
NCBI GI g3377797
BLAST score 143
E value 2.0e-09
Match length 53
% identity 60

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara



Seq. No. 39906

Seq. ID LIB3109-033-Q1-K1-E4

Method BLASTX
NCBI GI g3024019
BLAST score 305
E value 2.0e-37
Match length 121
% identity 66

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_2225879_dbj_BAA20876_ (AB004823) eukaryotic initiation
factor 5A2 [Solanum tuberosum] >gi_2225887_dbj_BAA20880_
(AB004827) eukaryotic initiation factor 5A1 [Solanum

tuberosum]

Seq. No.

Seq. ID LIB3109-033-Q1-K1-F6

39907

Method BLASTX
NCBI GI g3152587
BLAST score 261
E value 1.0e-23
Match length 119
% identity 53

NCBI Description (AC002986) Similar to CREB-binding protein homolog

gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No. 39908

Seq. ID LIB3109-033-Q1-K1-G11

Method BLASTN
NCBI GI g2444419
BLAST score 56
E value 1.0e-22
Match length 144
% identity 85

NCBI Description Glycine max ribosome-associated protein p40 mRNA, complete

cds

Seq. No. 39909

Seq. ID LIB3109-033-Q1-K1-G9 Method BLASTN

Method BLASTN
NCBI GI g4204764
BLAST score 46
E value 8.0e-17
Match length 219
% identity 77

NCBI Description Glycine max peroxidase (sEPb2) mRNA, partial cds

Seq. No.

39910

Seq. ID LIB3109-033-Q1-K1-H7

Method BLASTX
NCBI GI g4262228
BLAST score 240
E value 2.0e-25
Match length 118
% identity 63

NCBI Description (AC006200) putative receptor protein kinase [Arabidopsis



thaliana]

```
39911
Seq. No.
Seq. ID
                   LIB3109-034-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   g4558664
BLAST score
                   252
E value
                   1.0e-21
Match length
                   128
% identity
                   10
NCBI Description
                  (AC007063) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   39912
Seq. ID
                   LIB3109-034-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   g2792244
BLAST score
                   223
E value
                   3.0e-18
Match length
                   108
% identity
                   44
                  (AF032700) NBS-LRR type resistance protein [Oryza sativa]
NCBI Description
Seq. No.
                   39913
Seq. ID
                   LIB3109-034-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                   g1351033
BLAST score
                   154
E value
                   2.0e-10
Match length
                   73
                   47
% identity
NCBI Description
                  STEM 31 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
                   PROTEIN VSP25) >gi 170088 (M20037) vegetative storage
                  protein [Glycine max]
                   39914
Seq. No.
Seq. ID
                  LIB3109-035-Q1-K2-B7
Method
                  BLASTX
NCBI GI
                   q4512702
BLAST score
                   201
E value
                  1.0e-15
Match length
                  101
                   49
% identity
NCBI Description
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  39915
Seq. ID
                  LIB3109-035-Q1-K2-E6
Method
                  BLASTX
                  g114734
NCBI GI
BLAST score
                  207
E value
                  2.0e-16
Match length
                  64
% identity
                  67
NCBI Description
                  AUXIN-INDUCED PROTEIN AUX28 >gi 81759 pir A28993 aux28
                  protein - soybean >gi_169921 (J03919) auxin-regulated
                  protein (Aux28) [Glycine max]
```

Seq. No. 39916



```
Seq. ID
                   LIB3109-035-Q1-K3-C7
Method
                   BLASTN
NCBI GI
                   q886099
BLAST score
                   256
E value
                   1.0e-142
Match length
                   339
% identity
NCBI Description
                  Glycine max putative water channel protein (Pip1) mRNA,
                   complete cds
Seq. No.
                   39917
Seq. ID
                   LIB3109-035-Q1-K4-E6
Method
                   BLASTX
NCBI GI
                   q2459926
BLAST score
                   139
E value
                   4.0e-13
Match length
                   117
% identity
                   44
NCBI Description
                  (AF006197) annexin [Lavatera thuringiaca]
Seq. No.
                   39918
Seq. ID
                   LIB3109-035-Q1-K4-F12
Method
                   BLASTN
NCBI GI
                   g456713
BLAST score
                   326
E value
                   0.0e + 00
Match length
                   413
% identity
                   30
NCBI Description Glycine max gene for ubiquitin, complete cds
Seq. No.
                   39919
Seq. ID
                   LIB3109-035-Q1-K4-G12
Method
                   BLASTN
NCBI GI
                   g169980
BLAST score
                   137
E value
                   5.0e-71
Match length
                   273
% identity
                   88
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                   39920
Seq. ID
                   LIB3109-035-Q1-K5-B9
Method
                   BLASTX
NCBI GI
                   g132944
BLAST score
                   501
E value
                   5.0e-51
Match length
                   109
% identity
                   85
                  60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >qi 806279
```

(M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No.

39921

Seq. ID

LIB3109-035-Q1-K5-G12

Method BLASTN NCBI GI g4457218 BLAST score 101



E value 1.0e-49
Match length 205
% identity 87

NCBI Description Capsicum chinense acyl carrier protein (Acl1) mRNA,

complete cds

Seq. No.

Seq. ID LIB3109-035-Q1-K6-B8

39922

Method BLASTN
NCBI GI g459961
BLAST score 202
E value 1.0e-110
Match length 278
% identity 93

NCBI Description Glycine max proplastid omega-6 desaturase mRNA, complete

cds

Seq. No. 39923

Seq. ID LIB3109-035-Q1-K6-C11

Method BLASTX
NCBI GI g1806146
BLAST score 200
E value 8.0e-16
Match length 88
% identity 53

NCBI Description (X97317) cdc2MsF [Medicago sativa]

Seq. No. 39924

Seq. ID LIB3109-036-Q1-K1-A10

Method BLASTX
NCBI GI g3123349
BLAST score 216
E value 1.0e-17
Match length 81
% identity 53

NCBI Description (AJ005788) hypothetical protein [Cicer arietinum]

Seq. No. 39925

Seq. ID LIB3109-036-Q1-K1-A5

Method BLASTX
NCBI GI g136057
BLAST score 379
E value 2.0e-36
Match length 103
% identity 70

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase Coptis japonica >gi_556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 39926

Seq. ID LIB3109-036-Q1-K1-B2

Method BLASTX
NCBI GI g2828293
BLAST score 184
E value 1.0e-13
Match length 67



% identity

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No.

39927

Seq. ID

LIB3109-036-Q1-K1-E9

Method

BLASTX

NCBI GI

g1710530

BLAST score

285

E value Match length

2.0e-27 107

% identity

61

NCBI Description

60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256

ribosomal protein L27a - Arabidopsis thaliana

>gi_1107487_emb CAA63025 (X91959) 60S ribosomal protein

L27a [Arabidopsis thaliana]

Seq. No.

39928

Seq. ID

LIB3109-036-Q1-K1-F8

Method NCBI GI BLASTX g3252807

BLAST score

E value

277

1.0e-24

Match length

131

% identity

43

NCBI Description

(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.

39929

Seq. ID

LIB3109-036-Q1-K1-H12

Method

BLASTN

NCBI GI

g1196896

BLAST score

79

E value

2.0e-36

Match length

123

% identity

91

NCBI Description Glycine max acidic ribosomal protein PO mRNA, complete cds

Seq. No.

39930

Seq. ID Method

LIB3109-037-Q1-K1-A2

BLASTX

NCBI GI

g2827528

BLAST score E value

153 5.0e-10

Match length

48 60

% identity NCBI Description

(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.

39931

Seq. ID

LIB3109-037-Q1-K1-B4

Method

BLASTX

NCBI GI

q1709454

BLAST score

331

E value

6.0e-31

Match length

82

% identity NCBI Description

82 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR

(PDHE1-B) $>gi_1336097$ (U56697) pyruvate dehydrogenase Elbeta [Pisum sativum]

% identity

81



```
Seq. No.
                     39932
Seq. ID
                     LIB3109-037-Q1-K1-B8
Method
                     BLASTX
NCBI GI
                     g416650
BLAST score
                     376
E value
                     3.0e-36
Match length
                     109
% identity
                     63
NCBI Description
                     PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
                     {\tt PGNT35/PCNT111) > } {\tt gi\_100304\_pir\_S16268 \ auxin-induced}
                    protein (clone pGNT35) - common tobacco
>gi_19797_emb_CAA39706_ (X56265) auxin-induced protein
[Nicotiana tabacum] >gi_19801_emb_CAA39710_ (X56269)
                     auxin-induced protein [Nicotiana tabacum]
Seq. No.
                     39933
Seq. ID
                     LIB3109-037-Q1-K1-D12
Method
                     BLASTX
NCBI GI
                     g2244904
BLAST score
                     154
E value
                     2.0e-10
Match length
                     70
% identity
                     53
NCBI Description
                     (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
                     [Arabidopsis thaliana]
Seq. No.
                     39934
Seq. ID
                    LIB3109-037-Q1-K1-E8
Method
                    BLASTX
NCBI GI
                     g3482924
BLAST score
                     209
E value
                     1.0e-16
Match length
                     89
% identity
                     49
NCBI Description
                     (AC003970) Highly similar to cinnamyl alcohol
                    dehydrogenase, gi_1143445 [Arabidopsis thaliana]
Seq. No.
                    39935
Seq. ID
                    LIB3109-037-Q1-K1-H11
Method
                    BLASTX
NCBI GI
                    g2275199
BLAST score
                    164
E value
                    7.0e-12
Match length
                    66
% identity
                    52
NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]
                    39936
Seq. No.
Seq. ID
                    LIB3109-037-Q1-K1-H2
Method
                    BLASTN
NCBI GI
                    g3309268
BLAST score
                    42
                    3.0e-14
E value
Match length
                    178
```

NCBI Description Glycine max ferric leghemoglobin reductase-2 precursor



mRNA, complete cds

```
Seq. No.
                   39937
Seq. ID
                   LIB3109-038-Q1-K1-A4
Method
                   BLASTX
NCBI GI
                   g135406
BLAST score
                   343
E value
                   1.0e-32
                   74
Match length
% identity
                   89
                   TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
NCBI Description
                   alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                   alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                   alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                   39938
Seq. ID
                   LIB3109-038-Q1-K1-D4
Method
                   BLASTN
NCBI GI
                   g170091
BLAST score
                   179
E value
                   2.0e-96
Match length
                   226
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
Seq. No.
                   39939
Seq. ID
                   LIB3109-038-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                   g4510375
BLAST score
                   232
E value
                   1.0e-19
Match length
                   79
                   59
% identity
NCBI Description
                   (AC007017) putative homeotic protein BEL1 [Arabidopsis
                  thaliana]
                   39940
Seq. No.
Seq. ID
                  LIB3109-038-Q1-K1-F6
Method
                  BLASTN
NCBI GI
                  g984307
BLAST score
                  36
E value
                  3.0e-11
Match length
                  135
                  87
% identity
NCBI Description
                  Glycine max ribosomal protein S16 (rps16) gene, partial
```

cds, beta-carboxyltransferase (accD), photosystem I

component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 39941

Seq. ID LIB3109-038-Q1-K1-F8

Method BLASTN NCBI GI g169974 BLAST score 192 E value 1.0e-104

BLAST score

Match length

% identity

E value

151

50

62

4.0e-10



```
Match length
                   87
% identity
NCBI Description Glycine max vspA gene, complete cds
Seq. No.
                   39942
Seq. ID
                   LIB3109-038-Q1-K1-H5
Method
                   BLASTX
NCBI GI
                   q559713
BLAST score
                   178
                   3.0e-13
E value
                   95
Match length
% identity
                   42
NCBI Description
                   (D38552) The half39 protein is related to cyclophilin.
                   [Homo sapiens]
Seq. No.
                   39943
Seq. ID
                   LIB3109-041-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                   g1711615
BLAST score
                   114
                   2.0e-12
E value
Match length
                   98
% identity
                   49
NCBI Description
                  HIGH AFFINITY SULPHATE TRANSPORTER 1
                  >gi_1085847_pir__S51763 high affinity sulphate transporter
                   - Stylosanthes hamata >gi_607184_emb_CAA57710_ (X82255)
                  high affinity sulphate transporter [Stylosanthes hamata]
Seq. No.
                   39944
Seq. ID
                  LIB3109-041-Q1-K1-A4
Method
                  BLASTN
NCBI GI
                  g3021374
BLAST score
                  52
E value
                  1.0e-20
Match length
                  98
                  88
% identity
NCBI Description Glycine max mRNA for profilin, PRO1
                  39945
Seq. No.
Seq. ID
                  LIB3109-041-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g951449
BLAST score
                  429
E value
                  2.0e-42
Match length
                  128
                  61
% identity
NCBI Description
                  (L46681) aspartic protease precursor [Lycopersicon
                  esculentum]
Seq. No.
                  39946
Seq. ID
                  LIB3109-041-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1076512
```

6234



ferredoxin--nitrite reductase (EC 1.7.7.1) precursor - kidney bean >gi 500753 (U10419) nitrite reductase

[Phaseolus vulgaris]

Seq. No. 39947

NCBI Description

Seq. ID LIB3109-041-Q1-K1-C5

Method BLASTN
NCBI GI g1906001
BLAST score 123
E value 1.0e-62
Match length 325
% identity 93

NCBI Description Glycine max nitrite reductase gene, complete cds

Seq. No. 39948

Seq. ID LIB3109-041-Q1-K1-F2

Method BLASTX
NCBI GI g421954
BLAST score 167
E value 8.0e-12
Match length 51
% identity 51

NCBI Description hypothetical protein 3 - potato transposon Tst1

>gi_21433_emb_CAA36615_ (X52387) ORF3 [Solanum tuberosum]

Seq. No. 39949

Seq. ID LIB3109-042-Q1-K1-A6

Method BLASTX
NCBI GI g2833220
BLAST score 119
E value 2.0e-10
Match length 63
% identity 49

NCBI Description HYPOTHETICAL 35.7 KD PROTEIN IN DNL4-SLG1 INTERGENIC REGION

>gi_2132030_pir__S61990 hypothetical protein YOR006c yeast (Saccharomyces cerevisiae) >gi_1151002 (U43491)
hypothetical protein UND313 [Saccharomyces cerevisiae]

>gi_1420098_emb_CAA99194_ (Z74914) ORF YOR006c

[Saccharomyces cerevisiae]

Seq. No. 39950

Seq. ID LIB3109-042-Q1-K1-B7

Method BLASTX
NCBI GI g3309583
BLAST score 545
E value 4.0e-56
Match length 121
% identity 87

NCBI Description (AF073830) fructose-6-phosphate

2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No. 39951

Seq. ID LIB3109-042-Q1-K1-C5

Method BLASTX
NCBI GI g4220474
BLAST score 177
E value 5.0e-13

E value

Match length

% identity

4.0e-24

133 33



```
Match length
                   92
% identity
                   51
NCBI Description
                  (AC006069) putative myosin heavy chain [Arabidopsis
                  thaliana]
Seq. No.
                  39952
Seq. ID
                  LIB3109-042-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3094014
BLAST score
                  164
E value
                  9.0e-12
Match length
                  54
% identity
                  57
NCBI Description (AF060862) unknown [Homo sapiens]
Seq. No.
                  39953
                  LIB3109-043-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244996
BLAST score
                  147
E value
                  2.0e-09
Match length
                  40
% identity
                  60
NCBI Description (Z97341) similarity to a membrane-associated salt-inducible
                  protein [Arabidopsis thaliana]
Seq. No.
                  39954
Seq. ID
                  LIB3109-043-Q1-K1-B12
                  BLASTN
Method
NCBI GI
                  g2815245
BLAST score
                  32
E value
                  1.0e-08
Match length
                  32
% identity
                  100
NCBI Description C.arietinum mRNA for class I type 2 metallothionein (clone:
                  CanMT-2)
Seq. No.
                  39955
Seq. ID
                  LIB3109-043-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3510252
BLAST score
                  142
E value
                  6.0e-09
Match length
                  53
% identity
                  51
NCBI Description (AC005310) putative RNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  39956
                  LIB3109-043-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4322940
BLAST score
                  226
```

NCBI Description (AF096299) DNA-binding protein 2 [Nicotiana tabacum]

NCBI GI

```
Seq. No.
                   39957
Seq. ID
                   LIB3109-043-Q1-K1-H12
Method
                   BLASTX
NCBI GI
                   g2244759
BLAST score
                   155
E value
                   2.0e-10
Match length
                   56
% identity
                   54
NCBI Description
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
                   39958
Seq. No.
Seq. ID
                   LIB3109-044-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   g2341028
BLAST score
                   194
                   1.0e-20
E value
Match length
                   95
% identity
                   63
NCBI Description
                   (AC000104) Strong similarity to 60S ribosomal protein L17
                   (gb_X01694). EST gb_AA042332 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   39959
Seq. ID
                   LIB3109-045-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   g2232254
BLAST score
                   354
E value
                   9.0e-34
Match length
                   106
% identity
                   62
NCBI Description
                  (AF005237) old-yellow-enzyme homolog [Catharanthus roseus]
                   39960
Seq. No.
Seq. ID
                   LIB3109-045-Q1-K1-A7
Method
                   BLASTN
NCBI GI
                   g3982595
BLAST score
                   102
E value
                   2.0e-50
Match length
                   163
% identity
                   94
NCBI Description
                  Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                   39961
                  LIB3109-045-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2342477
BLAST score
                  293
E value
                  2.0e-26
Match length
                  106
% identity
                  51
NCBI Description
                  (AB006679) ATP binding protein [Homo sapiens]
Seq. No.
                  39962
Seq. ID
                  LIB3109-045-Q1-K1-E9
Method
                  BLASTX
```

q3075400



BLAST score 444
E value 3.0e-44
Match length 127
% identity 69

NCBI Description (AC004484) putative thromboxane-A synthase [Arabidopsis thaliana] >gi_3413720 (AC004747) putative thromboxin-A

synthase [Arabidopsis thaliana]

Seq. No. 39963

Seq. ID LIB3109-045-Q1-K1-F4

Method BLASTX
NCBI GI 94049399
BLAST score 211
E value 7.0e-17
Match length 121
% identity 38

NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]

Seq. No. 39964

Seq. ID LIB3109-045-Q1-K1-G2

Method BLASTN
NCBI GI g170091
BLAST score 226
E value 1.0e-124
Match length 298
% identity 94

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 39965

Seq. ID LIB3109-045-Q1-K1-H3

Method BLASTX
NCBI GI g4508069
BLAST score 316
E value 3.0e-29
Match length 114
% identity 51

NCBI Description (AC005882) 12246 [Arabidopsis thaliana]

Seq. No. 39966

Seq. ID LIB3109-045-Q1-K1-H4

Method BLASTX
NCBI GI g136057
BLAST score 278
E value 5.0e-25
Match length 67
% identity 78

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase Coptis japonica >gi_556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 39967

Seq. ID LIB3109-046-Q1-K1-A1

Method BLASTX NCBI GI g4544419 BLAST score 242



```
E value
Match length
                   80
% identity
                   60
NCBI Description
                  (AC006955) unknown protein [Arabidopsis thaliana]
Seq. No.
                   39968
Seq. ID
                   LIB3109-046-Q1-K1-A6
Method
                   BLASTX
NCBI GI
                   g4467147
BLAST score
                   168
E value
                   3.0e-14
Match length
                   96
% identity
                   52
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   39969
Seq. ID
                  LIB3109-046-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2326343
BLAST score
                  292
E value
                  2.0e-26
Match length
                  123
% identity
                   51
                   (Y11187) G14587-5 [Arabidopsis thaliana]
NCBI Description
                  >gi_2326350_emb_CAA72042_ (Y11155) hypothetical protein
                   [Arabidopsis thaliana]
Seq. No.
                  39970
Seq. ID
                  LIB3109-046-Q1-K1-B3
Method
                  BLASTX
NCBI GI
                  g1871177
BLAST score
                  178
E value
                  3.0e-21
Match length
                  76
% identity
                  76
NCBI Description
                  (U90439) unknown protein [Arabidopsis thaliana]
Seq. No.
                  39971
Seq. ID
                  LIB3109-046-Q1-K1-D4
Method
                  BLASTX
NCBI GI
                  g132468
BLAST score
                  236
E value
                  4.0e-20
Match length
                  95
% identity
                  44
                  PEPTIDE CHAIN RELEASE FACTOR 2 (RF-2) >gi_96819_pir__A36480
NCBI Description
                  translation releasing factor RF-2 - Salmonella typhimurium
                  >gi_154276 (M38590) peptide chain release factor 2
                  [Salmonella typhimurium]
Seq. No.
                  39972
Seq. ID
                  LIB3109-046-Q1-K1-E10
```

Method BLASTN
NCBI GI g871507
BLAST score 49

E value 2.0e-18 Match length 193



% identity 83

NCBI Description P.sativum mRNA for small GTP-binding protein (clone pGTP13)

Seq. No. 39973

Seq. ID LIB3109-046-Q1-K1-F3

Method BLASTN
NCBI GI g3982595
BLAST score 387
E value 0.0e+00
Match length 391
% identity 100

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 39974

Seq. ID LIB3109-046-Q1-K1-G12

Method BLASTX
NCBI GI g2230757
BLAST score 224
E value 1.0e-18
Match length 85
% identity 56

NCBI Description (Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No. 39975

Seq. ID LIB3109-046-Q1-K1-H4

Method BLASTX
NCBI GI g2055228
BLAST score 242
E value 1.0e-20
Match length 81
% identity 62

NCBI Description (AB000129) SRC1 [Glycine max]

Seq. No. 39976

Seq. ID LIB3109-047-Q1-K1-B8

Method BLASTX
NCBI GI g541943
BLAST score 242
E value 7.0e-21
Match length 70
% identity 63

NCBI Description metallothionein - soybean >gi 228682 prf 1808316A

metallothionein-like protein [Glycine max]

Seq. No. 39977

Seq. ID LIB3109-047-Q1-K1-B9

Method BLASTX
NCBI GI g3170230
BLAST score 431
E value 1.0e-42
Match length 122
% identity 69

NCBI Description (AF041848) fructose-6-phosphate 2-kinase

/fructose-2,6-bisphosphatase [Spinacia oleracea]

Seq. No. 39978

Seq. ID LIB3109-047-Q1-K1-C12

Match length

98



```
Method
                   BLASTX
NCBI GI
                   q2335098
BLAST score
                   144
E value
                   5.0e-09
Match length
                   66
% identity
                   47
NCBI Description
                  (AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.
                   39979
Seq. ID
                   LIB3109-047-Q1-K1-E3
Method
                   BLASTX
NCBI GI
                   q4191791
BLAST score
                   207
E value
                   4.0e-30
Match length
                   105
% identity
                   65
NCBI Description
                   (AC005917) putative sf21 {Helianthus annuus} protein
                   [Arabidopsis thaliana]
Seq. No.
                   39980
Seq. ID
                   LIB3109-047-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   q3719431
BLAST score
                   327
E value
                   2.0e-30
Match length
                   124
% identity
NCBI Description
                   (AF093107) delta-endotoxin [Bacillus thuringiensis]
Seq. No.
                   39981
Seq. ID
                  LIB3109-048-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                   g3892051
BLAST score
                   124
E value
                   7.0e-12
Match length
                   100
% identity
                   53
NCBI Description
                   (AC002330) predicted NADH dehydrogenase 24 kD subunit
                   [Arabidopsis thaliana]
Seq. No.
                  39982
Seq. ID
                  LIB3109-048-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3482977
BLAST score
                  166
E value
                  1.0e-11
Match length
                  87
% identity
                  41
NCBI Description
                  (AL031369) putative protein [Arabidopsis thaliana]
Seq. No.
                  39983
Seq. ID
                  LIB3109-050-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g1498053
BLAST score
                  314
E value
                  5.0e-29
```

Seq. No.

39989



```
% identity
NCBI Description
                  (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                  39984
                  LIB3109-050-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1354849
BLAST score
                  280
                  6.0e-25
E value
Match length
                  114
                  50
% identity
NCBI Description
                  (U57350) epoxide hydrolase [Nicotiana tabacum]
                  39985
Seq. No.
                  LIB3109-050-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2440044
BLAST score
                  290
E value
                   4.0e-26
Match length
                  96
% identity
                   60
NCBI Description
                  (AJ001293) major intrinsic protein PIPB [Craterostigma
                  plantagineum]
Seq. No.
                  39986
Seq. ID
                  LIB3109-052-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g1669341
BLAST score
                  373
E value
                  3.0e-36
Match length
                  84
                  80
% identity
NCBI Description
                  (D45066) AOBP (ascorbate oxidase promoter-binding protein)
                   [Cucurbita maxima]
Seq. No.
                  39987
Seq. ID
                  LIB3109-052-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4191785
BLAST score
                  290
E value
                  4.0e-26
                  87
Match length
% identity
                  62
NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana]
Seq. No.
                  39988
Seq. ID
                  LIB3109-052-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  q2252840
BLAST score
                  205
E value
                  3.0e~16
Match length
                  91
                  46
% identity
NCBI Description
                  (AF013293) contains regions of similarity to Haemophilus
                  influenzae permease (SP:P38767) [Arabidopsis thaliana]
```

Match length

% identity

91

46



Seq. ID LIB3109-052-Q1-K1-D8 Method BLASTN NCBI GI g3982595 BLAST score 156 E value 2.0e-82 Match length 240 % identity 91 NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds Seq. No. 39990 Seq. ID LIB3109-052-Q1-K1-F12 Method BLASTN NCBI GI g169974 BLAST score 40 E value 1.0e-13 Match length 96 % identity 85 NCBI Description Glycine max vspA gene, complete cds Seq. No. 39991 1998 m Seq. ID LIB3109-052-Q1-K1-G7 Method BLASTN NCBI GI q3982595 BLAST score 379 E value 0.0e + 00Match length 394 % identity 99 NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds Seq. No. 39992 Seq. ID LIB3109-053-Q1-K1-B5 Method BLASTX NCBI GI g1514649 BLAST score 444 E value 3.0e-44Match length 115 % identity 43 NCBI Description (X86021) potassium channel [Solanum tuberosum] Seq. No. 39993 Seq. ID LIB3109-053-Q1-K1-C1 Method BLASTX NCBI GI g2618686 BLAST score 257 E value 2.0e-22 Match length 110 % identity 41 NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana] Seq. No. 39994 Seq. ID LIB3109-053-Q1-K1-C10 Method BLASTX NCBI GI g4567310 BLAST score 179 E value 4.0e-13

% identity

NCBI Description

46





```
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                   39995
Seq. ID
                   LIB3109-053-Q1-K1-C12
Method
                   BLASTX
NCBI GI
                   g2288982
BLAST score
                   143
E value
                   7.0e-09
Match length
                   72
% identity
                   43
NCBI Description
                  (AC002335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   39996
Seq. ID
                   LIB3109-053-01-K1-D12
Method
                   BLASTX
NCBI GI
                   q4388820
BLAST score
                   256
E value
                   3.0e-22
Match length
                   54
% identity
                   83
                   (AC006528) putative myb DNA-binding protein [Arabidopsis
NCBI Description
Seq. No.
                   39997
Seq. ID
                   LIB3109-053-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   q3335350
BLAST score
                   250
E value
                   1.0e-21
Match length
                   92
% identity
                   52
NCBI Description
                   (AC004512) Similar to gb Z84386 anthranilate
                   N-hydroxycinnamoyl/benzoyltransferase from Dianthus
                   caryophyllus. [Arabidopsis thaliana]
Seq. No.
                   39998
Seq. ID
                   LIB3109-054-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   q1856971
BLAST score
                   186
E value
                   4.0e-14
Match length
                  71
% identity
                   52
NCBI Description
                   (D26058) This gene is specifically expressed at the S phase
                  during the cell cycle in the synchronous culture of
                  periwinkle cells. [Catharanthus roseus]
Seq. No.
                  39999
Seq. ID
                  LIB3109-054-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g4510342
BLAST score
                  166
                  1.0e-11
E value
Match length
                  96
```

[Arabidopsis thaliana]

(AC006921) putative serine/threonine protein kinase



```
Seq. No.
                    40000
Seq. ID
                   LIB3109-055-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   g2494034
BLAST score
                   151
E value
                   3.0e-10
Match length
                    69
% identity
                    48
                   DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
NCBI Description
                   KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)
                   diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.
                   40001
Seq. ID
                   LIB3109-055-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g3309086
BLAST score
                   157
E value
                   1.0e-10
Match length
                   105
% identity
                   39
                   (AF076253) calcineurin B-like protein 3 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   40002
Seq. ID
                   LIB3109-055-Q1-K1-E3
Method
                   BLASTN
NCBI GI
                   g3982595
BLAST score
                   224
E value
                   1.0e-123
Match length
                   312
% identity
                   93
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                   40003
Seq. ID
                   LIB3109-055-Q1-K1-F1
Method
                   BLASTN
NCBI GI
                   g3982595
BLAST score
                   392
E value
                   0.0e + 00
Match length
                   392
% identity
                   100
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                   40004
Seq. ID
                   LIB3109-056-Q1-K1-H10
Method
                   BLASTN
                   g169974
```

NCBI GI BLAST score 48 3.0e-18 E value Match length 212 % identity

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 40005

Seq. ID LIB3109-056-Q1-K1-H7



```
Method
                   BLASTX
NCBI GI
                   g4538911
BLAST score
                   108
E value
                   6.0e-12
Match length
                   63
% identity
                   65
NCBI Description
                  (AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   40006
Seq. ID
                   LIB3109-057-Q1-K1-D7
Method
                   BLASTN
NCBI GI
                   g4204764
BLAST score
                   136
E value
                   1.0e-70
Match length
                   264
% identity
                   88
NCBI Description Glycine max peroxidase (sEPb2) mRNA, partial cds
Seq. No.
                   40007
Seq. ID
                   LIB3109-057-Q1-K1-D8
Method
                   BLASTN
NCBI GI
                   g170087
BLAST score
                   107
E value
                   4.0e-53
Match length
                   251
% identity
                   86
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
Seq. No.
                   40008
Seq. ID
                   LIB3138-001-Q1-N1-A2
Method
                   BLASTN
NCBI GI
                   g4097879
BLAST score
                   163
E value
                   1.0e-86
Match length
                   371
% identity
                   86
NCBI Description
                  Bean pod mottle virus complete segment RNA1 polyprotein
                   gene, complete cds
Seq. No.
                   40009
Seq. ID
                  LIB3138-001-Q1-N1-A9
Method
                  BLASTN
NCBI GI
                   g210811
BLAST score
                   50
E value
                   3.0e-19
Match length
                  105
% identity
                  89
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40010
Seq. ID
                  LIB3138-001-Q1-N1-B1
Method
                  BLASTX
```

NCBI GI g3337356 BLAST score 254 E value 7.0e-22 Match length 70



% identity 74

NCBI Description (AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No. 40011

Seq. ID LIB3138-001-Q1-N1-B3

Method BLASTX
NCBI GI g1703456
BLAST score 156
E value 1.0e-10
Match length 79

Match length /9
% identity 52

NCBI Description CATION-TRANSPORTING ATPASE PAT1 >gi_1362215_pir__S57726

PAT1 protein - slime mold (Dictyostelium discoideum)

>gi_895788_emb_CAA61551_ (X89369) PAT1 protein

[Dictyostelium discoideum]

Seq. No. 40012

Seq. ID LIB3138-001-Q1-N1-B6

Method BLASTX
NCBI GI 94455275
BLAST score 200
E value 1.0e-15
Match length 107
% identity 43

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 40013

Seq. ID LIB3138-001-Q1-N1-B8

Method BLASTX
NCBI GI g282921
BLAST score 185
E value 6.0e-14
Match length 109
% identity 46

NCBI Description carbonate dehydratase (EC 4.2.1.1) precursor - garden pea

>gi_169057 (M63627) carbonic anhydrase [Pisum sativum]

>gi_227784_prf__1710354A carbonic anhydrase [Pisum sativum]

Seq. No. 40014

Seq. ID LIB3138-001-Q1-N1-C11

Method BLASTX
NCBI GI 9464719
BLAST score 223
E value 1.0e-18
Match length 69
% identity 64

NCBI Description 40S RIBOSOMAL PROTEIN RP41 (YS12) (S18A / S18B)

>gi_626900_pir__S41784 ribosomal protein S11.e, cytosolic -

yeast (Saccharomyces cerevisiae) >gi_295653 (L15408)

ribosomal protein S18 [Saccharomyces cerevisiae] >gi_311132 (L17004) ribosomal protein S18 [Saccharomyces cerevisiae]

>gi_602085_emb_CAA84990_ (Z35917) ORF YBR048w

[Saccharomyces cerevisiae] >gi_642297 emb CAA87804

(Z47814) Rps18ap [Saccharomyces cerevisiae]

>gi_1216233_emb_CAA65218_ (X95966) 40S ribosomal protein [Saccharomyces cerevisiae] >gi_1431458_emb_CAA98846_

BLAST score

% identity

E value Match length 70 3.0e-31

158

86





Seq. No. 40015 Seq. ID LIB3138-001-Q1-N1-C9 Method BLASTN NCBI GI g456713 BLAST score 41 E value 7.0e-14 Match length 84 % identity 30 NCBI Description Glycine max gene for ubiquitin, complete cds Seq. No. 40016 Seq. ID LIB3138-001-Q1-N1-E5 Method BLASTX NCBI GI q3367638 BLAST score 432 E value 5.0e-43Match length 99 80 % identity NCBI Description (AJ000331) monogalactosyldiacylglycerol synthase [Arabidopsis thaliana] Seq. No. 40017 Seq. ID LIB3138-001-Q1-N1-E7 Method BLASTX NCBI GI q399307 BLAST score 166 E value 4.0e-13 Match length 82 % identity 56 NCBI Description PRENYL TRANSFERASE >gi 99282 pir A40433 prephytoene pyrophosphatase dehydrogenase (crtE) homolog - Cyanophora paradoxa >gi_336639 (M37111) prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] >gi_1016130 (U30821) prenyl transferase [Cyanophora paradoxa] 40018 Seq. No. Seq. ID LIB3138-001-Q1-N1-F10 Method BLASTN NCBI GI g210811 BLAST score 162 E value 5.0e-86 Match length 302 % identity 88 NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA Seq. No. 40019 Seq. ID LIB3138-001-Q1-N1-F4 Method BLASTN NCBI GI g16508

NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene



sam-1 >gi 166871 gb M55077 ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

Seq. No. 40020 Seq. ID LIB3138-002-Q1-N1-A10 Method BLASTX NCBI GI g3914019 BLAST score 173 E value 6.0e-13 Match length 86 % identity 55

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi 2305014

(AF004317) S-adenosyl-L-methionine synthetase homolog [Musa

acuminata]

Seq. No. 40021

Seq. ID LIB3138-002-Q1-N1-B9

Method BLASTX NCBI GI g138364 BLAST score 365 E value 5.0e-35 Match length 114 % identity 69

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) $>gi_75639_pir_GNWXG7$ genome polyprotein M -

bean pod mottle vīrus (straīn Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40022

Seq. ID LIB3138-002-Q1-N1-C2

Method BLASTX NCBI GI g3746838 BLAST score 163 3.0e-11 E value Match length 80 % identity 20

NCBI Description (AF083383) 38kDa splicing factor; SPF 38 [Homo sapiens]

Seq. No. 40023

Seq. ID LIB3138-002-Q1-N1-D3

Method BLASTX NCBI GI g4097880 BLAST score 144 E value 1.0e-14 Match length 81 % identity

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

40024 Seq. No.

LIB3138-002-Q1-N1-D4 Seq. ID

Method BLASTN NCBI GI g4097879 BLAST score 60 E value 3.0e-25 Match length 120 % identity 88



NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No. 40025

Seq. ID LIB3138-002-Q1-N1-D5

Method BLASTX
NCBI GI g2494266
BLAST score 407
E value 6.0e-40
Match length 116
% identity 70

NCBI Description GTP-BINDING PROTEIN LEPA >gi_1653961_dbj_BAA18871_ (D90917)

LepA [Synechocystis sp.]

Seq. No. 40026

Seq. ID LIB3138-003-Q1-N1-A10

Method BLASTN
NCBI GI g210811
BLAST score 137
E value 5.0e-71
Match length 342
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40027

Seq. ID LIB3138-003-Q1-N1-A3

Method BLASTN
NCBI GI g210811
BLAST score 229
E value 1.0e-126
Match length 389
% identity 90

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40028

Seq. ID LIB3138-003-Q1-N1-A8

Method BLASTX
NCBI GI g1723487
BLAST score 151
E value 7.0e-10
Match length 92
% identity 37

NCBI Description HYPOTHETICAL 97.1 KD PROTEIN C32A11.02C IN CHROMOSOME I

>gi_1213266_emb_CAA93699_ (Z69796) unknown

[Schizosaccharomyces pombe]

Seq. No. 40029

Seq. ID LIB3138-003-Q1-N1-B11

Method BLASTX
NCBI GI g4097880
BLAST score 352
E value 1.0e-33
Match length 92
% identity 74

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

```
Seq. No.
                    40030
 Seq. ID
                   LIB3138-003-Q1-N1-E10
 Method
                   BLASTN
 NCBI GI
                   g1419473
 BLAST score
                   35
 E value
                   4.0e-10
 Match length
                   168
 % identity
                   88
 NCBI Description A.thaliana chloroplast ndhA gene
 Seq. No.
                   40031
 Seq. ID
                   LIB3138-003-Q1-N1-F11
 Method
                   BLASTN
 NCBI GI
                   g3832511
 BLAST score
                   49
 E value
                   2.0e-18
 Match length
                   121
 % identity
                   85
 NCBI Description
                   Astragalus membranaceus granule-bound glycogen (starch)
                   synthase mRNA, complete cds
 Seq. No.
                   40032
 Seq. ID
                   LIB3138-003-Q1-N1-F3
 Method
                   BLASTX
NCBI GI
                   g461812
 BLAST score
                   188
 E value
                   4.0e-14
 Match length
                   67
 % identity
                   57
 NCBI Description
                   CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
                   GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                   Cytochrome P-450 protein [Catharanthus roseus]
                   >gi 445604 prf 1909351A cytochrome P450 [Catharanthus
                   roseus]
 Seq. No.
                   40033
 Seq. ID
                   LIB3138-003-Q1-N1-G2
Method
                   BLASTX
NCBI GI
                   g1169201
BLAST score
                   233
E value
                   2.0e-19
Match length
                   116
% identity
                   48
NCBI Description
                   DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                   >gi_421830_pir_ S33707 DRT112 protein - Arabidopsis
                   thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
```

Seq. No. 40034 Seq. ID LIB3138-003-Q1-N1-G5

Method BLASTX
NCBI GI g3738303
BLAST score 232
E value 3.0e-19
Match length 74
% identity 64

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

Method



>gi 4249399 (AC006072) unknown protein [Arabidopsis

thaliana] Seq. No. 40035 Seq. ID LIB3138-003-Q1-N1-G8 Method BLASTX NCBI GI g1350548 BLAST score 166 E value 1.0e-11 Match length 100 % identity 39 NCBI Description (L47609) heat shock-like protein [Picea glauca] Seq. No. 40036 Seq. ID LIB3138-003-Q1-N1-H12 Method BLASTN NCBI GI g531828 BLAST score 53 E value 6.0e-21 Match length 193 % identity 82 NCBI Description Cloning vector pSport1, complete cds Seq. No. 40037 Seq. ID LIB3138-003-01-N1-H9 Method BLASTX NCBI GI q3650030 BLAST score 190 2.0e-14 E value Match length 98 % identity 41 NCBI Description (AC005396) unknown protein [Arabidopsis thaliana] Seq. No. 40038 Seq. ID LIB3138-004-Q1-N1-A12 Method BLASTX NCBI GI q444791 BLAST score 474 E value 3.0e-49 Match length 113 % identity 24 NCBI Description ubiquitin [Bos taurus] Seq. No. 40039 Seq. ID LIB3138-004-Q1-N1-A3 Method BLASTN NCBI GI g4097879 BLAST score 38 E value 3.0e-12 Match length 102 % identity 85 NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

_

LIB3138-004-Q1-N1-B10

40040

BLASTN



```
NCBI GI
                   g4097879
BLAST score
                   64
E value
                   1.0e-27
Match length
                   112
% identity
                   89
NCBI Description
                   Bean pod mottle virus complete segment RNA1 polyprotein
                   gene, complete cds
                   40041
Seq. No.
Seq. ID
                   LIB3138-004-Q1-N1-B3
Method
                   BLASTX
NCBI GI
                   q2738248
BLAST score
                   170
E value
                   5.0e-17
Match length
                   105
% identity
                   58
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   40042
Seq. ID
                   LIB3138-004-Q1-N1-C7
Method
                   BLASTX
NCBI GI
                   q400638
BLAST score
                   330
E value
                   7.0e-31
Match length
                   97
% identity
                   71
NCBI Description
                  NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1
                   >gi_1334564_emb_CAA38809_ (X55026) NADH-ubiquinone
                   oxidoreductase subunit 1 [Podospora anserina]
Seq. No.
                   40043
Seq. ID
                   LIB3138-004-Q1-N1-C9
Method
                  BLASTX
NCBI GI
                   q4538939
BLAST score
                   194
E value
                   2.0e-20
Match length
                   97
% identity
NCBI Description
                   (AL049483) Col-O casein kinase I-like protein [Arabidopsis
                  thaliana]
Seq. No.
                   40044
Seq. ID
                  LIB3138-004-Q1-N1-D11
Method
                  BLASTX
NCBI GI
                  q231610
BLAST score
                  157
                  1.0e-10
E value
Match length
                  37
% identity
                  89
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
```

>gi_67880_pir __PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152 (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 40045



```
Seq. ID
                   LIB3138-004-Q1-N1-F8
Method
                   BLASTX
NCBI GI
                   g3688191
BLAST score
                   283
E value
                   2.0e-25
Match length
                   69
% identity
                   71
                   (AJ010090) MAP3K alpha protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   40046
Seq. No.
Seq. ID
                   LIB3138-004-Q1-N1-G2
Method
                   BLASTX
NCBI GI
                   q1764098
BLAST score
                   317
E value
                   2.0e-29
Match length
                   112
% identity
                   52
NCBI Description
                  (U81794) putative permease [Uromyces fabae]
Seq. No.
                   40047
Seq. ID
                   LIB3138-005-Q1-N1-A12
Method
                   BLASTX
NCBI GI
                   g2598039
BLAST score
                   193
E value
                   9.0e-15
Match length
                   137
% identity
                   37
NCBI Description
                   (AJ001273) manganese resistance 1 protein [Saccharomyces
                   cerevisiae]
Seq. No.
                   40048
Seq. ID
                  LIB3138-005-Q1-N1-B3
Method
                  BLASTX
NCBI GI
                  q3152598
BLAST score
                   155
                   2.0e-10
E value
Match length
                   94
% identity
                   47
NCBI Description
                  (AC002986) Contains similarity to C2-HC type zinc finger
                  protein C.e-MyT1 gb_U67079 from C. elegans and to
                  hypersensitivity-related gene 201 isolog T28M21.14 from A.
                  thaliana BAC gb_AF002109. [Arabidopsis thaliana]
Seq. No.
                  40049
Seq. ID
                  LIB3138-005-Q1-N1-C10
Method
                  BLASTN
                  g3885514
                  60
                  5.0e-25
                  202
```

NCBI GI BLAST score E value Match length % identity 88

NCBI Description Medicago sativa clone MS56 unknown mRNA

Seq. No.

40050

Seq. ID LIB3138-005-Q1-N1-D7

Method BLASTN



NCBI GI g4097879
BLAST score 151
E value 2.0e-79
Match length 335
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40051

Seq. ID LIB3138-005-Q1-N1-E4

Method BLASTN
NCBI GI g3552012
BLAST score 76
E value 2.0e-34
Match length 278

Match length 278 % identity 84

NCBI Description Glycine max proline-rich protein precursor, mRNA, complete

cds

Seq. No. 40052

Seq. ID LIB3138-005-Q1-N1-G8

Method BLASTN
NCBI GI 94097879
BLAST score 71
E value 1.0e-31
Match length 127
% identity 89

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40053

Seq. ID LIB3138-005-Q1-N1-H2

Method BLASTX
NCBI GI g229707
BLAST score 441
E value 8.0e-44
Match length 97
% identity 82

NCBI Description Bean pod mottle virus

Seq. No. 40054

Seq. ID LIB3138-005-Q1-N1-H4

Method BLASTX
NCBI GI g3676762
BLAST score 259
E value 1.0e-22
Match length 81
% identity 62

NCBI Description (AF087136) RS6/L7A ribosomal protein homolog

[Schizosaccharomyces pombe]

Seq. No. 40055

Seq. ID LIB3138-006-Q1-N1-A9

Method BLASTN
NCBI GI g3021374
BLAST score 203
E value 1.0e-110



```
Match length 279 % identity 93
```

NCBI Description Glycine max mRNA for profilin, PRO1

Seq. No.

40056

Seq. ID

LIB3138-006-Q1-N1-B11

Method

BLASTX

NCBI GI

g4097880

BLAST score E value 259 8.0e-23

Match length

87 61

% identity NCBI Description

(U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40057

Seq. ID

LIB3138-006-Q1-N1-B3

Method NCBI GI BLASTX g138364

BLAST score E value

257 2.0e-22

Match length % identity

2.0e-2 87 66

40058

NCBI Description

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No.

Seq. ID

LIB3138-006-Q1-N1-C10

Method BLASTN
NCBI GI g938299
BLAST score 40
E value 4.0e-13
Match length 92

% identity 89

NCBI Description V.ungiculata mRNA for unknown protein (A3 gene)

Seq. No.

40059

Seq. ID

LIB3138-006-Q1-N1-C3

Method BLASTN
NCBI GI g4097879
BLAST score 168
E value 1.0e-89
Match length 356
% identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40060

Seq. ID

LIB3138-006-Q1-N1-D1

Method BLASTX
NCBI GI g2804298
BLAST score 256
E value 4.0e-22
Match length 128
% identity 38

NCBI Description (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]

```
40061
Seq. No.
Seq. ID
                  LIB3138-006-Q1-N1-D2
Method
                  BLASTX
NCBI GI
                  g3269300
BLAST score
                   409
E value
                   4.0e-40
                   92
Match length
                  76
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                   40062
Seq. ID
                  LIB3138-006-Q1-N1-D9
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  276
E value
                  7.0e-25
Match length
                  76
                  74
% identity
NCBI Description
                  (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  40063
Seq. ID
                  LIB3138-006-Q1-N1-E12
Method
                  BLASTX
NCBI GI
                  q138364
BLAST score
                  335
E value
                  1.0e-31
Match length
                  82
                  78
% identity
NCBI Description
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  40064
Seq. ID
                  LIB3138-006-Q1-N1-E4
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  127
E value
                  5.0e-65
Match length
                  304
% identity
                  87
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40065
Seq. ID
                  LIB3138-006-Q1-N1-G12
Method
                  BLASTX
NCBI GI
                  g123537
BLAST score
                  190
E value
                  2.0e-14
Match length
                  95
                  45
% identity
NCBI Description
                  12 KD HEAT SHOCK PROTEIN (GLUCOSE AND LIPID-REGULATED
                  PROTEIN) >gi_72231_pir__HHBY12 heat shock protein 12 -
```

yeast (Saccharomyces cerevisiae) >gi_3800_emb_CAA39306_
(X55785) hsp12 [Saccharomyces cerevisiae] >gi_171607



(M60827) 15 kD glucose and lipid regulated protein [Saccharomyces cerevisiae] >gi_559934_emb_CAA86349 (Z46255) hsp12, glp1, len: 109, CAI: 0.65, HS12_YEAST P22943 12 KD HEAT SHOCK PROTEIN [Saccharomyces cerevisiae] >gi_836740_dbj_BAA09224_ (D50617) 12KD heat shock protein [Saccharomyces cerevisiae] >gi_1100790_dbj_BAA08003 (D44596) 15kD glucose and lipid regulated protein [Saccharomyces cerevisiae] >gi_1742028_dbj_BAA14033_ (D89864) Sc-Hsp12p [Saccharomyces pastorianus]

 Seq. No.
 40066

 Seq. ID
 LIB3138-007-Q1-N1-B9

 Method
 BLASTN

 NCBL GI
 TARRESTO

NCBI GI g4097879 BLAST score 88

BLAST score 88 E value 6.0e-42 Match length 224 % identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40067

Seq. ID LIB3138-007-Q1-N1-E12

Method BLASTN
NCBI GI 94097879
BLAST score 87
E value 3.0e-41
Match length 310

% identity 83
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40068

Seq. ID LIB3138-007-Q1-N1-G1

Method BLASTX
NCBI GI g138364
BLAST score 270
E value 3.0e-24
Match length 67
% identity 76

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40069

Seq. ID LIB3138-007-Q1-N1-G11

Method BLASTN
NCBI GI g4097879
BLAST score 112
E value 4.0e-56
Match length 352
% identity 83

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40070



```
Seq. ID
                   LIB3138-007-Q1-N1-H10
Method
                   BLASTN
NCBI GI
                   g3033512
BLAST score
                   105
E value
                   3.0e-52
Match length
                   185
% identity
                   89
NCBI Description
                  Phaseolus vulgaris rubisco activase (Rca1) mRNA, complete
                   cds
                   40071
Seq. No.
Seq. ID
                   LIB3138-008-Q1-N1-A12
Method
                   BLASTX
NCBI GI
                   g229707
BLAST score
                   315
E value
                   4.0e-29
Match length
                   86
% identity
                   73
NCBI Description Bean pod mottle virus
Seq. No.
                   40072
Seq. ID
                   LIB3138-008-Q1-N1-A2
Method
                  BLASTN
NCBI GI
                   g4097879
BLAST score
                   84
E value
                   2.0e-39
Match length
                   372
% identity
                   82
NCBI Description
                  Bean pod mottle virus complete segment RNA1 polyprotein
                   gene, complete cds
Seq. No.
                   40073
Seq. ID
                  LIB3138-008-Q1-N1-B3
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  86
E value
                  1.0e-40
Match length
                  262
% identity
                  84
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40074
Seq. ID
                  LIB3138-008-Q1-N1-B5
Method
                  BLASTX
NCBI GI
                  g586542
BLAST score
                  213
E value
                  4.0e-17
Match length
                  92
% identity
                  47
                  GENERAL AMINO ACID PERMEASE AGP2 >gi_626793_pir__S46001
NCBI Description
```

probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae) >gi_496863_emb_CAA53491_

(X75891) YBR1007 [Saccharomyces cerevisiae] >gi_536423 emb_CAA85089 (Z36001) ORF YBR132c

[Saccharomyces cerevisiae] >gi_1582519_prf__2118402G

YBR1007 gene [Saccharomyces cerevisiae]

Match length

NCBI Description

% identity

88 69



```
Seq. No.
                  40075
Seq. ID
                  LIB3138-008-Q1-N1-B8
Method
                  BLASTX
NCBI GI
                  q138364
BLAST score
                  354
                  9.0e-34
E value
                  110
Match length
% identity
                  66
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  40076
                  LIB3138-008-Q1-N1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  81
E value
                  7.0e-38
Match length
                  129
% identity
                  91
NCBI Description
                  Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
                  40077
Seq. No.
Seq. ID
                  LIB3138-008-Q1-N1-C10
Method
                  BLASTX
NCBI GI
                  g1256839
BLAST score
                  475
E value
                  8.0e-48
Match length
                  128
% identity
NCBI Description
                  (U53329) Ran1-like protein kinase [Fusarium solani f. sp.
                  pisi]
                  40078
Seq. No.
                  LIB3138-008-Q1-N1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2944178
BLAST score
                  191
                  9.0e-15
E value
                  77
Match length
% identity
                  55
                  (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  40079
Seq. ID
                  LIB3138-008-Q1-N1-C6
Method
                  BLASTX
NCBI GI
                  q4204697
BLAST score
                  341
E value
                  3.0e-32
```

At5P2 [Arabidopsis thaliana]

(AF117063) putative inositol polyphosphate 5-phosphatase

```
Seq. No.
                   40080
Seq. ID
                   LIB3138-008-Q1-N1-D7
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   128
E value
                   1.0e-65
Match length
                   242
% identity
                   90
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
Seq. No.
                   40081
Seq. ID
                  LIB3138-008-Q1-N1-D9
Method
                  BLASTX
NCBI GI
                   g229707
BLAST score
                   461
E value
                   3.0e-46
Match length
                  113
                   77
% identity
NCBI Description Bean pod mottle virus
Seq. No.
                  40082
Seq. ID
                  LIB3138-008-Q1-N1-E7
Method
                  BLASTN
NCBI GI
                  g533295
BLAST score
                  47
E value
                  2.0e-17
Match length
                  107
```

 Seq. No.
 40083

 Seq. ID
 LIB3138-008-Q1-N1-E8

 Method
 BLASTX

 NCBI GI
 g3647355

 BLAST score
 237

 E value
 5.0e-20

E value 5.0e Match length 99 % identity 47

NCBI Description (Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA

Seq. No. 40084

Seq. ID LIB3138-008-Q1-N1-F2

Method BLASTX
NCBI GI g2500493
BLAST score 326
E value 2.0e-30
Match length 90
% identity 64

NCBI Description PUTATIVE 40S RIBOSOMAL PROTEIN IN SNF2-CPA1 INTERGENIC REGION >gi_2119080_pir_S67197 ribosomal protein S10.e.A -

% identity

NCBI Description

53



yeast (Saccharomyces cerevisiae) >qi 1420650 emb CAA99521

(Z75201) ORF YOR293w [Saccharomyces cerevisiae] Seq. No. 40085 Seq. ID LIB3138-008-Q1-N1-F3 Method BLASTX NCBI GI g4455169 BLAST score 218 E value 8.0e-18 Match length 79 57 % identity NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana] 40086 Seq. No. Seq. ID LIB3138-008-Q1-N1-F4 Method BLASTN NCBI GI g806807 BLAST score 130 E value 6.0e-67 230 Match length % identity 89 Pisum sativum chaperonin precursor mRNA, chloroplast gene NCBI Description encoding chloroplast protein, complete cds Seq. No. 40087 Seq. ID LIB3138-008-Q1-N1-F6 Method BLASTX NCBI GI g282921 BLAST score 160 E value 6.0e-11 Match length 98 % identity 41 NCBI Description carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi 169057 (M63627) carbonic anhydrase [Pisum sativum] >gi_227784_prf 1710354A carbonic anhydrase [Pisum sativum] Seq. No. 40088 Seq. ID LIB3138-008-Q1-N1-G3 Method BLASTX NCBI GI g229707 BLAST score 194 E value 6.0e-15 Match length 81 % identity 56 NCBI Description Bean pod mottle virus Seq. No. 40089 LIB3138-008-Q1-N1-G4 Seq. ID Method BLASTX NCBI GI g1488043 BLAST score 170 7.0e-20 E value Match length 116

(U63784) PAPS-reductase-like protein [Catharanthus roseus]



```
Seq. No.
Seq. ID
                   LIB3138-008-Q1-N1-G5
Method
                   BLASTX
NCBI GI
                   g4097880
BLAST score
                   388
                   1.0e-37
E value
                   123
Match length
% identity
                   63
NCBI Description
                  (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   40091
Seq. ID
                   LIB3138-008-Q1-N1-H10
Method
                   BLASTX
NCBI GI
                   g2245066
BLAST score
                   164
E value
                   2.0e-11
                   69
Match length
                   52
% identity
NCBI Description
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
Seq. No.
                   40092
Seq. ID
                   LIB3138-008-Q1-N1-H12
Method
                   BLASTN
                   g496493
NCBI GI
BLAST score
                   149
E value
                   3.0e-78
Match length
                   374
% identity
                   87
                  P.sativum (Rosakrone) mRNA for nonphosphorylating,
NCBI Description
                  NADP-specific, glyceraldehyde-3-phosphate dehydrogenase
Seq. No.
                   40093
Seq. ID
                  LIB3138-009-Q1-N1-A12
Method
                  BLASTX
NCBI GI
                   g4097880
BLAST score
                   200
                   4.0e-24
E value
Match length
                   90
% identity
                   64
NCBI Description
                  (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   40094
Seq. ID
                  LIB3138-009-Q1-N1-A5
Method
                  BLASTN
                   g4097879
NCBI GI
BLAST score
                   67
E value
                   3.0e-29
Match length
                  196
% identity
                   87
NCBI Description
                  Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
Seq. No.
                   40095
```

Seq. ID LIB3138-009-Q1-N1-B12

Method BLASTX NCBI GI g2702274 BLAST score 240



```
E value
                  2.0e-20
Match length
                  69
% identity
                  67
NCBI Description
                  (AC003033) unknown protein [Arabidopsis thaliana]
```

Seq. No. 40096 Seq. ID LIB3138-009-Q1-N1-B3

Method BLASTN NCBI GI g210811 BLAST score 67 E value 2.0e-29

Match length 180 % identity 91

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40097

Seq. ID LIB3138-009-Q1-N1-B8

Method BLASTN NCBI GI g3021374 BLAST score 55 E value 3.0e-22 Match length 123 86 % identity

NCBI Description Glycine max mRNA for profilin, PRO1

Seq. No. 40098

Seq. ID LIB3138-009-Q1-N1-C12

Method BLASTX NCBI GI g4097880 BLAST score 537 E value 4.0e-55 Match length 121 86 % identity

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40099

Seq. ID LIB3138-009-Q1-N1-D11

Method BLASTX NCBI GI g138364 BLAST score 222 E value 2.0e-18 Match length 77 58 % identity

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40100

Seq. ID LIB3138-009-Q1-N1-D7

Method BLASTX NCBI GI q4097880 BLAST score 277 E value 5.0e-46Match length 124 % identity 78





```
NCBI Description
                  (U70866) polyprotein [Bean pod mottle virus]
                  40101
Seq. No.
Seq. ID
                  LIB3138-009-Q1-N1-E10
Method*
                  BLASTX
NCBI GI
                  g3236238
BLAST score
                  182
E value
                  5.0e-14
                  42
Match length
                  76
% identity
NCBI Description
                  (AC004684) putative ARF1 GTPase activating protein
                   [Arabidopsis thaliana] >gi 4519792 dbj BAA75744.1
                   (AB017876) Asp1 [Arabidopsis thaliana]
                  40102
Seq. No.
Seq. ID
                  LIB3138-009-Q1-N1-F10
Method
                  BLASTN
NCBI GI
                  g313266
BLAST score
                  58
                  7.0e-24
E value
Match length
                  82
% identity
                  93
NCBI Description T.aestivum gene for phosphoglycerate kinase
Seq. No.
                  40103
Seq. ID
                  LIB3138-009-Q1-N1-F6
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  163
E value
                  1.0e-86
Match length
                  347
% identity
                  87
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                  40104
Seq. ID
                  LIB3138-009-Q1-N1-F8
Method
                  BLASTX
NCBI GI
                  g100196
BLAST score
                  205
E value
                  3.0e-16
Match length
                  84
% identity
                  52
NCBI Description
                  chlorophyll a/b-binding protein (cab-11) - tomato
                  40105
Seq. No.
Seq. ID
                  LIB3138-009-Q1-N1-F9
Method
                  BLASTX
NCBI GI
                  q1717779
BLAST score
                  319
E value
                  1.0e-29
Match length
                  108
% identity
```

Seq. No. 40106

NCBI Description

THIOREDOXIN REDUCTASE >gi 757510 dbj BAA08090 (D45049)

Thioredoxin Reductase (NADPH) [Neurospora crassa]



```
LIB3138-009-Q1-N1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  130
E value
                  7.0e-67
Match length
                  309
                  86
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
                  40107
Seq. No.
                  LIB3138-010-Q1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g138364
BLAST score
                  568
E value
                  1.0e-58
Match length
                  137
% identity
                  81
NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
                  40108
Seq. No.
Seq. ID
                  LIB3138-010-Q1-N1-A3
                  BLASTN
Method
NCBI GI
                  g210811
                  52
BLAST score
                  2.0e-20
E value
                  107
Match length
% identity
                  89
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40109
Seq. ID
                  LIB3138-010-Q1-N1-B1
Method
                  BLASTX
                  g4097880
NCBI GI
BLAST score
                  230
E value
                  3.0e-19
                  97
Match length
                  54
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  40110
                  LIB3138-010-Q1-N1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  180
E value
                  1.0e-96
Match length
                  336
                  89
% identity
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
```

Seq. ID LIB3138-010-Q1-N1-D3



```
BLASTX
Method
NCBI GI
                  q1296805
BLAST score
                   300
E value
                  2.0e-27
                  82
Match length
% identity
                  70
NCBI Description
                   (X90929) C-terminal peptidase of the D1 protein [Hordeum
                  vulgare]
Seq. No.
                   40112
Seq. ID
                  LIB3138-010-Q1-N1-E4
Method
                  BLASTX
NCBI GI
                  g3128213
BLAST score
                  241
                  2.0e-20
E value
Match length
                  100
% identity
                  26
NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  40113
Seq. ID
                  LIB3138-010-Q1-N1-G1
Method
                  BLASTX
NCBI GI
                  q229708
BLAST score
                  264
E value
                  4.0e-23
Match length
                  109
% identity
                  52
NCBI Description Bean pod mottle virus
Seq. No.
                  40114
Seq. ID
                  LIB3138-010-Q1-N1-G12
Method
                  BLASTX
NCBI GI
                  g131218
BLAST score
                  141
                  1.0e-08
E value
Match length
                  42
% identity
                  64
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IX (PSI-J)
NCBI Description
                  >gi 2924269_emb CAA77421_ (Z00044) PSI J-protein [Nicotiana
                  tabacum]
                  40115
Seq. No.
Seq. ID
                  LIB3138-010-Q1-N1-G6
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  82
                  3.0e-38
E value
Match length
                  383
                  81
% identity
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
```

Seq. No. 40116

Seq. ID LIB3138-010-Q1-N1-H11

Method BLASTX NCBI GI g138364 BLAST score 371



E value 1.0e-35 Match length 125 % identity 64

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40117

Seq. ID LIB3138-010-Q1-N1-H12

Method BLASTX
NCBI GI g229707
BLAST score 307
E value 1.0e-28
Match length 78
% identity 76

NCBI Description Bean pod mottle virus

Seq. No. 40118

Seq. ID LIB3138-010-Q1-N1-H3

Method BLASTN
NCBI GI g210811
BLAST score 121
E value 1.0e-61
Match length 297
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40119

Seq. ID LIB3138-011-Q1-N1-B6

Method BLASTN
NCBI GI g4097879
BLAST score 86
E value 1.0e-40
Match length 206
% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40120

Seq. ID LIB3138-011-Q1-N1-C8

Method BLASTX
NCBI GI g4097880
BLAST score 260
E value 1.0e-22
Match length 73
% identity 74

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 40121

Seq. ID LIB3138-011-Q1-N1-D4

Method BLASTN
NCBI GI g4097879
BLAST score 42
E value 2.0e-14
Match length 94



% identity

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40122

Seq. ID LIB3138-011-Q1-N1-D6 BLASTX

Method NCBI GI

g1172441 376

BLAST score E value

3.0e-36 113

75

Match length % identity

NCBI Description

POSSIBLE TRANSCRIPTION FACTOR POSF21 >qi 99685 pir S21883

DNA-binding protein POSF21 - Arabidopsis thaliana >gi 16429_emb_CAA43366_ (X61031) posF21 [Arabidopsis

thaliana]

Seq. No.

40123

Seq. ID

LIB3138-011-Q1-N1-F3

Method NCBI GI BLAST score BLASTX q3033389 159

E value Match length

9.0e-11 132

% identity

NCBI Description

(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No.

40124

Seq. ID

LIB3138-011-Q1-N2-A10 BLASTN

Method NCBI GI BLAST score

g210811 52

E value Match length 2.0e-20

% identity

103 89

NCBI Description

Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. Seq. ID

40125

Method

LIB3138-011-Q1-N2-A7

NCBI GI

BLASTX g3874271

BLAST score E value

316 1.0e-29

Match length % identity

79 72

NCBI Description

(Z81467) predicted using Genefinder; Similarity to Drosophila UDP-glucose:glycoprotein glucosyltransferase

(TR:Q09332); cDNA EST yk250b10.3 comes from this gene; cDNA EST yk250b10.5 comes from this gene [Caenorhabditis

elegans] >gi 3876437 emb CAB04207 (Z81516) predicted using

Genefinder; Similarity to Drosophila

UDP-glucose:glycoprotein glucosyltransferase (TR:Q09332);

cDNA EST yk250b10.3 comes from this gene; cDNA EST

yk250b10.5 comes from this gene [Caenorhabditis elegans]

Seq. No.

40126

NCBI GI

BLAST score



```
LIB3138-011-Q1-N2-F5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4097879
BLAST score
                  91
                  2.0e-43
E value
                  307
Match length
                  86
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  40127
Seq. No.
Seq. ID
                  LIB3138-012-Q1-N1-A2
                  BLASTX
Method
NCBI GI
                  g4097880
BLAST score
                  141
E value
                  5.0e-09
                  84
Match length
                  40
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                  40128
Seq. ID
                  LIB3138-012-Q1-N1-A8
Method
                  BLASTN
NCBI GI
                  q938299
BLAST score
                  52
                  2.0e-20
E value
Match length
                  148
                  84
% identity
NCBI Description V.ungiculata mRNA for unknown protein (A3 gene)
                  40129
Seq. No.
Seq. ID
                  LIB3138-012-Q1-N1-A9
                  BLASTX
Method
NCBI GI
                  g3114719
BLAST score
                  229
E value
                  6.0e-19
Match length
                  135
                  18
% identity
NCBI Description
                  (Z68906) ATP-binding multidrug cassette transporter
                  [Botryotinia fuckeliana]
Seq. No.
                  40130
Seq. ID
                  LIB3138-012-Q1-N1-B10
Method
                  BLASTN
NCBI GI
                  q210811
BLAST score
                  115
E value
                  6.0e-58
                  300
Match length
% identity
                  87
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                  40131
Seq. ID
                  LIB3138-012-Q1-N1-B7
Method
                  BLASTN
```

6270

g3033512

104



E value 2.0e-51
Match length 347
% identity 82

NCBI Description Phaseolus vulgaris rubisco activase (Rcal) mRNA, complete

cds

Seq. No. 40132

Seq. ID LIB3138-012-Q1-N1-C3

Method BLASTX
NCBI GI g3063458
BLAST score 307
E value 4.0e-28
Match length 118
% identity 49

NCBI Description (AC003981) F22013.20 [Arabidopsis thaliana]

Seq. No. 40133

Seq. ID LIB3138-012-Q1-N1-C5

Method BLASTX
NCBI GI g138364
BLAST score 288
E value 6.0e-26
Match length 116
% identity 52

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40134

Seq. ID LIB3138-012-Q1-N1-C6

Method BLASTX
NCBI GI g138364
BLAST score 250
E value 1.0e-21
Match length 98
% identity 52

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40135

Seq. ID LIB3138-012-Q1-N1-D11

Method BLASTX
NCBI GI g3367594
BLAST score 273
E value 3.0e-24
Match length 91
% identity 57

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 40136

Seq. ID LIB3138-012-Q1-N1-D5

Method BLASTX NCBI GI g138364 BLAST score 162



```
E value

3.0e-11

Match length
60
% identity

NCBI Description

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
bean pod mottle virus (strain Kentucky G7) >gi_210812
(M62738) coat protein [Bean pod mottle virus]

Seq. No.

40137

Seq. ID

LIB3138-012-Q1-N1-E11
```

Method BLASTN

NCBI GI g210811

BLAST score 159

E value 4.0e-84

Match length 339

% identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40138 Seq. ID LIB3138-

Seq. ID LIB3138-012-Q1-N1-H12

Method BLASTX
NCBI GI g1053216
BLAST score 163
E value 3.0e-11
Match length 69
% identity 55

NCBI Description (U39475) chlorophyll a/b-binding protein [Glycine max]

Seq. No. 40139

Seq. ID LIB3138-012-Q1-N1-H8

Method BLASTN
NCBI GI g210811
BLAST score 70
E value 4.0e-31
Match length 166
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40140

Seq. ID LIB3138-013-Q1-N1-A5

Method BLASTX
NCBI GI 94490682
BLAST score 232
E value 2.0e-19
Match length 115
% identity 48

NCBI Description (AJ132376) cdc37 protein [Schizosaccharomyces pombe]

>gi_4490684_emb_CAB38758.1_ (AJ132377) cdc37 protein

[Schizosaccharomyces pombe]

Seq. No. 40141

Seq. ID LIB3138-013-Q1-N1-B1

Method BLASTN NCBI GI g210811 BLAST score 100

6272

, e.e., 1



5.0e-49 E value Match length 332 % identity Bean pod mottle virus coat protein gene, complete cds, NCBI Description complete middle component (M) RNA Seq. No. 40142 Seq. ID LIB3138-013-Q1-N1-B11 Method BLASTX NCBI GI q115471 BLAST score 298 E value 5.0e-27 Match length 121 57 % identity CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE NCBI Description DEHYDRATASE) >gi_100078_pir__S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792 (X52558) precursor peptide (AA -104 to 224) [Pisum sativum] Seq. No. 40143 Seq. ID LIB3138-013-Q1-N1-D2 Method BLASTN NCBI GI q602564 BLAST score 127 5.0e-65 E value Match length 379 83 % identity NCBI Description C.paradisi (Macf) INO1 gene Seq. No. 40144 LIB3138-013-Q1-N1-D4 Seq. ID Method BLASTN NCBI GI g537626 BLAST score 114 2.0e-57 E value Match length 262 % identity 86 Glycine max inducible nitrate reductase 2 (INR2) mRNA, NCBI Description complete cds 40145 Seq. No. LIB3138-013-Q1-N1-F1 Seq. ID Method BLASTX NCBI GI g473874 207 BLAST score

2.0e-16 E value Match length 134 % identity 9

(U08285) a membrane-associated salt-inducible protein NCBI Description

[Nicotiana tabacum]

Seq. No.

40146

Seq. ID

LIB3138-013-Q1-N1-G3

Method BLASTX g1123105 NCBI GI BLAST score 199 E value 1.0e-15



```
Match length 98
% identity 44
NCBI Description (U42438) similar to S. cerevisiae longevity-assurance protein 1 (SP:P38703) [Caenorhabditis elegans]

Seq. No. 40147
Seq. ID LIB3138-013-Q1-N1-G6
Method BLASTX
```

NCBI GI g4097880 BLAST score 416 E value 6.0e-41 Match length 120 % identity 72

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

 Seq. No.
 40148

 Seq. ID
 LIB3138-013-Q1-N1-H10

 Method
 BLASTN

Method BLASTN
NCBI GI g210811
BLAST score 128
E value 7.0e-66
Match length 180
% identity 93

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40149

Seq. ID LIB3138-014-Q1-N1-A1

Method BLASTX
NCBI GI g4455232
BLAST score 178
E value 4.0e-13
Match length 99
% identity 53

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No.

40150

Seq. ID LIB3138-014-Q1-N1-A12

Method BLASTN
NCBI GI g1055367
BLAST score 54
E value 1.0e-21
Match length 194
% identity 82

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 40151

Seq. ID LIB3138-014-Q1-N1-B12

Method BLASTN
NCBI GI g210811
BLAST score 95
E value 4.0e-46
Match length 251
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Match length

NCBI Description

% identity

263

88



40152 Seq. No. Seq. ID LIB3138-014-Q1-N1-B4 Method BLASTN g4097879 NCBI GI BLAST score 54 2.0e-21 E value Match length * 122 % identity 86 NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds Seq. No. 40153 Seq. ID LIB3138-014-Q1-N1-D4 Method BLASTX NCBI GI q138364 BLAST score 212 E value 3.0e-17 Match length 98 51 % identity GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi 210812 (M62738) coat protein [Bean pod mottle virus] Seq. No. 40154 Seq. ID LIB3138-014-Q1-N1-F12 Method BLASTN NCBI GI g2687434 BLAST score 82 2.0e-38 E value 206 Match length % identity 85 Eucryphia lucida large subunit 26S ribosomal RNA gene, NCBI Description partial sequence 40155 Seq. No. Seq. ID LIB3138-014-Q1-N1-F2 Method BLASTX g4049353 NCBI GI BLAST score 156 2.0e-10 E value Match length 68 57 % identity (AL034567) putative protein [Arabidopsis thaliana] NCBI Description 40156 Seq. No. Seq. ID LIB3138-014-Q1-N1-F5 Method BLASTN NCBI GI g210811 BLAST score 110 5.0e-55 E value

complete middle component (M) RNA

Bean pod mottle virus coat protein gene, complete cds,



```
Seq. No.
Seq. ID
                  LIB3138-014-Q1-N1-F6
Method
                  BLASTX
NCBI GI
                  g3348073
BLAST score
                  595
E value
                  7.0e-62
Match length
                  130
% identity
                  85
NCBI Description
                  (AF077766) plasma membrane H(+)-ATPase 1 [Filobasidiella
                  neoformans]
Seq. No.
                  40158
Seq. ID
                  LIB3138-014-Q1-N1-G11
Method
                  BLASTX
NCBI GI
                  q2496789
BLAST score
                  173
E value
                  2.0e-12
Match length
                  57
                  63
% identity
                  1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (DXP
NCBI Description
                  REDUCTOISOMERASE) >gi 1001556 dbj BAA10183 (D64000)
                  hypothetical protein [Synechocystis sp.]
Seq. No.
                  40159
Seq. ID
                  LIB3138-014-Q1-N2-C3
Method
                  BLASTX
NCBI GI
                  q3738194
BLAST score
                  140
E value
                  1.0e-08
Match length
                  44
% identity
                  59
NCBI Description (AL031854) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  40160
Seq. ID
                  LIB3138-014-Q1-N2-D7
Method
                  BLASTX
NCBI GI
                  g3329368
BLAST score
                  212
E value
                  5.0e-17
Match length
                  120
% identity
                  35
NCBI Description
                  (AF031244) nodulin-like protein [Arabidopsis thaliana]
Seq. No.
                  40161
Seq. ID
                  LIB3138-014-Q1-N2-E1
Method
                  BLASTX
                  q4481810
                  141
                  1.0e-08
                  62
```

NCBI GI BLAST score E value Match length 40 % identity

NCBI Description (AL035632) BACN32G11.d [Drosophila melanogaster]

Seq. No. 40162

Seq. ID LIB3138-014-Q1-N2-E10

Method BLASTX NCBI GI g399024



BLAST score E value 1.0e-13 Match length 84 % identity 48

FRUCTOSE-BISPHOSPHATE ALDOLASE 1, CHLOROPLAST PRECURSOR NCBI Description >gi_322710_pir__S29047 fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - garden pea (fragment)

>gi_169037 (M97476) aldolase [Pisum sativum]

Seq. No. 40163

Seq. ID LIB3138-014-Q1-N2-F1

Method BLASTN NCBI GI q210811 BLAST score 150 E value 8.0e-79 Match length 352 % identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40164

Seq. ID LIB3138-014-Q1-N2-H5

Method BLASTX NCBI GI g3860272 BLAST score 263 2.0e-23 E value 72 Match length % identity 78

NCBI Description (AC005824) putative suppressor protein [Arabidopsis

thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1

protein [Arabidopsis thaliana]

Seq. No. 40165

Seq. ID LIB3138-015-Q1-N1-C8

Method BLASTX NCBI GI q913445 BLAST score 260 E value 1.0e-22 Match length 84 % identity 64

NCBI Description (S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv.

red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

Seq. No. 40166

Seq. ID LIB3138-015-Q1-N1-D12

BLASTX Method NCBI GI g4580513 BLAST score 393 E value 3.0e-38 Match length 98 76 % identity

NCBI Description (AF036300) scarecrow-like 1 [Arabidopsis thaliana]

Seq. No.

40167

Seq. ID LIB3138-015-Q1-N1-D4

Method BLASTN



```
NCBI GI
                    g210811
 BLAST score
                    160
 E value
                    1.0e-84
Match length
                   364
 % identity
                   86
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
 Seq. No.
                   40168
Seq. ID
                   LIB3138-015-Q1-N1-E4
Method
                   BLASTX
NCBI GI
                   g4377999
BLAST score
                   547
E value
                   3.0e-56
Match length
                   125
% identity
                   78
NCBI Description
                   (AF076951) Cu-Zn superoxide dismutase [Glomerella
                   cingulata]
Seq. No.
                   40169
Seq. ID
                   LIB3138-015-Q1-N1-F4
Method
                   BLASTX
NCBI GI
                   g4538960
                   244
BLAST score
E value
                   1.0e-26
Match length
                   122
% identity
                   47
NCBI Description
                   (AL049488) potassium uptake transporter-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   40170
Seq. ID
                   LIB3138-015-Q1-N1-G10
                   BLASTX
Method
NCBI GI
                   g229707
BLAST score
                   227
E value
                   5.0e-19
Match length
                   54
% identity
                   81
NCBI Description
                  Bean pod mottle virus
Seq. No.
                   40171
Seq. ID
                  LIB3138-015-Q1-N1-H1
                  BLASTN
Method
NCBI GI
                   q4406529
BLAST score
                   171
E value
                   3.0e-91
Match length
                  374
% identity
                  86
                  Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
NCBI Description
                  encoding chloroplast protein, complete cds
Seq. No.
                  40172
Seq. ID
                  LIB3138-015-Q1-N2-D11
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3582333
BLAST score 151
E value 8.0e-10



```
Match length
                  32
% identity
                  (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  40173
Seq. No.
                  LIB3138-015-Q1-N2-E5
Seq. ID
                  BLASTN
Method
                  q1163180
NCBI GI
BLAST score
                  33
E value
                  2.0e-09
                  67
Match length
% identity
                  87
NCBI Description Glycine max arginine decarboxylase mRNA, complete cds
Seq. No.
                  40174
                  LIB3138-015-Q1-N2-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894598
BLAST score
                  236
                  8.0e-20
E value
Match length
                  87
% identity
                  51
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  LIB3138-015-Q1-N2-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4510385
BLAST score
                   211
                   3.0e-17
E value
Match length
                   83
% identity
                   51
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   40176
                  LIB3138-015-Q1-N2-H3
Seq. ID
                  BLASTX
Method
                   q138364
NCBI GI
BLAST score
                   222
                   7.0e-27
E value
                   88
Match length
                   72
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                   40177
Seq. No.
Seq. ID
                   LIB3138-015-Q1-N2-H8
                   BLASTX
Method
                   g3298542
NCBI GI
                   157
BLAST score
```

1.0e-10 E value Match length 85 45 % identity

(AC004681) putative cellulose synthase [Arabidopsis NCBI Description

thaliana]



```
40178
Seq. No.
                  LIB3138-016-Q1-N1-B11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g21002
BLAST score
                  42
                  2.0e-14
E value
                  106
Match length
                  85
% identity
NCBI Description Bean DNA for glycine-rich cell wall protein GRP 1.8
Seq. No.
                  40179
                  LIB3138-016-Q1-N1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1785622
BLAST score
                  404
E value
                  2.0e-39
Match length
                  115
% identity
                  (Z84202) ORFc [Arabidopsis thaliana]
NCBI Description
                  40180
Seq. No.
Seq. ID
                  LIB3138-016-Q1-N1-C2
Method
                  BLASTN
                  q4097879
NCBI GI
BLAST score
                  132
                   4.0e-68
E value
Match length
                   308
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                   40181
                   LIB3138-016-Q1-N1-C8
Seq. ID
Method
                   BLASTN
                   g4097879
NCBI GI
BLAST score
                   162
                   7.0e-86
E value
Match length
                   338
% identity
                   87
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
Seq. No.
                   40182
                   LIB3138-016-Q1-N1-E2
Seq. ID
Method
                   BLASTX
                   g4097880
NCBI GI
                   322
BLAST score
                   3.0e-32
E value
                   90
Match length
                   80
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
```

Seq. No. 40183

Seq. ID LIB3138-016-Q1-N1-E5

BLASTX Method NCBI GI g3281868

6280



```
BLAST score
                  8.0e-09
E value
                  53
Match length
                  51
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  40184
                  LIB3138-016-Q1-N1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  140
E value
                  7.0e-73
Match length
                  304
% identity
                  87
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                   40185
                  LIB3138-017-Q1-N1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                   85
E value
                   3.0e-40
Match length
                   193
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   40186
Seq. ID
                   LIB3138-017-Q1-N1-D2
Method
                   BLASTX
NCBI GI
                   g2911079
BLAST score
                   196
                   2.0e-15
E value
Match length
                   65
% identity
                   57
                   (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   40187
                   LIB3138-017-Q1-N1-E1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   55
E value
                   4.0e-22
Match length
                   239
% identity
                   85
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   40188
                   LIB3138-017-Q1-N1-E6
Seq. ID
Method
                   BLASTN
                   g4097879
NCBI GI
```

BLAST score 45 2.0e-16 E value

Match length 105 86 % identity



NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No. 40189

Seg. ID LIB3138-017-Q1-N1-F10

Method BLASTN
NCBI GI g4097879
BLAST score 181
E value 3.0e-97
Match length 404
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40190

Seq. ID LIB3138-017-Q1-N1-G2

Method BLASTN
NCBI GI g210811
BLAST score 83
E value 6.0e-39
Match length 222
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40191

Seq. ID LIB3138-017-Q1-N1-H3

Method BLASTN
NCBI GI 94097879
BLAST score 98
E value 1.0e-47
Match length 299
% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40192

Seq. ID LIB3138-017-Q1-N1-H4

Method BLASTX
NCBI GI g2459443
BLAST score 222
E value 2.0e-18
Match length 63
% identity 68

NCBI Description (AC002332) putative NAD(P)-dependent cholesterol

dehydrogenase [Arabidopsis thaliana]

Seq. No. 40193

Seq. ID LIB3138-017-Q1-N1-H8

Method BLASTN
NCBI GI g4097879
BLAST score 83
E value 7.0e-39
Match length 211
% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds



```
40194
Seq. No.
Seq. ID
                  LIB3138-018-Q1-N1-A3
                  BLASTX
Method
NCBI GI
                  g138364
                  279
BLAST score
                  2.0e-35
E value
Match length
                  104
                  76
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                  (M62738) coat protein [Bean pod mottle virus]
                  40195
Seq. No.
Seq. ID
                  LIB3138-018-Q1-N1-B9
Method
                  BLASTX
                  g138364
NCBI GI
                  135
BLAST score
                  2.0e-11
E value
                  90
Match length
% identity
                  49
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
                  40196
Seq. No.
Seq. ID
                  LIB3138-018-Q1-N1-D11
                  BLASTX
Method
NCBI GI
                  g409547
BLAST score
                  339
                  5.0e-32
E value
Match length
                  112
% identity
                  53
                  (L07492) sugar transport protein [Saccharomyces cerevisiae]
NCBI Description
Seq. No.
                  40197
Seq. ID
                  LIB3138-018-Q1-N1-E4
Method
                  BLASTX
NCBI GI
                  g2129879
BLAST score
                  238
                  5.0e-20
E value
Match length
                  111
                  50
% identity
NCBI Description
                  chlorophyll a/b-binding protein type II precursor,
                  photosystem I - garden pea >gi 602359 emb CAA57492
                  (X81962) Type II chlorophyll a/b binding protein from
                  photosystem I [Pisum sativum]
Seq. No.
                  40198
Seq. ID
                  LIB3138-018-Q1-N1-E5
```

Method BLASTN NCBI GI q210811 BLAST score 206 E value 1.0e-112 Match length 377



% identity 89
NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No. 40199

Seq. ID LIB3138-018-Q1-N1-E7

Method BLASTN
NCBI GI g210811
BLAST score 175
E value 9.0e-94
Match length 335
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40200

Seq. ID LIB3138-018-Q1-N1-E9

Method BLASTX
NCBI GI g229708
BLAST score 166
E value 7.0e-12
Match length 82
% identity 54

NCBI Description Bean pod mottle virus

Seq. No. 40201

Seq. ID LIB3138-018-Q1-N1-G10

Method BLASTN
NCBI GI g4406529
BLAST score 108
E value 1.0e-53
Match length 375
% identity 82

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40202

Seq. ID LIB3138-018-Q1-N1-G9

Method BLASTX
NCBI GI g131768
BLAST score 244
E value 1.0e-20
Match length 111
% identity 50

NCBI Description QUINATE PERMEASE (QUINATE TRANSPORTER)

>qi 101798 pir S08498 quinate transport protein -

Emericella nidulans >gi_2400_emb_CAA31879_ (X13525) quinate

permease [Emericella nidulans]

Seq. No. 40203

Seq. ID LIB3138-018-Q1-N1-H1

Method BLASTN
NCBI GI 94406529
BLAST score 132
E value 5.0e-68
Match length 279
% identity 87



NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No. 40204

Seq. ID LIB3138-018-Q1-N1-H2

Method BLASTN
NCBI GI g210811
BLAST score 139
E value 3.0e-72
Match length 311
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40205

Seq. ID LIB3138-019-Q1-N1-A9

Method BLASTN
NCBI GI g4406529
BLAST score 158
E value 1.0e-83
Match length 341
% identity 87

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40206

Seq. ID LIB3138-019-Q1-N1-B3

Method BLASTX
NCBI GI g3183392
BLAST score 258
E value 2.0e-22
Match length 93
% identity 52

NCBI Description HYPOTHETICAL 24.1 KD PROTEIN C17A5.08 IN CHROMOSOME I

PRECURSOR >gi_2370480_emb_CAB11508_ (Z98849) hypothetical

transmembrane protein [Schizosaccharomyces pombe]

Seq. No. 40207

Seq. ID LIB3138-019-Q1-N1-B7

Method BLASTX
NCBI GI g626677
BLAST score 296
E value 3.0e-27
Match length 75
% identity 71

NCBI Description NMD3 protein - yeast (Saccharomyces cerevisiae) >gi_458900

(U00027) Nmd3p: Putative Upf1p interacting protein

[Saccharomyces cerevisiae]

Seq. No. 40208

Seq. ID LIB3138-019-Q1-N1-C1

Method BLASTX
NCBI GI g2754849
BLAST score 214
E value 3.0e-17
Match length 47
% identity 87

6285



```
NCBI Description (AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]
```

Seq. No. 40209

Seq. ID LIB3138-019-Q1-N1-D4

Method BLASTX
NCBI GI g3850583
BLAST score 141
E value 1.0e-08
Match length 33
% identity 79

NCBI Description (AC005278) Contains similarity to transcription initiation

factor IIE, alpha subunit gb_X63468 from Homo sapiens.

[Arabidopsis thaliana]

Seq. No. 40210

Seq. ID LIB3138-019-Q1-N1-F11

Method BLASTN
NCBI GI 94406529
BLAST score 198
E value 1.0e-107
Match length 377
% identity 88

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40211

Seq. ID LIB3138-019-Q1-N1-H4

Method BLASTX
NCBI GI g2842480
BLAST score 401
E value 4.0e-40
Match length 117
% identity 28

NCBI Description (AL021749) ADP, ATP carrier-like protein [Arabidopsis

thaliana]

Seq. No. 40212

Seq. ID LIB3138-019-Q1-N1-H6

Method BLASTN
NCBI GI g2198850
BLAST score 54
E value 2.0e-21
Match length 102
% identity 88

NCBI Description Zea mays cystathionine gamma-synthase (CGS1) mRNA, complete

cds

Seq. No. 40213

Seq. ID LIB3138-020-Q1-N1-C6

Method BLASTN
NCBI GI g257814
BLAST score 129
E value 1.0e-66
Match length 185
% identity 92

NCBI Description phenylalanine ammonia-lyase [soybeans, mRNA, 1427 nt]



```
Seq. No.
                  40214
                  LIB3138-020-Q1-N1-C8
Seq. ID
Method
                  BLASTX
                  g138364
NCBI GI
                  233
BLAST score
E value
                  8.0e-20
                  66
Match length
                  73
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                  40215
Seq. No.
                  LIB3138-020-Q1-N1-E2
Seq. ID
                  BLASTN
Method
NCBI GI
                  q927506
                   42
BLAST score
                   2.0e-14
E value
                  74
Match length
                   89
% identity
NCBI Description P.sativum mRNA for fructose-1, 6-biphosphate aldolase
                   (clone aldcyt1)
Seq. No.
                   40216
                  LIB3138-020-Q1-N1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q836954
                   426
BLAST score
                   4.0e-42
E value
                   129
Match length
% identity
                  (U20948) receptor protein kinase [Ipomoea trifida]
NCBI Description
Seq. No.
                   40217
                   LIB3138-020-Q1-N1-G4
Seq. ID
Method
                   BLASTN
                   q4097879
NCBI GI
BLAST score
                   142
                   3.0e-74
E value
Match length
                   258
                   89
% identity
                   Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   40218
Seq. No.
                   LIB3138-020-Q1-N1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4115936
                   172
BLAST score
                   3.0e-12
E value
                   94
Match length
                   33
% identity
                   (AF118223) No definition line found [Arabidopsis thaliana]
NCBI Description
```

6287

40219

Seq. No.



```
LIB3138-021-Q1-N1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82065
BLAST score
                  227
                  7.0e-19
E value
Match length
                  81
% identity
                  ribosomal protein S3a - Madagascar periwinkle
NCBI Description
                  >gi 217903 dbj BAA00860 (D01058) ORF [Catharanthus roseus]
Seq. No.
                  40220
Seq. ID
                  LIB3138-021-Q1-N1-B6
Method
                  BLASTN
                  q4097879
NCBI GI
                  208
BLAST score
                  1.0e-113
E value
                  495
Match length
                  86
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  40221
Seq. ID
                  LIB3138-021-Q1-N1-B8
Method
                  BLASTN
                  q767700
NCBI GI
                  99
BLAST score
                  3.0e-48
E value
                  187
Match length
% identity
                   88
                  Carrot mRNA for DNA-binding protein (transcriptional
NCBI Description
                  regulator), partial cds, CHB6
Seq. No.
                   40222
                  LIB3138-021-Q1-N1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4115931
BLAST score
                   257
                   6.0e-26
E value
Match length
                   93
% identity
                   55
                   (AF118223) contains similarity to Guillardia theta ABC
NCBI Description
                   transporter (GB:AF041468) [Arabidopsis thaliana]
Seq. No.
                   40223
Seq. ID
                   LIB3138-021-Q1-N1-H9
Method
                   BLASTN
NCBI GI
                   g4097879
BLAST score
                   35
                   4.0e-10
E value
Match length
                   43
                   95
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
```

Seq. No. 40224 Seq. ID LIB313

Seq. ID LIB3138-022-Q1-N1-A10

Method BLASTN



NCBI GI g4097879 BLAST score 198 E value 1.0e-107 Match length 442 % identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40225

Seq. ID LIB3138-022-Q1-N1-A12

Method BLASTX
NCBI GI g2388943
BLAST score 158
E value 1.0e-10
Match length 115
% identity 36

NCBI Description (Z98978) SPAC27E2.03c, putative gtp-binding protein,

len:392a a, similar eg. to YBR025C, YBN5 YEAST, P38219, hypothetica 1 44.2 kd protein, (394aa), fasta scores, opt:1664, E():0, (63.7% identity in 391 aa overlap), also

sim

Seq. No. 40226

Seq. ID LIB3138-022-Q1-N1-B2

Method BLASTX
NCBI GI g4097880
BLAST score 409
E value 6.0e-75
Match length 168
% identity 85

% identity 85
NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40227

Seq. ID LIB3138-022-Q1-N1-B3

Method BLASTX
NCBI GI g138364
BLAST score 371
E value 3.0e-53
Match length 148
% identity 74

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40228

Seq. ID LIB3138-022-Q1-N1-B7

Method BLASTN
NCBI GI g4406529
BLAST score 156
E value 2.0e-82
Match length 341
% identity 86

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40229



```
LIB3138-022-Q1-N1-C4
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4097879
BLAST score
                  299
E value
                  1.0e-167
Match length
                  659
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  40230
Seq. No.
Seq. ID
                  LIB3138-022-Q1-N1-D9
                  BLASTX
Method
NCBI GI
                  q4097880
BLAST score
                  452
                  4.0e-45
E value
                  116
Match length
% identity
                  78
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                  40231
                  LIB3138-022-Q1-N1-F11
Seq. ID
Method
                  BLASTX
                  q138364
NCBI GI
BLAST score
                  591
E value
                  5.0e-68
                  168
Match length
                  78
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                   40232
                  LIB3138-022-Q1-N1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4097880
                   408
BLAST score
                   1.0e-49
E value
Match length
                  155
% identity
                   71
NCBI Description
                   (U70866) polyprotein [Bean pod mottle virus]
                   40233
Seq. No.
                  LIB3138-022-Q1-N1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3599999
                  759
BLAST score
                  7.0e-81
E value
                  193
Match length
                   74
% identity
                  (AF066054) formaldehyde dehydrogenase [Pichia pastoris]
NCBI Description
```

Seq. No. 40234

Seq. ID LIB3138-023-Q1-N1-D4

Method BLASTX NCBI GI g539244

BLAST score

E value Match length 213 7.0e-17

58



```
BLAST score
                  4.0e-18
E value
                  114
Match length
                  43
% identity
                  hypothetical protein YKR028w - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi_486457_emb_CAA82100_ (Z28253) ORF YKR028w
                   [Saccharomyces cerevisiae]
                  40235
Seq. No.
                  LIB3138-023-Q1-N1-D7
Seq. ID
                  BLASTX
Method
                  g4490297
NCBI GI
BLAST score
                  133
E value
                   2.0e-11
                   105
Match length
                   39
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   40236
Seq. No.
                   LIB3138-023-Q1-N1-D8
Seq. ID
                   BLASTX
Method
                   g2414666
NCBI GI
                   328
BLAST score
                   1.0e-30
E value
Match length
                   125
                   54
% identity
                  (Z99262) pyridoxal reductase. [Schizosaccharomyces pombe]
NCBI Description
                   40237
Seq. No.
                   LIB3138-024-Q1-N1-A11
Seq. ID
                   BLASTN
Method
                   q210811
NCBI GI
                   125
BLAST score
                   1.0e-63
E value
                   277
Match length
                   86
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   40238
Seq. No.
                   LIB3138-024-Q1-N1-A9
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   95
BLAST score
E value
                   5.0e-46
                   283
Match length
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   40239
Seq. ID
                   LIB3138-024-Q1-N1-B4
Method
                   BLASTX
                   g1296805
NCBI GI
```



```
% identity
                  (X90929) C-terminal peptidase of the D1 protein [Hordeum
NCBI Description
                  vulgare]
                  40240
Seq. No.
                  LIB3138-024-Q1-N1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2980765
                  322
BLAST score
                  1.0e-29
E value
                  123
Match length
                  50
% identity
NCBI Description (AL022198) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  40241
                  LIB3138-024-Q1-N1-C12
Seq. ID
                  BLASTX
Method
                  g138364
NCBI GI
                  182
BLAST score
                  3.0e-26
E value
Match length
                  107
% identity
                  61
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
                  40242
Seq. No.
                  LIB3138-024-Q1-N1-C6
Seq. ID
Method
                  BLASTN
                  g210811
NCBI GI
                  174
BLAST score
                  5.0e-93
E value
Match length
                  410
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  40243
Seq. No.
                  LIB3138-024-Q1-N1-D11
Seq. ID
                  BLASTX
Method
                  q138364
NCBI GI
BLAST score
                   452
                   3.0e-45
E value
Match length
                   100
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   40244
Seq. No.
                   LIB3138-024-Q1-N1-G7
```

Seq. ID

Method BLASTN NCBI GI g210811 303 BLAST score 1.0e-170 E value



```
Match length
% identity
                  89
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  40245
Seq. No.
Seq. ID
                  LIB3138-024-Q1-N1-H11
Method
                  BLASTX
NCBI GI
                  q4097880
BLAST score
                  530
E value
                  4.0e-54
Match length
                  164
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   40246
Seq. No.
                  LIB3138-024-Q1-N1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4101473
                  157
BLAST score
                   2.0e-10
E value
                   37
Match length
% identity
NCBI Description (AF003382) KEA1 [Arabidopsis thaliana]
                   40247
Seq. No.
                  LIB3138-024-Q1-N1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4097880
BLAST score
                   425
E value
                   5.0e-42
Match length
                   125
% identity
                   69
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   40248
                   LIB3138-024-Q1-N1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1840116
                   339
BLAST score
                   8.0e-32
E value
Match length
                   101
% identity
                   69
                   (U85497) ADP-glucose pyrophosphorylase large subunit
NCBI Description
                   [Lycopersicon esculentum]
```

Seq. No. 40249

Seq. ID LIB3138-024-Q1-N1-H6

Method BLASTX
NCBI GI g1840116
BLAST score 484
E value 1.0e-48
Match length 139
% identity 70

NCBI Description (U85497) ADP-glucose pyrophosphorylase large subunit

[Lycopersicon esculentum]

. ...



78

% identity

NCBI Description

```
Seq. No.
                  LIB3138-025-Q1-N1-A5
Seq. ID
                  BLASTX
Method
                  q116324
NCBI GI
BLAST score
                  165
E value
                  1.0e-11
Match length
                  65
% indentity
                  51
                  ENDOCHITINASE PR4 PRECURSOR >gi 100000 pir S16579
NCBI Description
                  chitinase (EC 3.2.1.14) precursor - kidney bean
Seq. No.
                  40251
                  LIB3138-025-Q1-N1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2498183
BLAST score
                  362
E value
                  1.0e-34
                  97
Match length
% identity
                   69
                  BLI-3 PROTEIN >gi_602075_emb_CAA57098_ (X81318) bli-3
NCBI Description
                   [Neurospora crassa] >gi 1092170 prf 2023159A bli-3 gene
                   [Neurospora crassa]
Seq. No.
                   40252
Seq. ID
                  LIB3138-025-Q1-N1-D1
Method
                  BLASTX
NCBI GI
                  q3152599
BLAST score
                   283
E value
                   2.0e-25
Match length
                   89
% identity
                   30
                   (ACO02986) Strong similarity to lupeol synthase gb_U49919
NCBI Description
                   and cycloartenol synthase gb U02555 from A. thaliana (the
                   third gene with similar homology). [Arabidopsis thaliana]
Seq. No.
                   40253
Seq. ID
                  LIB3138-025-Q1-N1-E1
Method
                  BLASTX
NCBI GI
                   g4097880
                   204
BLAST score
                   2.0e-16
E value
Match length
                   81
                   58
% identity
NCBI Description
                   (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   40254
Seq. ID
                   LIB3138-025-Q1-N1-E11
Method
                   BLASTX
NCBI GI
                   g138364
BLAST score
                   481
                   1.0e-48
E value
                   127
Match length
```

6294

(M62738) coat protein [Bean pod mottle virus]

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi_210812



```
40255
Seq. No.
                  LIB3138-025-Q1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g138364
                  220
BLAST score
E value
                  2.0e-18
                  67
Match length
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
                  40256
Seq. No.
                  LIB3138-025-Q1-N1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q138364
BLAST score
                  422
                  9.0e-42
E value
Match length
                  110
                  79
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  40257
Seq. ID
                  LIB3138-025-Q1-N1-F9
                  BLASTX
Method
                  g2494215
NCBI GI
                  248
BLAST score
                  2.0e-21
E value
Match length
                  87
% identity
                  DYNEIN, 78 KD INTERMEDIATE CHAIN, FLAGELLAR OUTER ARM
NCBI Description
                   (IC78) >gi 1361948 pir A57037 dynein intermediate chain,
                   78k - Chlamydomonas reinhardtii >gi 642541 (U19120)
                   outer-arm dynein Mr78,000 intermediate chain subunit
                   [Chlamydomonas reinhardtii]
                   40258
Seq. No.
                   LIB3138-025-Q1-N1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   33
E value
                   1.0e-09
Match length
                   89
% identity
                   84
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
```

complete middle component (M) RNA Seq. No. 40259

40259 LIB3138-025-Q1-N1-G2

Seq. ID LIB3138-Method BLASTN NCBI GI g2832611

BLAST score 33



```
2.0e-09
E value
                  61
Match length
                  92
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
NCBI Description
                   (ESSAII project)
                  40260
Seq. No.
                  LIB3138-025-Q1-N1-G7
Seq. ID
Method
                  BLASTX
                  g2864614
NCBI GI
                  225
BLAST score
E value
                  1.0e-18
Match length
                  91
                   45
% identity
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   40261
                   LIB3138-027-Q1-N1-B10
Seq. ID
                   BLASTX
Method
                   q115471
NCBI GI
                                                  7
                   206
BLAST score
                   2.0e-16
E value
Match length
                   107
% identity
                   48
                  CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                   DEHYDRATASE) >gi 100078 pir S10200 carbonate dehydratase
                   (EC 4.2.1.1) precursor - garden pea >gi 20673 emb CAA36792
                   (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]
                   40262
Seq. No.
                   LIB3138-027-Q1-N1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2673914
BLAST score
                   214
                   3.0e-17
E value
                   47
Match length
                   87
% identity
                   (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   40263
Seq. No.
                   LIB3138-027-Q1-N1-C12
Seq. ID
                   BLASTX
Method
                   g2827522
NCBI GI
                   148
BLAST score
                   2.0e-09
E value
                   43
Match length
% identity
                   63
                   (AL021633) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   40264
                   LIB3138-027-Q1-N1-E8
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
BLAST score
                   104
                   2.0e-51
E value
                   368
Match length
```

82

% identity



```
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
                  40265
Seq. No.
                  LIB3138-027-Q1-N1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2392021
BLAST score
                  133
E value
                  1.0e-13
Match length
                  80
% identity
                  (D63425) phopholipid hydroperoxide glutathione
NCBI Description
                  peroxidase-like protein [Spinacia oleracea]
Seq. No.
                  40266
Seq. ID
                  LIB3138-027-Q1-N1-H11
Method
                  BLASTX
NCBI GI
                  g2832652
BLAST score
                  301
                  2.0e-27
E value
Match length
                  72
                  83
% identity
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
                   40267
Seq. No.
                  LIB3138-027-Q1-N1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q462414
BLAST score
                   310
E value
                   1.0e-28
Match length
                  118
                   56
% identity
                  AMINO-ACID PERMEASE INDA1 >gi_422225_pir__S33212 INDA1
NCBI Description
                  protein - fungus (Trichoderma harzianum)
                   >gi 296570 emb CAA80308 (Z22594) INDA1 [Trichoderma
                  harzianum]
                   40268
Seq. No.
                   LIB3138-028-Q1-N1-A9
Seq. ID
                   BLASTX
Method
                   g4097880
NCBI GI
                   224
BLAST score
                   1.0e-18
E value
Match length
                   70
% identity
                   66
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   40269
```

LIB3138-028-Q1-N1-B7 Seq. ID

Method BLASTX g1351408 NCBI GI 209 BLAST score 8.0e-17 E value Match length 61 % identity 64

VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) NCBI Description

>gi 1076563 pir S51117 cystein proteinase - sweet orange

6297



>gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

40270 Seq. No. Seq. ID LIB3138-028-Q1-N1-D5 BLASTN Method g1053215 NCBI GI BLAST score 34 4.0e-10 E value 45 Match length 96 % identity Glycine max chlorophyll a/b-binding protein (cab3) mRNA, NCBI Description nuclear gene encoding chloroplast protein, complete cds 40271 Seq. No. LIB3138-028-Q1-N1-E3 Seq. ID BLASTX Method g3482967 NCBI GI 168 BLAST score 6.0e-12 E value Match length 39 % identity 82 (AL031369) Protein phosphatase 2C-like protein [Arabidopsis NCBI Description thaliana] >gi 4559345 gb AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana] 40272 Seq. No. LIB3138-028-Q1-N1-F10 Seq. ID BLASTX Method g3269291 NCBI GI BLAST score 176 5.0e-13 E value 86 Match length % identity 44 (AL030978) putative receptor protein kinase [Arabidopsis NCBI Description thaliana] 40273 Seq. No. LIB3138-028-Q1-N1-F8 Seq. ID BLASTX Method g2253010 NCBI GI BLAST score 201 4.0e-22 E value 85 Match length 65 % identity (Y14199) MAP3K delta-1 protein kinase [Arabidopsis NCBI Description thaliana] 40274 Seq. No. Seq. ID LIB3138-028-Q1-N1-G4 BLASTX Method NCBI GI g229708 BLAST score 460

6298

3.0e-46

111

77

E value

Match length

% identity

NCBI Description

Seq. No. Seq. ID

2. The

40280

LIB3138-029-Q1-N1-E2



```
NCBI Description Bean pod mottle virus
                  40275
Seq. No.
Seq. ID
                  LIB3138-029-Q1-N1-B11
Method
                  BLASTX
                  g138364
NCBI GI
                  300
BLAST score
E value
                  2.0e-27
                  98
Match length
                  69
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                  40276
Seq. No.
                  LIB3138-029-Q1-N1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4097880
                  305
BLAST score
                  2.0e-28
E value
Match length
                  74
                  81
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   40277
Seq. No.
Seq. ID
                  LIB3138-029-Q1-N1-C8
Method
                  BLASTX
                  g229707
NCBI GI
                   323
BLAST score
                   5.0e-30
E value
                   132
Match length
% identity
                   55
NCBI Description
                  Bean pod mottle virus
                   40278
Seq. No.
Seq. ID
                   LIB3138-029-Q1-N1-D12
                   BLASTX
Method
NCBI GI
                   q4097880
                   203
BLAST score
                   4.0e-16
E value
                   87
Match length
                   62
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   40279
Seq. ID
                   LIB3138-029-Q1-N1-D2
                   BLASTN
Method
                   g169974
NCBI GI
                   159
BLAST score
                   3.0e-84
E value
                   283
Match length
                   89
% identity
```

6299

Glycine max vspA gene, complete cds



```
Method
                  BLASTX
                  q138364
NCBI GI
                  271
BLAST score
                  5.0e-24
E value
                  102
Match length
                  59
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                   40281
                  LIB3138-029-Q1-N1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2773269
BLAST score
                   62
                   2.0e-26
E value
Match length
                   157
                   89
% identity
                  Glycine max ferredoxin-dependent glutamate synthase (glu)
NCBI Description
                  mRNA, partial cds
Seq. No.
                   40282
Seq. ID
                   LIB3138-029-Q1-N1-F6
                   BLASTX
Method
                   g2258315
NCBI GI
BLAST score
                   272
E value
                   5.0e-24
                   91
Match length
                   57
% identity
                   (AF004878) resistance complex protein I2C-1 [Lycopersicon
NCBI Description
                   esculentum]
                   40283
Seq. No.
                   LIB3138-029-Q1-N1-G3
Seq. ID
Method
                   BLASTN
                   g210811
NCBI GI
BLAST score
                   116
                   2.0e-58
E value
                   304
Match length
% identity
                   85
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   40284
                   LIB3138-029-Q1-N1-G6
Seq. ID
Method
                   BLASTX
                   g138364
NCBI GI
BLAST score
                   175
                   5.0e-20
E value
                   109
Match length
                   57
% identity
```

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]



```
Seq. No.
Seq. ID
                   LIB3138-029-Q1-N1-G8
Method
                   BLASTX
NCBI GI
                   g229707
BLAST score
                    463
E value
                   2.0e-46
Match length
                   114
                   73
% identity
NCBI Description Bean pod mottle virus
Seq. No.
                   40286
Seq. ID
                   LIB3138-029-Q1-N1-H11
Method
                   BLASTN
NCBI GI
                   q210811
BLAST score
                   41
E value
                   6.0e-14
                   77
Match length
% identity
                   88
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
Seq. No.
                   40287
Seq. ID
                   LIB3138-029-Q1-N1-H4
Method
                   BLASTN
NCBI GI
                   q496493
BLAST score
                   194
E value
                   1.0e-105
Match length
                   346
% identity
                   89
NCBI Description
                   P.sativum (Rosakrone) mRNA for nonphosphorylating,
                   NADP-specific, glyceraldehyde-3-phosphate dehydrogenase
Seq. No.
                   40288
Seq. ID
                   LIB3138-029-Q1-N1-H7
Method
                   BLASTX
NCBI GI
                   q123537
BLAST score
                   152
                   6.0e-10
E value
Match length
                   85
% identity
                   40
NCBI Description
                   12 KD HEAT SHOCK PROTEIN (GLUCOSE AND LIPID-REGULATED
                   PROTEIN) >gi_72231 pir HHBY12 heat shock protein 12
                   yeast (Saccharomyces cerevisiae) >gi_3800_emb_CAA39306_
                   (X55785) hsp12 [Saccharomyces cerevisiae] >gi 171607
                   (M60827) 15 kD glucose and lipid regulated protein
                   [Saccharomyces cerevisiae] >gi_559934_emb_CAA86349
(Z46255) hsp12, glp1, len: 109, CAI: 0.65, HS12_YEAST
```

P22943 12 KD HEAT SHOCK PROTEIN [Saccharomyces cerevisiae] >gi_836740_dbj_BAA09224_ (D50617) 12KD heat shock protein [Saccharomyces cerevisiae] >gi 1100790 dbj BAA08003 (D44596) 15kD glucose and lipid regulated protein [Saccharomyces cerevisiae] >gi_1742028_dbj_BAA14033

(D89864) Sc-Hsp12p [Saccharomyces pastorianus]

Seq. No. 40289

Seq. ID LIB3138-030-Q1-N1-A11

Method BLASTX

```
NCBI GI
                   g1666171
BLAST score
                  200
                  1.0e-15
E value
Match length
                  62
% identity
                  85
NCBI Description (Y09105) unknown [Nicotiana plumbaginifolia]
Seq. No.
                  40290
Seq. ID
                  LIB3138-030-Q1-N1-B2
Method
                  BLASTX
NCBI GI
                  q3874889
BLAST score
                  208
E value
                  2.0e-16
Match length
                  62
% identity
                  53
NCBI Description
                  (Z48045) similarity to the transmembranous domains of yeast
                  ERS1 protein; cDNA EST EMBL: D69878 comes from this gene;
                  cDNA EST EMBL: D66181 comes from this gene; cDNA EST
                  yk413c7.5 comes from this gene [Caenorhabditis elegans]
                  40291
Seq. No.
Seq. ID
                  LIB3138-030-Q1-N1-F3
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  283
E value
                  2.0e-25
Match length
                  88
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  40292
Seq. ID
                  LIB3138-030-Q1-N1-G10
Method
                  BLASTX
NCBI GI
                  q3122833
BLAST score
                  469
E value
                  4.0e-47
                  129
Match length
                  71
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S5 >gi 1685071 (U78085) ribosomal
                  protein S5 [Mus musculus]
Seq. No.
                  40293
Seq. ID
                  LIB3138-030-Q1-N1-G4
                  BLASTX
                  g138364
                  343
```

Method NCBI GI BLAST score E value 2.0e-41 Match length 123 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40294

Seq. ID LIB3138-030-Q1-N1-H2

Method BLASTX ij.



```
NCBI GI g2132069
BLAST score 267
E value 2.0e-23
Match length 119
% identity 45
NCBI Description hypothetical protein YOR150w - yeast (Saccharomyces cerevisiae) >gi_1293710 (U55020) O3530p [Saccharomyces cerevisiae] >gi_1420377_emb_CAA99356_ (Z75058) ORF YOR150w
```

Seq. No. 40295

Seq. ID LIB3138-030-Q1-N1-H4

[Saccharomyces cerevisiae]

gene, complete cds

Method BLASTN
NCBI GI g4097879
BLAST score 48
E value 6.0e-18
Match length 143

% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

Seq. No. 40296

Seq. ID LIB3138-031-Q1-N1-A9

Method BLASTX
NCBI GI g138364
BLAST score 364
E value 6.0e-35
Match length 114
% identity 68

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40297

Seq. ID LIB3138-031-Q1-N1-B9

Method BLASTN
NCBI GI g20728
BLAST score 34
E value 5.0e-10
Match length 85
% identity 92

NCBI Description Pea chloroplast GAPA mRNA encoding

glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A

(EC 1.2.1.13)

Seq. No. 40298

Seq. ID LIB3138-031-Q1-N1-C12

Method BLASTN
NCBI GI g169036
BLAST score 32
E value 8.0e-09
Match length 40
% identity 95

NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No. 40299



```
Seq. ID LIB3138-031-Q1-N1-C4 Method BLASTN
```

NCBI GI g210811 BLAST score 162 E value 6.0e-86 Match length 314 % identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40300

Seq. ID LIB3138-031-Q1-N1-E4

Method BLASTX
NCBI GI g229707
BLAST score 303
E value 4.0e-28
Match length 77
% identity 73

NCBI Description Bean pod mottle virus

Seq. No. 40301

Seq. ID LIB3138-031-Q1-N1-E6

Method BLASTX
NCBI GI g3080398
BLAST score 273
E value 4.0e-24
Match length 80
% identity 33

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 40302

Seq. ID LIB3138-031-Q1-N1-E7

Method BLASTX
NCBI GI g2960358
BLAST score 236
E value 5.0e-20
Match length 73
% identity 64

NCBI Description (AJ224895) caffeoyl-CoA 3-O-methyltransferase [Populus

balsamifera subsp. trichocarpa] >gi_2960360_emb_CAA12200_(AJ224896) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa] >gi_3550590_emb_CAA11495_(AJ223620) caffeoyl CoA 3-O-methyltransferase [Populus

balsamifera subsp. trichocarpa]

Seq. No. 40303

Seq. ID LIB3138-031-Q1-N1-F10

Method BLASTX
NCBI GI g1170409
BLAST score 179
E value 2.0e-13
Match length 68
% identity 56

NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)

>gi_549887 (U09336) homeobox protein [Arabidopsis thaliana]
>gi_549888 (U09337) homeobox protein [Arabidopsis thaliana]
>gi_4490724_emb_CAB38927.1_ (AL035709) homeobox protein

% identity

95



HAT22 [Arabidopsis thaliana]

```
Seq. No.
                   40304
Seq. ID
                   LIB3138-031-Q1-N1-F4
Method
                   BLASTX
                   g2653397
NCBI GI
BLAST score
                   212
E value
                   1.0e-17
Match length
                   63
% identity
                   62
NCBI Description
                   (AL009147) 1-evidence=predicted by content;
                   1-method=genefinder;084; 1-method score=86.60;
                   1-evidence end; 2-evidence=predicted by motif;
                   2-match_accession=PROSITE:PS00070;
                   2-match_description=Aldehyde dehydrogenases cysteine a
Seq. No.
                   40305
Seq. ID
                   LIB3138-031-Q1-N1-G1
Method
                   BLASTX
NCBI GI
                   g3513747
BLAST score
                   255
                   5.0e-22
E value
Match length
                   113
% identity
                   48
                   (AF080118) contains similarity to reverse transcriptases
NCBI Description
                   (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
Seq. No.
                   40306
Seq. ID
                   LIB3138-032-Q1-N1-A11
Method
                   BLASTN
NCBI GI
                   g170643
BLAST score
                   72
E value
                   3.0e-32
Match length
                   116
% identity
                   91
NCBI Description
                  Vigna aconitifolia
                   5'-phosphoribosyl-4-(N-succinocarboxamide)-5-
                   aminoimidazole synthetase mRNA
Seq. No.
                   40307
Seq. ID
                  LIB3138-032-Q1-N1-A5
Method
                  BLASTX
NCBI GI
                   g4097880
BLAST score
                   306
E value
                   4.0e-28
Match length
                  107
% identity
                   59
NCBI Description
                  (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   40308
Seq. ID
                  LIB3138-032-Q1-N1-B3
Method
                  BLASTN
NCBI GI
                  q169157
BLAST score
                  54
E value
                  2.0e-21
Match length
                   66
```



```
NCBI Description
                   Pisum sativum serine hydroxymethyltransferase mRNA,
                   complete cds
Seq. No.
                   40309
Seq. ID
                   LIB3138-032-Q1-N1-B7
Method
                   BLASTX
NCBI GI
                   g4097880
BLAST score
                   197
E value
                   1.0e-26
Match length
                   120
% identity
                   55
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   40310
Seq. ID
                   LIB3138-032-Q1-N1-E1
Method
                   BLASTX
NCBI GI
                   g4097880
BLAST score
                   202
                   5.0e-16
E value
Match length
                   71
% identity
                   63
NCBI Description
                   (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   40311
Seq. ID
                  LIB3138-032-Q1-N1-E7
Method
                  BLASTN
NCBI GI
                   g4097879
BLAST score
                   155
E value
                   9.0e-82
Match length
                   346
% identity
                   86
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                   40312
                  LIB3138-032-Q1-N1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q210811
BLAST score
                  93
E value
                  8.0e-45
Match length
                  377
% identity
                  81
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  40313
```

1

Seq. No.

Seq. ID LIB3138-032-Q1-N1-F11

Method BLASTX NCBI GI g2501578 BLAST score 218 E value 8.0e-18 Match length 84 % identity 55

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__\$60047

ethylene-responsive protein 1 - Para rubber tree

>gi_1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

6306



Seq. No. 40314

Seq. ID LIB3138-033-Q1-N1-A2

Method BLASTX
NCBI GI g138364
BLAST score 313
E value 1.0e-31
Match length 110
% identity 69

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40315

Seq. ID LIB3138-033-Q1-N1-B8

Method BLASTN
NCBI GI g210811
BLAST score 112
E value 3.0e-56
Match length 296
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40316

Seq. ID LIB3138-033-Q1-N1-C3

Method BLASTX
NCBI GI g138364
BLAST score 525
E value 9.0e-54
Match length 125
% identity 84

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40317

Seq. ID LIB3138-033-Q1-N1-C9

Method BLASTX
NCBI GI g124366
BLAST score 262
E value 7.0e-23
Match length 104
% identity 59

NCBI Description ACETOLACTATE SYNTHASE I PRECURSOR (ACETOHYDROXY-ACID

SYNTHASE I) (ALS I) >gi_320132_pir__S17691 acetolactate

synthase (EC 4.1.3.18) 1 precursor - rape

>gi_17772_emb_CAA77613_ (Z11524) actohydroxyacid synthase I

[Brassica napus]

Seq. No. 40318

Seq. ID LIB3138-033-Q1-N1-D1

Method BLASTX NCBI GI g3236238 BLAST score 509



E value 7.0e-52 Match length 107 % identity 86

NCBI Description (AC004684) putative ARF1 GTPase activating protein

[Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_

(AB017876) Aspl [Arabidopsis thaliana]

Seq. No. 40319

Seq. ID LIB3138-033-Q1-N1-E1

Method BLASTN
NCBI GI g210811
BLAST score 34
E value 1.0e-09
Match length 74

Match length 74 % identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40320

Seq. ID LIB3138-033-Q1-N1-E11

Method BLASTN
NCBI GI g1370286
BLAST score 81
E value 1.0e-37
Match length 226
% identity 84

NCBI Description P.sativum mRNA for pore protein

Seq. No. 40321

Seq. ID LIB3138-033-Q1-N1-F12

Method BLASTN
NCBI GI g210811
BLAST score 80
E value 2.0e-37
Match length 155
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40322

Seq. ID LIB3138-033-Q1-N1-F2

Method BLASTX
NCBI GI g138364
BLAST score 166
E value 4.0e-21
Match length 113
% identity 50

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40323

Seq. ID LIB3138-033-Q1-N1-F9

Method BLASTX NCBI GI g4519671 BLAST score 285

E value

Match length

% identity

1.0e-09

74

86



```
E value
                   6.0e-26
Match length
                   76
 % identity
                   74
NCBI Description
                   (AB017693) transfactor [Nicotiana tabacum]
Seq. No.
                   40324
Seq. ID
                   LIB3138-034-Q1-N1-A2
Method
                   BLASTX
NCBI GI
                   q4097880
BLAST score
                   251
                   7.0e-22
E value
Match length
                   85
% identity
                   60
NCBI Description
                   (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   40325
Seq. ID
                   LIB3138-034-Q1-N1-A4
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   162
E value
                   6.0e-86
Match length
                   326
% identity
                   87
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
Seq. No.
                   40326
Seq. ID
                   LIB3138-034-Q1-N1-A5
Method
                   BLASTX
NCBI GI
                   q138364
BLAST score
                   149
                   7.0e-10
E value
Match length
                   74
% identity
                   45
NCBI Description
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                   40327
Seq. ID
                   LIB3138-034-Q1-N1-B12
Method
                   BLASTX
NCBI GI
                   g3021409
BLAST score
                   144
E value
                   2.0e-09
Match length
                   73
% identity
NCBI Description
                  (Y12781) transducin (beta) like 1 protein [Homo sapiens]
Seq. No.
                   40328
Seq. ID
                  LIB3138-034-Q1-N1-B8
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  34
```

6309



NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No. 40329

Seq. ID LIB3138-034-Q1-N1-E1

Method BLASTN
NCBI GI 9467614
BLAST score 300
E value 1.0e-168
Match length 332
% identity 98

NCBI Description A.alternata AltA2 mRNA for aldehyde dehydrogenase

Seq. No. 40330

Seq. ID LIB3138-034-Q1-N1-E11

Method BLASTX
NCBI GI g229707
BLAST score 490
E value 1.0e-49
Match length 118
% identity 80

NCBI Description Bean pod mottle virus

Seq. No. 40331

Seq. ID LIB3138-034-Q1-N1-F12

Method BLASTX
NCBI GI g138364
BLAST score 365
E value 4.0e-35
Match length 100
% identity 72

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40332

Seq. ID LIB3138-034-Q1-N1-F3

Method BLASTX
NCBI GI g229707
BLAST score 351
E value 2.0e-33
Match length 89
% identity 78

NCBI Description Bean pod mottle virus

Seq. No. 40333

Seq. ID LIB3138-034-Q1-N1-G12

Method BLASTX
NCBI GI g1173285
BLAST score 495
E value 3.0e-50
Match length 123
% identity 79

NCBI Description 40S RIBOSOMAL PROTEIN S9 >gi_1362936_pir__ S55917 ribosomal protein S9 - human >gi_550023 (U14971) ribosomal protein S9 [Homo sapiens] >gi_1096943_prf__2113200F ribosomal protein



S9 [Homo sapiens] >gi 4506745 ref NP 001004.1 pRPS9 ribosomal protein S9

Seq. No. 40334 Seq. ID LIB3138-034-Q1-N1-G9

Method BLASTX NCBI GI g138364 BLAST score 433 E value 4.0e-43 Match length 102 % identity 78

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40335

Seq. ID LIB3138-034-Q1-N1-H2

Method BLASTX NCBI GI g3914449 BLAST score 205 E value 3.0e-16 Match length 41 % identity 98

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT

7) >gi_3172331 (AF041258) 26S proteasome subunit 7 [Prunus

persica]

Seq. No. 40336

Seq. ID LIB3138-034-Q1-N1-H6

Method BLASTX NCBI GI q4097880 BLAST score 263 E value 3.0e-23 Match length 85 % identity 64

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40337

Seq. ID LIB3138-035-Q1-N1-A7

Method BLASTX NCBI GI q854536 BLAST score 397 E value 1.0e-38 Match length 112 % identity 67

NCBI Description (Z46259) RPD3 gene [Saccharomyces cerevisiae]

>gi_2253190_emb_CAA96262_ (Z71605) ORF YNL330c

[Saccharomyces cerevisiae]

Seq. No. 40338

Seq. ID LIB3138-035-Q1-N1-B2

Method BLASTN NCBI GI g2245073 BLAST score 40 E value 2.0e-13 Match length 56



% identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No.

40339

Seq. ID

LIB3138-035-Q1-N1-B5

Method NCBI GI BLASTX g138364 375

BLAST score E value

2.0e-36

Match length % identity

86 83

NCBI Description

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No.

40340

Seq. ID

LIB3138-035-Q1-N1-D12

Method NCBI GI

BLASTN

BLAST score

g4097879

124

E value

3.0e-63

Match length

317

% identity

87

NCBI Description

Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40341

Seq. ID

LIB3138-035-Q1-N1-D7

Method

BLASTN

NCBI GI

g4097879

BLAST score

36

E value Match length 3.0e-11

% identity

52 92

NCBI Description

Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40342

Seq. ID

LIB3138-035-Q1-N1-E2

Method NCBI GI

BLASTN g1053215

BLAST score

312

E value

1.0e-175

Match length

352 97

% identity NCBI Description

Glycine max chlorophyll a/b-binding protein (cab3) mRNA,

nuclear gene encoding chloroplast protein, complete cds

Seq. No.

40343

Seq. ID

LIB3138-035-Q1-N1-E3

Method NCBI GI BLASTN

g210811

BLAST score

88

E value

6.0e-42

Match length

268



% identity 83

NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No. 40344

Seq. ID LIB3138-035-Q1-N1-E5

Method BLASTX
NCBI GI g138364
BLAST score 242
E value 2.0e-37
Match length 103

% identity 62 NCBI Description GENOME POLYPROTEIN M (CONTAINS: CO

ICBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40345

Seq. ID LIB3138-035-Q1-N1-E7

Method BLASTN
NCBI GI g210811
BLAST score 144
E value 4.0e-75
Match length 344
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40346

Seq. ID LIB3138-035-Q1-N1-E9

Method BLASTX
NCBI GI 94107323
BLAST score 588
E value 5.0e-61
Match length 122

% identity 87

NCBI Description (AL035077) 60s ribosomal protein 110 [Schizosaccharomyces

pombe]

Seq. No. 40347

Seq. ID LIB3138-035-Q1-N1-F5

Method BLASTN
NCBI GI g4097879
BLAST score 81
E value 1.0e-37
Match length 169

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40348

% identity

Seq. ID LIB3138-035-Q1-N1-G2

Method BLASTX
NCBI GI g1619300
BLAST score 199
E value 1.0e-15
Match length 48



% identity NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 40349

Seq. ID LIB3138-035-Q1-N1-G3

Method BLASTX NCBI GI g3914605 BLAST score 223 2.0e-18 E value Match length 90 % identity 56

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >qi 541930 pir \$39551

ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi 415852 emb CAA79857 (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

40350 Seq. No.

Seq. ID LIB3138-035-Q1-N1-G8

Method BLASTN NCBI GI g4097879 BLAST score 80 E value 5.0e-37 Match length 108 % identity 94

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40351

Seq. ID LIB3138-035-Q1-N1-H2

Method BLASTN NCBI GI g1619902 BLAST score 68 8.0e-30 E value Match length 200

% identity

NCBI Description Glycine max thiol protease isoform B mRNA, partial cds

Seq. No. 40352

Seq. ID LIB3138-035-Q1-N1-H5

Method BLASTN NCBI GI q4406529 BLAST score 93 E value 5.0e-45 193 Match length % identity 87

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40353

Seq. ID LIB3138-036-Q1-N1-A11

Method BLASTX NCBI GI g4097880 BLAST score 448 E value 9.0e-45 Match length 113



% identity

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40354

Seq. ID

LIB3138-036-Q1-N1-A12

Method

BLASTN

g4097879

NCBI GI

BLAST score

78

E value Match length 7.0e-36 182

% identity

86

NCBI Description

Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40355

Seq. ID

LIB3138-036-Q1-N1-B10

Method NCBI GI BLASTN g1665864

BLAST score

176

E value

2.0e-94

Match length

355

% identity

88

NCBI Description B.taurus MHC class 1 protein molecule D18.4

Seq. No.

40356

Seq. ID

LIB3138-036-Q1-N1-B11

Method

BLASTN

NCBI GI

g163345

BLAST score

40

E value

3.0e-13

Match length

117

% identity

88

NCBI Description Bovine MHC class I AW10 mRNA (haplotype AW10), 3' end

Seq. No.

40357

Seq. ID Method

LIB3138-036-Q1-N1-B9

NCBI GI

BLASTX

BLAST score

q4097880

E value

140

Match length

4.0e-13

% identity

75 59

NCBI Description

(U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40358

Seq. ID

LIB3138-036-Q1-N1-C1

Method

BLASTN

NCBI GI

q456713

BLAST score

41

E value

6.0e-14

Match length

169 81

% identity

NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No.

40359

Seq. ID

LIB3138-036-Q1-N1-C9

Method

BLASTX



```
NCBI GI
                   g3915826
BLAST score
                  308
                  5.0e-31
E value
Match length
                  91
                  77
```

% identity

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No.

40360

Seq. ID

LIB3138-036-Q1-N1-E1

Method BLASTN NCBI GI q2976 BLAST score 131 2.0e-67 E value Match length 231 % identity 89

NCBI Description Neurospora crassa mRNA for mitochondrial ADP/ATP carrier

Seq. No.

40361

Seq. ID

LIB3138-036-Q1-N1-E10

Method BLASTX NCBI GI g138364 BLAST score 142 1.0e-18 E value Match length 100 % identity 55

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >qi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No.

40362

Seq. ID LIB3138-036-Q1-N1-E5

Method BLASTN NCBI GI g210811 BLAST score 206 E value 1.0e-112 Match length 365

89 % identity

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

40363

Seq. ID

LIB3138-036-Q1-N1-F3

Method BLASTX NCBI GI g138364 BLAST score 599 E value 2.0e-62 Match length 133 % identity 86

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >qi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No.

40364

Seq. ID

LIB3138-036-Q1-N1-F9

Method

BLASTX



NCBI GI g2494369 BLAST score 106 E value 2.0e-09 Match length 54 % identity 63

NCBI Description LAMIN B RECEPTOR (INTEGRAL NUCLEAR ENVELOPE INNER MEMBRANE PROTEIN) (LMN2R) >gi_627510_pir__A53616 lamin B receptor -

human >gi_438639 (L25931) lamin B receptor [Homo sapiens] >gi_4504961 ref NP 002287.1 pLBR lamin B receptor

Seq. No. 40365

Seq. ID LIB3138-036-Q1-N1-G2

Method BLASTN
NCBI GI g210811
BLAST score 126
E value 1.0e-64
Match length 258
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40366

Seq. ID LIB3138-036-Q1-N1-G3

Method BLASTN
NCBI GI g210811
BLAST score 176
E value 3.0e-94
Match length 392
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40367

Seq. ID LIB3138-036-Q1-N1-H12

Method BLASTN
NCBI GI g287733
BLAST score 212
E value 1.0e-116
Match length 212
% identity 100

NCBI Description B.taurus mRNA for F1-ATPase gamma-subunit

Seq. No.

40368

Seq. ID LIB3138-037-Q1-N1-A11

Method BLASTX
NCBI GI g576509
BLAST score 238
E value 3.0e-20
Match length 63
% identity 73

NCBI Description (L36857) GTP-binding protein [Pisum sativum]

Seq. No.

40369

Seq. ID LIB3138-037-Q1-N1-A12

Method BLASTX NCBI GI g138364 BLAST score 236

6317



E value 6.0e-20 Match length 111 % identity 45

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40370

Seq. ID LIB3138-037-Q1-N1-C3

Method BLASTX
NCBI GI 94097880
BLAST score 259
E value 4.0e-26
Match length 92
% identity 63

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 40371

Seq. ID LIB3138-037-Q1-N1-C8

Method BLASTN
NCBI GI g210811
BLAST score 80
E value 4.0e-37
Match length 240
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40372

Seq. ID LIB3138-037-Q1-N1-C9

Method BLASTX
NCBI GI g4097880
BLAST score 283
E value 1.0e-25
Match length 91
% identity 66

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 40373

Seq. ID LIB3138-037-Q1-N1-F1

Method BLASTX
NCBI GI g3281857
BLAST score 164
E value 9.0e-12
Match length 75
% identity 45

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 40374

Seq. ID LIB3138-037-Q1-N1-G1

Method BLASTX
NCBI GI g4097880
BLAST score 137
E value 9.0e-09
Match length 60
% identity 50



```
NCBI Description
                  (U70866) polyprotein [Bean pod mottle virus]
                  40375
Seq. No.
Seq. ID
                  LIB3138-037-Q1-N1-H6
Method
                  BLASTN
NCBI GI
                  g1053215
BLAST score
                  156
                  2.0e-82
E value
                  247
Match length
% identity
                  91
NCBI Description
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
                  nuclear gene encoding chloroplast protein, complete cds
                  40376
Seq. No.
Seq. ID
                  LIB3138-037-Q1-N1-H8
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  34
                  9.0e-10
E value
                  58
Match length
% identity
                  90
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40377
Seq. ID
                  LIB3138-038-Q1-N1-B3
Method
                  BLASTN
NCBI GI
                  g1055367
BLAST score
                  307
                  1.0e-172
E value
                  386
Match length
                  95
% identity
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
Seq. No.
                  40378
Seq. ID
                  LIB3138-038-Q1-N1-B9
Method
                  BLASTX
                  g1350740
NCBI GI
BLAST score
                  258
                  2.0e-22
E value
Match length
                  96
% identity
                  56
NCBI Description
                  60S RIBOSOMAL PROTEIN L36 (L39) >gi 1051262 (U37010)
                  ribosomal protein L39 [Candida albicans]
Seq. No.
                  40379
Seq. ID
                  LIB3138-039-Q1-N1-B12
Method
                  BLASTN
NCBI GI
                  g2677827
```

NCBI GI g2677827
BLAST score 39
E value 1.0e-12
Match length 59
% identity 92

NCBI Description Prunus armeniaca cysteine protease mRNA, complete cds

Seq. No. 40380



```
Seq. ID
                  LIB3138-039-Q1-N1-B9
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  205
E value
                  1.0e-111
Match length
                  405
% identity
                  88
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  40381
Seq. ID
                  LIB3138-039-Q1-N1-D4
Method
                  BLASTX
NCBI GI
                  g2062169
BLAST score
                  389
E value
                  5.0e-38
Match length
                  92
% identity
                  41
                  (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                  thaliana]
                                            1.50
Seq. No.
                  40382
Seq. ID
                  LIB3138-039-Q1-N1-F1
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  77
E value
                  2.0e-35
Match length
                  196
% identity
NCBI Description
                  Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
Seq. No.
                  40383
Seq. ID
                  LIB3138-039-Q1-N1-F5
Method
                  BLASTX
NCBI GI
                  g730680
BLAST score
                  305
                  3.0e-28
E value
Match length
                  81
% identity
                  68
                  40S RIBOSOMAL PROTEIN SA (P40) (STUBARISTA PROTEIN)
NCBI Description
                  (LAMININ RECEPTOR HOMOLOG) (K14) >gi 158031 (M90422) p40
                  [Drosophila melanogaster] >gi 3292889 emb CAA19839
                  (AL031027) EG:80H7.6 [Drosophila melanogaster]
                  40384
Seq. No.
Seq. ID
                  LIB3138-039-Q1-N1-G8
Method
                  BLASTN
NCBI GI
                  g20728
```

BLAST score 94 2.0e-45 E value Match length 276 % identity 88

NCBI Description Pea chloroplast GAPA mRNA encoding

glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A

(EC 1.2.1.13)



```
Seq. No.
Seq. ID
                  LIB3138-039-Q1-N1-G9
Method
                  BLASTX
NCBI GI
                  g138364
BLAST score
                  415
E value
                  8.0e-41
Match length
                  125
% identity
                  66
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                  (M62738) coat protein [Bean pod mottle virus]
```

Seq. No. 40386 Seq. ID LIB3138-039-Q1-N1-H9 Method BLASTX NCBI GI g3158474 BLAST score 374

4.0e-36 E value Match length 106 % identity 72

NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 40387 Seq. ID LIB3138-040-Q1-N1-B10 Method BLASTX NCBI GI g138364 BLAST score 285 E value 9.0e-26

Match length 99 % identity 61 NCBI Description

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi 210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 40388

Seq. ID LIB3138-040-Q1-N1-D11

Method BLASTX NCBI GI g4102999 BLAST score 192 E value 1.0e-14 Match length 86 % identity 50

NCBI Description (AF019630) pathogenicity protein [Magnaporthe grisea]

Seq. No. 40389

Seq. ID LIB3138-040-Q1-N1-D12

Method BLASTX NCBI GI g3021267 BLAST score 165 E value 1.0e-11 Match length 90 % identity 42

NCBI Description (AL022347) serine/threonine kinase - like protein

[Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  LIB3138-040-Q1-N1-D4
                  BLASTX
Method
                  g3135253
NCBI GI
BLAST score
                  313
E value
                  7.0e-29
Match length
                  112
% identity
                  50
                  (AC003058) putative receptor protein kinase [Arabidopsis
NCBI Description
Seq. No.
                  40391
                  LIB3138-040-Q1-N1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  45
E value
                  3.0e-16
Match length
                  125
% identity
NCBI Description
                  Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
Seq. No.
                  40392
Seq. ID
                  LIB3138-040-Q1-N1-F5
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  69
E value
                  2.0e-30
Match length
                  228
% identity
                  84
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  40393
Seq. ID
                  LIB3138-040-Q1-N1-F9
Method
                  BLASTX
NCBI GI
                  g4567251
BLAST score
                  147
                  2.0e-09
E value
                  34
Match length
                  68
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  40394
Seq. ID
                  LIB3138-040-Q1-N1-H1
Method
                  BLASTX
NCBI GI
                  g2331137
BLAST score
                  178
                  1.0e-13
E value
```

Match length 45 78 % identity

(AF010582) glyceraldehyde-3-phosphate dehydrogenase [Oryza NCBI Description

sativa]

Seq. No.

40395

Seq. ID LIB3138-041-Q1-N1-A10

Method BLASTN



```
NCBI GI g4115721
BLAST score 254
E value 1.0e-141
Match length 401
% identity 94
NCBI Description Alternary
```

NCBI Description Alternaria alternata gene for 1,3,8-trihydroxynaphthalene

reductase, complete cds

Seq. No. 40396

Seq. ID LIB3138-041-Q1-N1-A6

Method BLASTX
NCBI GI 94490315
BLAST score 161
E value 5.0e-11
Match length 34
% identity 88

NCBI Description (AL035678) hypothetical protein [Arabidopsis thaliana]

Seq. No. 40397

Seq. ID LIB3138-041-Q1-N1-B1

Method BLASTX
NCBI GI g138364
BLAST score 353
E value 1.0e-33
Match length 100
% identity 72

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40398

Seq. ID LIB3138-041-Q1-N1-B3

Method BLASTN
NCBI GI 94097879
BLAST score 162
E value 6.0e-86
Match length 326
% identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40399

Seq. ID LIB3138-041-Q1-N1-B5

Method BLASTN
NCBI GI g210811
BLAST score 146
E value 2.0e-76
Match length 338
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40400

Seq. ID LIB3138-041-Q1-N1-C5

Method BLASTX NCBI GI g138364



BLAST score 502 E value 6.0e-51 Match length 117 % identity 85

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639 pir_GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40401

Seq. ID LIB3138-041-Q1-N1-D11

Method BLASTX
NCBI GI g2501021
BLAST score 362
E value 1.0e-34
Match length 133
% identity 57

NCBI Description LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)

>gi_1652562_dbj_BAA17483_ (D90906) lysyl-tRNA synthetase

[Synechocystis sp.]

Seq. No. 40402

Seq. ID LIB3138-041-Q1-N1-E4

Method BLASTX
NCBI GI g3688350
BLAST score 272
E value 4.0e-24
Match length 122
% identity 48

NCBI Description (AL030996) dJ1189B24.4 (novel PUTATIVE protein similar to

hypothetical proteins S. pombe C22F3.14C and C. elegans

C16A3.8) [Homo sapiens]

Seq. No. 40403

Seq. ID LIB3138-041-Q1-N1-F12

Method BLASTX
NCBI GI g2492597
BLAST score 150
E value 4.0e-10
Match length 70
% identity 49

NCBI Description HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN SLL0182

>gi_1001688_dbj_BAA10424_ (D64002) ABC transporter

[Synechocystis sp.]

Seq. No. 40404

Seq. ID LIB3138-041-Q1-N1-F5

Method BLASTX
NCBI GI g2224901
BLAST score 210
E value 8.0e-17
Match length 53
% identity 68

NCBI Description (U67134) PcMYB1 protein [Petroselinum crispum]

Seq. No. 40405

Seq. ID LIB3138-041-Q1-N1-G6



Method BLASTN
NCBI GI g4097879
BLAST score 163
E value 1.0e-86
Match length 347
% identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40406

Seq. ID LIB3138-041-Q1-N1-H3

Method BLASTX
NCBI GI g138364
BLAST score 418
E value 3.0e-41
Match length 103
% identity 80

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40407

Seq. ID LIB3138-042-Q1-N1-A10

Method BLASTX
NCBI GI g138364
BLAST score 205
E value 1.0e-17
Match length 89
% identity 59

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40408

Seq. ID LIB3138-042-Q1-N1-A12

Method BLASTN
NCBI GI g210811
BLAST score 59
E value 1.0e-24
Match length 211
% identity 82

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40409

Seq. ID LIB3138-042-Q1-N1-A2

Method BLASTN
NCBI GI g2661020
BLAST score 140
E value 5.0e-73
Match length 220
% identity 91

NCBI Description Glycine max catalase (cat4) mRNA, complete cds

Seq. No. 40410



```
Seq. ID
                   LIB3138-042-Q1-N1-B10
 Method
                   BLASTX
 NCBI GI
                   q138364
 BLAST score
                   530
 E value
                   3.0e-54
 Match length
                   130
 % identity
                   77
NCBI Description
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle vīrus (straīn Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
 Seq. No.
                   40411
 Seq. ID
                   LIB3138-042-Q1-N1-B12
Method
                   BLASTX
NCBI GI
                   q138364
BLAST score
                   446
E value
                   2.0e-44
Match length
                   100
% identity
                   80
NCBI Description
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                   40412
Seq. ID
                   LIB3138-042-Q1-N1-C10
Method
                   BLASTX
NCBI GI
                   q229708
BLAST score
                   303
E value
                   7.0e-28
Match length
                   95
% identity
                   68
NCBI Description Bean pod mottle virus
Seq. No.
                   40413
Seq. ID
                  LIB3138-042-Q1-N1-C2
Method
                  BLASTX
NCBI GI
                  q4325282
BLAST score
                  201
E value
                   9.0e-16
Match length
                  77
% identity >
NCBI Description
                  (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
                  >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                  [Arabidopsis thaliana]
Seq. No.
                  40414
Seq. ID
                  LIB3138-042-Q1-N1-D11
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  137
E value
                  4.0e-71
Match length
                  312
% identity
```

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

87

complete middle component (M) RNA



 Seq. No.
 40415

 Seq. ID
 LIB3138-042-Q1-N1-D9

 Method
 BLASTN

 NCBI GI
 g4406529

 BLAST score
 60

 Fundamental Score
 3.00-25

E value 3.0e-25
Match length 140
% identity 86

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40416

Seq. ID LIB3138-042-Q1-N1-E12

Method BLASTX
NCBI GI g3482940
BLAST score 156
E value 2.0e-10
Match length 93
% identity 35

NCBI Description (AC005315) putative ligand-gated ionic channel [Arabidopsis

thaliana]

Seq. No. 40417

Seq. ID LIB3138-042-Q1-N1-F7

Method BLASTX
NCBI GI g229708
BLAST score 160
E value 7.0e-11
Match length 54
% identity 63

NCBI Description Bean pod mottle virus

Seq. No. 40418

Seq. ID LIB3138-042-Q1-N1-F9

Method BLASTN
NCBI GI g1079735
BLAST score 151
E value 2.0e-79
Match length 195
% identity 94

NCBI Description Glycine soja ribulose 1,5-bisphosphate carboxylase small

subunit precursor (rbcS) gene, nuclear gene encoding

chloroplast protein, complete cds

Seq. No. 40419

Seq. ID LIB3138-042-Q1-N1-G12

Method BLASTX
NCBI GI 94406530
BLAST score 241
E value 2.0e-20
Match length 89
% identity 61

NCBI Description (AF126870) rubisco activase [Vigna radiata]

Seq. No. 40420

Seq. ID LIB3138-042-Q1-N1-H12



Method BLASTX g138364 NCBI GI BLAST score 226 E value 1.0e-18 78 Match length 60 % identity

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

40421 Seq. No.

Seq. ID LIB3138-043-Q1-N1-C1

Method BLASTX NCBI GI g138364 BLAST score 249 2.0e-21 E value 92 Match length 60 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40422

Seq. ID LIB3138-043-Q1-N1-C2

Method BLASTX NCBI GI g4097880 BLAST score 196 E value 5.0e-21 Match length 131 % identity 40

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40423

Seq. ID LIB3138-043-Q1-N1-D8

Method BLASTX NCBI GI g138364 BLAST score 186 7.0e-30 E value Match length 121 % identity 67

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40424

Seq. ID LIB3138-043-Q1-N1-E1

Method BLASTX NCBI GI q138364 BLAST score 393 E value 3.0e-38 Match length 117 % identity

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -





bean pod mottle virus (strain Kentucky G7) >gi_210812
(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40425

Seq. ID LIB3138-043-Q1-N1-H10

Method BLASTN
NCBI GI g4097879
BLAST score 91
E value 1.0e-43

Match length 127 % identity 93

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40426

Seq. ID LIB3138-044-Q1-N1-A11

Method BLASTX
NCBI GI g4097880
BLAST score 250
E value 5.0e-39
Match length 113
% identity 84

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 40427

Seq. ID LIB3138-044-Q1-N1-A9

Method BLASTX
NCBI GI g229707
BLAST score 341
E value 2.0e-32
Match length 76
% identity 83

NCBI Description Bean pod mottle virus

Seq. No. 40428

Seq. ID LIB3138-044-Q1-N1-C12

Method BLASTX
NCBI GI g4097880
BLAST score 279
E value 5.0e-25
Match length 92
% identity 63

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40429

Seq. ID LIB3138-044-Q1-N1-D10

Method BLASTN
NCBI GI 94097879
BLAST score 151
E value 2.0e-79
Match length 371
% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40430

Seq. ID LIB3138-044-Q1-N1-D5

6329



```
Method BLASTN
NCBI GI g210811
BLAST score 109
E value 2.0e-54
Match length 233
% identity 87
NCBI Description Bean po
```

NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

 Seq. No.
 40431

 Seq. ID
 LIB3138-044-Q1-N1-E4

 Method
 BLASTN

 NCBI GI
 g4097879

 BLAST score
 38

 E value
 4.0e-12

E value 4.0e-12
Match length 58
% identity 91

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40432

Seq. ID LIB3138-044-Q1-N1-G5

Method BLASTX
NCBI GI g2760843
BLAST score 477
E value 4.0e-48
Match length 124
% identity 73

NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]

Seq. No. 40433

Seq. ID LIB3138-044-Q1-N1-G6

Method BLASTX
NCBI GI g1061040
BLAST score 248
E value 2.0e-21
Match length 88
% identity 59

NCBI Description (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]

>gi 1587694 prf 2207220A sterol C-methyltransferase

[Arabidopsis thaliana]

Seq. No. 40434

Seq. ID LIB3138-044-Q1-N1-H11

Method BLASTN
NCBI GI 94097879
BLAST score 87
E value 3.0e-41
Match length 282
% identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40435

Seq. ID LIB3138-044-Q1-N1-H12

Method BLASTX NCBI GI g229708



BLAST score 226 E value 6.0e-19 Match length 87 % identity 57

NCBI Description Bean pod mottle virus

Seq. No. 40436

Seq. ID LIB3138-044-Q1-N1-H8

Method BLASTX
NCBI.GI g3935187
BLAST score 358
E value 4.0e-34
Match length 123
% identity 58

NCBI Description (AC004557) F17L21.30 [Arabidopsis thaliana]

Seq. No. 40437

Seq. ID LIB3138-045-Q1-N1-C2

Method BLASTX
NCBI GI g138364
BLAST score 199
E value 8.0e-23
Match length 117
% identity 57

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40438

Seq. ID LIB3138-045-Q1-N1-D10

Method BLASTX
NCBI GI g138364
BLAST score 164
E value 2.0e-11
Match length 57
% identity 61

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40439

Seq. ID LIB3138-045-Q1-N1-D3

Method BLASTX
NCBI GI g1723376
BLAST score 288
E value 8.0e-26
Match length 110
% identity 48

NCBI Description HYPOTHETICAL 20.1 KD PROTEIN IN YCF37-PSAF INTERGENIC REGION (ORF174) >gi 2147509 pir S73113 hypothetical

protein 174 - Porphyra purpurea chloroplast >gi_1276658

(U38804) ORF174 [Porphyra purpurea]

Seq. No. 40440

Seq. ID LIB3138-045-Q1-N1-D8



```
Method BLASTX
NCBI GI g1350956
BLAST score 184
E value 5.0e-14
Match length 61
% identity 64
```

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

Seq. No. 40441

Seq. ID LIB3138-045-Q1-N1-F4

Method BLASTN
NCBI GI g4097879
BLAST score 236
E value 1.0e-130
Match length 480
% identity 88

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40442

Seq. ID LIB3138-045-Q1-N1-G9

Method BLASTN
NCBI GI g4097879
BLAST score 181
E value 3.0e-97
Match length 416
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40443

Seq. ID LIB3138-046-Q1-N1-A12

Method BLASTN
NCBI GI g210811
BLAST score 120
E value 6.0e-61
Match length 288
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40444

Seq. ID LIB3138-046-Q1-N1-A2

Method BLASTN
NCBI GI g210811
BLAST score 149
E value 4.0e-78
Match length 373
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40445

Seq. ID LIB3138-046-Q1-N1-B6

Method BLASTX NCBI GI g229708 BLAST score 195



E value 2.0e-15 Match length 68 % identity 57

NCBI Description Bean pod mottle virus

Seq. No.

Seq. ID LIB3138-046-Q1-N1-D11

40446

Method BLASTX
NCBI GI g282921
BLAST score 245
E value 7.0e-30
Match length 119
% identity 66

NCBI Description carbonate dehydratase (EC 4.2.1.1) precursor - garden pea

>gi_169057 (M63627) carbonic anhydrase [Pisum sativum]

>gi_227784_prf__1710354A carbonic anhydrase [Pisum sativum]

Seq. No. 40447

Seq. ID LIB3138-046-Q1-N1-F12

Method BLASTX
NCBI GI g2462929
BLAST score 155
E value 2.0e-20
Match length 82
% identity 60

NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No. 40448

Seq. ID LIB3138-046-Q1-N1-F2

Method BLASTX
NCBI GI g309673
BLAST score 198
E value 1.0e-15
Match length 70
% identity 67

NCBI Description (L19651) light harvesting protein [Pisum sativum]

Seq. No. 40449

Seq. ID LIB3138-046-Q1-N1-F5

Method BLASTX
NCBI GI g3914473
BLAST score 185
E value 2.0e-14
Match length 56
% identity 66

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_479684_pir__S35151 photosystem I chain XI - spinach >gi_396275 emb_CAA45775 (X64445) subunit XI of

photosystem I reaction center [Spinacia oleracea]

Seq. No. 40450

Seq. ID LIB3138-046-Q1-N1-G3

Method BLASTX
NCBI GI 9731453
BLAST score 198
E value 8.0e-16
Match length 64



% identity

PROBABLE ATP-DEPENDENT TRANSPORTER YER036C NCBI Description

> >gi 1077646 pir S50539 hypothetical protein YER036c yeast (Saccharomyces cerevisiae) >gi 603269 (U18796)

Yer036cp [Saccharomyces cerevisiae]

40451 Seq. No.

LIB3138-046-Q1-N1-G9 Seq. ID

Method BLASTX NCBI GI g731453 BLAST score 180 1.0e-14 E value 66 Match length

70 % identity

PROBABLE ATP-DEPENDENT TRANSPORTER YERO36C NCBI Description

> >gi 1077646 pir S50539 hypothetical protein YER036c yeast (Saccharomyces cerevisiae) >gi 603269 (U18796)

Yer036cp [Saccharomyces cerevisiae]

40452 Seq. No.

Seq. ID LIB3138-046-Q1-N1-H5

Method BLASTX NCBI GI g1778093 BLAST score 214 2.0e-17 E value 82 Match length % identity 54

NCBI Description (U64902) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 40453

LIB3138-046-Q1-N1-H8 Seq. ID

Method BLASTX NCBI GI g3298547 BLAST score 125 2.0e-11 E value Match length 91

48 % identity

(AC004681) putative condensin protein [Arabidopsis NCBI Description

thaliana]

Seq. No.

40454

Seq. ID LIB3138-047-Q1-N1-A11

Method BLASTX NCBI GI q229708 BLAST score 382 E value 5.0e-37 Match length 115 69 % identity

NCBI Description Bean pod mottle virus

Seq. No.

40455

LIB3138-047-Q1-N1-A12 Seq. ID

Method BLASTX NCBI GI q4097880 BLAST score 247



E value 4.0e-21 Match length 109 50 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No.

40456

Seq. ID

LIB3138-047-Q1-N1-A4

Method NCBI GI BLASTN g4406529

BLAST score E value

40 2.0e-13

Match length % identity

60 92

NCBI Description

Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No.

40457

Seq. ID

LIB3138-047-Q1-N1-A8

Method

BLASTN q2598656

NCBI GI BLAST score

34

E value Match length

7.0e-10 102

% identity

83

NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No.

40458

Seq. ID

LIB3138-047-Q1-N1-B10

Method BLASTX NCBI GI g400890 BLAST score 353 E value 1.0e-33 Match length 111 45 % identity

NCBI Description

PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi_282837_pir__S26953 photosystem II 22K protein precursor - $spinach \ge gi_21307_{emb}CAA48557_ (X68552)_22kD-protein of$ PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864) photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

Seq. No.

40459

Seq. ID

LIB3138-047-Q1-N1-B6

Method BLASTN g210811 NCBI GI BLAST score 129 E value 3.0e-66 Match length 385 % identity 83

NCBI Description

Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

40460

Seq. ID

LIB3138-047-Q1-N1-C12

Method BLASTX NCBI GI q1134882 BLAST score 166



```
E value
                   2.0e-15
Match length
                   127
% identity
                   43
```

(Z68291) cysteine protease [Pisum sativum] NCBI Description

Seq. No.

40461

Seq. ID

LIB3138-047-Q1-N1-C3

Method NCBI GI

BLASTN q1150683

BLAST score

34

E value Match length 1.0e-09 125

% identity

87

NCBI Description V.radiata atpB, rbcL and trnK genes

Seq. No.

Seq. ID

40462

Method

LIB3138-047-Q1-N1-D11 BLASTN

NCBI GI BLAST score

g210811 72

E value Match length 2.0e-32 184 85

% identity NCBI Description

Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

40463

Seq. ID

LIB3138-047-Q1-N1-E10

Method NCBI GI BLAST score BLASTX g3342800 355

8.0e-34 E value Match length

94 % identity 78

NCBI Description

(AF061837) putative cytosolic 6-phosphogluconate

dehydrogenase [Zea mays]

Seq. No.

40464

Seq. ID

LIB3138-047-Q1-N1-E3

Method BLASTN NCBI GI g210811 BLAST score 142 E value 4.0e-74 Match length 294 87 % identity

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

40465

Seq. ID

LIB3138-047-Q1-N1-F12

Method BLASTX NCBI GI g138364 BLAST score 394 E value 2.0e-38 Match length 100 % identity 79

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT



PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >qi 210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 40466 Seq. ID LIB3138-047-Q1-N1-F2 Method BLASTN NCBI GI g210811 BLAST score 154 E value 4.0e-81 Match length 382 % identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40467 Seq. ID

LIB3138-047-Q1-N1-F5 Method BLASTX NCBI GI g4097880 BLAST score 441 -E value 7.0e-44 Match length 128

% identity 69

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No. 40468

Seq. ID LIB3138-047-Q1-N1-G8

Method BLASTX NCBI GI g3789942 BLAST score 214 1.0e-17 E value Match length 78 % identity 11

(AF093505) polyubiquitin [Saccharum hybrid cultivar NCBI Description

H32-8560]

Seq. No. 40469

Seq. ID LIB3138-047-Q1-N1-H9

Method BLASTX NCBI GI g4097880 BLAST score 204 E value 3.0e-16 Match length 65 % identity 65

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40470

Seq. ID LIB3138-048-Q1-N1-A7

Method BLASTX NCBI GI g229708 BLAST score 191 E value 5.0e-15 Match length 59 68 % identity

NCBI Description Bean pod mottle virus

40471

Seq. No.

NCBI GI

E value

BLAST score

g229708

4.0e-10

153



```
LIB3138-048-Q1-N1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2959324
BLAST score
                  411
E value
                  2.0e-40
Match length
                  109
% identity
                  71
NCBI Description (Y15224) Importin alpha-like protein [Arabidopsis thaliana]
Seq. No.
                  40472
Seq. ID
                  LIB3138-048-Q1-N1-A9
Method
                  BLASTN
NCBI GI
                  g1619904
BLAST score
                  59
E value
                  2.0e-24
Match length
                  134
% identity
                  87
NCBI Description Glycine max thiol protease isoform A mRNA, partial cds
                  40473
Seq. No.
Seq. ID
                  LIB3138-048-Q1-N1-B6
Method
                  BLASTN
NCBI GI
                  q1079735
BLAST score
                  103
                  4.0e-51
E value
Match length
                  155
% identity
                  92
NCBI Description Glycine soja ribulose 1,5-bisphosphate carboxylase small
                  subunit precursor (rbcS) gene, nuclear gene encoding
                  chloroplast protein, complete cds
Seq. No.
                  40474
Seq. ID
                  LIB3138-048-Q1-N1-D11
Method
                  BLASTX
NCBI GI
                  g229708
BLAST score
                  259
E value
                  8.0e-23
Match length
                  84
% identity
                  61
NCBI Description Bean pod mottle virus
Seq. No.
                  40475
Seq. ID
                  LIB3138-048-Q1-N1-D4
Method
                  BLASTX
NCBI GI
                  g229708
BLAST score
                  388
E value
                  1.0e-37
Match length
                  109
% identity
                  65
NCBI Description Bean pod mottle virus
Seq. No.
                  40476
Seq. ID
                  LIB3138-048-Q1-N1-D7
Method
                  BLASTX
```



Match length 67 % identity 51

NCBI Description Bean pod mottle virus

Seq. No. 40477

Seq. ID LIB3138-048-Q1-N1-E1

Method BLASTX
NCBI GI g4455207
BLAST score 206
E value 9.0e-17
Match length 75
% identity 55

NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 40478

Seq. ID LIB3138-048-Q1-N1-E6

Method BLASTX
NCBI GI g4335771
BLAST score 394
E value 2.0e-38
Match length 126
% identity 62

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 40479

Seq. ID LIB3138-048-Q1-N1-F9

Method BLASTN
NCBI GI g210811
BLAST score 53
E value 6.0e-21
Match length 173
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40480

Seq. ID LIB3138-048-Q1-N1-G1

Method BLASTX
NCBI GI g3493611
BLAST score 183
E value 1.0e-13
Match length 37
% identity 84

NCBI Description (AF068318) regulatory subunit of protein kinase CK2; CK2

beta-subunit [Arabidopsis thaliana]

Seq. No. 40481

Seq. ID LIB3138-048-Q1-N1-G5

Method BLASTX
NCBI GI g229708
BLAST score 181
E value 1.0e-13
Match length 57
% identity 63

NCBI Description Bean pod mottle virus

Seq. No. 40482



Seq. ID LIB3138-048-Q1-N1-G6

Method BLASTX
NCBI GI g229708
BLAST score 203
E value 2.0e-16
Match length 62
% identity 74

NCBI Description Bean pod mottle virus

Seq. No. 40483

Seq. ID LIB3138-048-Q1-N1-H7

Method BLASTX
NCBI GI g1711574
BLAST score 353
E value 6.0e-34
Match length 79
% identity 85

NCBI Description SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR

(SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA)

>gi 2130169 pir S65966 succinate--CoA ligase (GDP-forming)

(EC 6.2.1.4) alpha chain precursor - slime mold

(Dictyostelium discoideum) >gi_780694 (U23408) succinyl

coenzyme A synthetase alpha subunit [Dictyostelium

discoideum]

Seq. No. 40484

Seq. ID LIB3138-048-Q1-N1-H9

Method BLASTN
NCBI GI g4097879
BLAST score 115
E value 5.0e-58
Match length 275
% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40485

Seq. ID LIB3138-049-Q1-N1-A4

Method BLASTN
NCBI GI g4406529
BLAST score 201
E value 1.0e-109
Match length 340
% identity 90

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40486

Seq. ID LIB3138-049-Q1-N1-B1

Method BLASTN
NCBI GI g210811
BLAST score 132
E value 4.0e-68
Match length 280
% identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA



Seq. No. 40487 Seq. ID LIB3138-049-Q1-N1-B2 Method BLASTX NCBI GI q1680686 BLAST score 207 E value 1.0e-16 Match length 90 % identity 48 NCBI Description (U51330) rust resistance kinase Lr10 [Triticum aestivum] Seq. No. 40488 Seq. ID LIB3138-049-Q1-N1-B6 Method BLASTX NCBI GI g4512666 BLAST score 151 4.0e-10 E value Match length 81 % identity 41 (AC006931) putative mei2 protein [Arabidopsis thaliana] NCBI Description Seq. No. 40489 Seq. ID LIB3138-049-Q1-N1-B7 Method BLASTN NCBI GI g515746 BLAST score 135 4.0e-70 E value Match length 161 98 % identity NCBI Description Soybean chloroplast fructose-1, 6-bisphosphatase (FBP) mRNA, complete cds 40490 Seq. No. Seq. ID LIB3138-049-Q1-N1-E1 Method BLASTX NCBI GI g3650379 BLAST score 472 E value 2.0e-47 Match length 124 74 % identity NCBI Description (AL031740) 60s ribosomal protein 110a. [Schizosaccharomyces pombe] Seq. No. 40491 Seq. ID LIB3138-049-Q1-N1-E12 Method BLASTN NCBI GI g210811 BLAST score 66 E value 6.0e-29 Match length 133 % identity Bean pod mottle virus coat protein gene, complete cds, NCBI Description complete middle component (M) RNA

Seq. No. 40492

Seq. ID LIB3138-049-Q1-N1-E7

Method BLASTX

6341



NCBI GI g1172704 BLAST score 171 E value 3.0e-12 Match length 123 % identity 40

NCBI Description PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN)

>gi_633940 (L39082) transport protein [Arabidopsis
thaliana] >gi_4406786_gb_AAD20096_ (AC006532) histidine

transport protein PTR2-B [Arabidopsis thaliana]

Seq. No. 40493

Seq. ID LIB3138-049-Q1-N1-F2

Method BLASTN
NCBI GI g2275060
BLAST score 130
E value 6.0e-67
Match length 254
% identity 88

NCBI Description Neurospora crassa mRNA encoding GTP-binding protein (Ran),

partial

Seq. No. 40494

Seq. ID LIB3138-049-Q1-N1-H9

Method BLASTX
NCBI GI g1709846
BLAST score 114
E value 2.0e-12
Match length 99
% identity 34

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)

22 kDa component of photosystem II [Lycopersicon

esculentum]

Seq. No. 40495

Seq. ID LIB3138-050-Q1-N1-A10

Method BLASTN
NCBI GI g4115721
BLAST score 61
E value 8.0e-26
Match length 165
% identity 85

NCBI Description Alternaria alternata gene for 1,3,8-trihydroxynaphthalene

reductase, complete cds

Seq. No. 40496

Seq. ID LIB3138-050-Q1-N1-A4

Method BLASTX
NCBI GI g138364
BLAST score 324
E value 2.0e-30
Match length 88
% identity 69

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]



```
Seq. No.
Seq. ID
                  LIB3138-050-Q1-N1-B3
Method
                  BLASTX
NCBI GI
                  g3242705
BLAST score
                   290
E value
                  3.0e-26
Match length
                  118
% identity
                  54
                   (AC003040) putative nicotinate phosphoribosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  40498
Seq. ID
                  LIB3138-050-Q1-N1-B4
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  116
E value
                  1.0e-58
Match length
                  340
% identity
                  84
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40499
Seq. ID
                  LIB3138-050-Q1-N1-B6
Method
                  BLASTX
NCBI GI
                  g2213598
BLAST score
                  153
E value
                  4.0e-10
Match length
                  125
% identity
NCBI Description (AC000348) T7N9.18 [Arabidopsis thaliana]
Seq. No.
                  40500
Seq. ID
                  LIB3138-050-Q1-N1-C1
Method
                  BLASTN
NCBI GI
                  g4389416
BLAST score
                  35
E value
                  3.0e-10
Match length
                  59
% identity
                  90
NCBI Description Glycine max nitrate reductase (nr2) gene, partial cds
Seq. No.
                  40501
Seq. ID
                  LIB3138-050-Q1-N1-D4
Method
                  BLASTX
NCBI GI
                  q229707
BLAST score
                  145
E value
                  2.0e-09
Match length
                  82
% identity
                  40
NCBI Description Bean pod mottle virus
```

Seq. No. 40502

Seq. ID LIB3138-050-Q1-N1-E4

Method BLASTX NCBI GI g138364 BLAST score 233



```
E value
                     1.0e-19
 Match length
                    50
 % identity
                    82
 NCBI Description
                    GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                    PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                    bean pod mottle virus (strain Kentucky G7) >gi_210812
                    (M62738) coat protein [Bean pod mottle virus]
 Seq. No.
                    40503
 Seq. ID
                    LIB3138-050-Q1-N1-F1
 Method
                    BLASTX
 NCBI GI
                    q138364
 BLAST score
                    184
E value
                    5.0e-37
Match length
                    124
 % identity
                    70
NCBI Description
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                    PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                    bean pod mottle vīrus (strain Kentucky G7) >gi 210812
                    (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                    40504
Seq. ID
                    LIB3138-050-Q1-N1-F11
Method
                    BLASTX
NCBI GI
                    q4097880
BLAST score
                    143
E value
                    3.0e-09
Match length
                    64
% identity
                    48
NCBI Description
                  (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   40505
Seq. ID
                   LIB3138-050-Q1-N1-F5
Method
                   BLASTX
NCBI GI
                   q132951
BLAST score
                   581
E value
                   3.0e-60
Match length
                   128
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L16 (YL16) (39A) (RP39)
                   >gi_2119108_pir__S59767 ribosomal protein L11.e.A,
                   cytosolic - yeast (Saccharomyces cerevisiae) >gi_914973 (U32445) 60S ribosomal protein L16 (Swiss Prot. accession
                   number P06380) [Saccharomyces cerevisiae]
Seq. No.
                   40506
Seq. ID
                   LIB3138-050-Q1-N1-G1
Method
                   BLASTX
NCBI GI
                   g4097880
BLAST score
                   231
E value
                   8.0e-29
```

Match length 121 % identity 63

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 40507

Seq. ID LIB3138-050-Q1-N1-G10



Method BLASTX
NCBI GI g138364
BLAST score 256
E value 2.0e-22
Match length 87
% identity 67

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40508

Seq. ID LIB3138-050-Q1-N1-G3

Method BLASTN
NCBI GI g210811
BLAST score 92
E value 2.0e-44
Match length 236
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40509

Seq. ID LIB3138-050-Q1-N1-H1

Method BLASTX
NCBI GI g138364
BLAST score 160
E value 7.0e-11
Match length 117
% identity 36

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40510

Seq. ID LIB3138-050-Q1-N1-H2

Method BLASTX
NCBI GI g138364
BLAST score 272
E value 2.0e-37
Match length 96
% identity 70

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40511

Seq. ID LIB3138-050-Q1-N1-H4

Method BLASTX
NCBI GI g3738215
BLAST score 359
E value 2.0e-34
Match length 102
% identity 69

NCBI Description (AL031853) putative helicase [Schizosaccharomyces pombe]

```
40512
Seq. No.
Seq. ID
                  LIB3138-051-Q1-N1-A2
Method
                  BLASTN
NCBI GI
                  g2318116
BLAST score
                  85
E value
                  2.0e-40
Match length
                  137
                  91
% identity
NCBI Description
                  Pisum sativum Mg-chelatase subunit D (ChlD) mRNA, complete
                  cds
Seq. No.
                  40513
Seq. ID
                  LIB3138-051-Q1-N1-A8
Method
                  BLASTX
NCBI GI
                  g3510256
BLAST score
                  147
                  3.0e-15
E value
Match length
                  87
                  60
% identity
NCBI Description
                 (AC005310) unknown protein [Arabidopsis thaliana]
                  40514
Seq. No.
                  LIB3138-051-Q1-N1-B8
```

Seq. ID Method BLASTX NCBI GI g2494243 BLAST score 343 2.0e-32 E value

Match length 103 66 % identity

ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) NCBI Description

>gi_1235573_emb_CAA65434_ (X96614) EF1-alpha translation

elongation factor [Podospora curvicolla]

Seq. No. 40515

Seq. ID LIB3138-051-Q1-N1-C7

Method BLASTX NCBI GI q123537 BLAST score 149 9.0e-10 E value Match length 89 % identity 42

NCBI Description 12 KD HEAT SHOCK PROTEIN (GLUCOSE AND LIPID-REGULATED

PROTEIN) >gi_72231_pir__HHBY12 heat shock protein 12 yeast (Saccharomyces cerevisiae) >gi_3800_emb_CAA39306_ (X55785) hsp12 [Saccharomyces cerevisiae] >gi 171607 (M60827) 15 kD glucose and lipid regulated protein [Saccharomyces cerevisiae] >gi_559934_emb_CAA86349 (Z46255) hsp12, glp1, len: 109, CAI: 0.65, HS12 YEAST P22943 12 KD HEAT SHOCK PROTEIN [Saccharomyces cerevisiae] >gi 836740 dbj BAA09224 (D50617) 12KD heat shock protein

[Saccharomyces cerevisiae] >gi 1100790 dbj BAA08003 (D44596) 15kD glucose and lipid regulated protein [Saccharomyces cerevisiae] >gi 1742028 dbj BAA14033

(D89864) Sc-Hsp12p [Saccharomyces pastorianus]

Seq. No. 40516



Seq. ID LIB3138-051-Q1-N1-D1 Method BLASTX NCBI GI g138364 BLAST score 559

BLAST score 559
E value 1.0e-57
Match length 111
% identity 92

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

No. 40517

Seq. No. 40517 Seq. ID LIB3138-051-Q1-N1-E5

Method BLASTX
NCBI GI 94415924
BLAST score 273
E value 4.0e-24
Match length 110
% identity 50

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 40518

Seq. ID LIB3138-051-Q1-N1-G2

Method BLASTX
NCBI GI g1906600
BLAST score 399
E value 7.0e-39
Match length 98
% identity 74

NCBI Description (U85769) MepB [Aspergillus fumigatus]

Seq. No. 40519

Seq. ID LIB3138-051-Q1-N1-H10

Method BLASTN
NCBI GI g4097879
BLAST score 146
E value 2.0e-76
Match length 334
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40520

Seq. ID LIB3138-052-Q1-N1-A6

Method BLASTX
NCBI GI g138364
BLAST score 115
E value 2.0e-12
Match length 70
% identity 58

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]



```
Seq. No.
Seq. ID
                  LIB3138-052-Q1-N1-A8
Method
                  BLASTN
NCBI GI
                  g1053215
BLAST score
                  128
                  3.0e-66
E value
Match length
                  132
                  99
% identity
NCBI Description
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
                  nuclear gene encoding chloroplast protein, complete cds
```

40522 Seq. No. Seq. ID LIB3138-052-Q1-N1-C11 BLASTN Method NCBI GI g169362

BLAST score 54 1.0e-21 E value Match length 81 93 % identity

NCBI Description P.vulgaris PVPR3 protein mRNA, complete cds

Seq. No. 40523 Seq. ID LIB3138-052-Q1-N1-C6 Method BLASTX NCBI GI g138364 BLAST score 298 2.0e-27 E value

79 Match length 76 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639 pir GNWXG7 genome polyprotein M bean pod mottle vīrus (straīn Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40524

Seq. ID LIB3138-052-Q1-N1-E2

Method BLASTN q2924257 NCBI GI BLAST score 128 E value 1.0e-65 Match length 168 % identity 94

NCBI Description Tobacco chloroplast genome DNA

Seq. No.

40525

Seq. ID LIB3138-052-Q1-N1-E9

Method BLASTX NCBI GI q3668093 BLAST score 239 3.0e-20 E value Match length 107 % identity 48

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.

40526

Seq. ID LIB3138-052-Q1-N1-F6

Method BLASTN



NCBI GI g210811 BLAST score 74 E value 2.0e-33 Match length 250 % identity 83

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40527

Seq. ID LIB3138-052-Q1-N1-F8

Method BLASTX
NCBI GI g2131776
BLAST score 172
E value 2.0e-12
Match length 77
% identity 42

NCBI Description hypothetical protein YLR099c - yeast (Saccharomyces

cerevisiae) >gi_1256849 (U53876) Ylr099cp [Saccharomyces cerevisiae] >gi_1360481_emb_CAA97663_ (Z73271) ORF YLR099c

[Saccharomyces cerevisiae]

Seq. No. 40528

Seq. ID LIB3138-052-Q1-N1-G5

Method BLASTN
NCBI GI g4406529
BLAST score 98
E value 4.0e-48
Match length 106
% identity 98

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40529

Seq. ID LIB3138-052-Q1-N1-G6

Method BLASTN
NCBI GI g210811
BLAST score 71
E value 1.0e-31
Match length 175
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40530

Seq. ID LIB3138-052-Q1-N1-H7

Method BLASTX
NCBI GI 94417287
BLAST score 260
E value 4.0e-23
Match length 68
% identity 71

NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 40531

Seq. ID LIB3138-053-Q1-N1-A2

Method BLASTX NCBI GI g2281972



BLAST score 264 E value 4.0e-23 Match length 62 % identity 85

NCBI Description (Z98056) 40s ribosomal protein s15 or s22

[Schizosaccharomyces pombe] >gi_2414597_emb_CAB16574_ (Z99295) 40s ribosomal protein s15a [Schizosaccharomyces pombe] >gi_3219307_dbj_BAA28848_ (AB015353) ribosomal

protein S22 homolog [Schizosaccharomyces pombe]

Seq. No. 40532

Seq. ID LIB3138-053-Q1-N1-C1

Method BLASTX
NCBI GI g138364
BLAST score 567
E value 1.0e-58
Match length 122
% identity 84

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40533

Seq. ID LIB3138-053-Q1-N1-D6

Method BLASTX
NCBI GI g121736
BLAST score 418
E value 4.0e-41
Match length 124
% identity 65

NCBI Description GLUTATHIONE S-TRANSFERASE 1 (SR8) (CLASS-THETA)

>gi_99589_pir__S16604 glutathione transferase (EC 2.5.1.18)

CARSR8 - clove pink >gi_18330 emb_CAA41279 (X58390) glutathione s-transferase [Dianthus caryophyllus] >gi_167968 (M64268) glutathione transferase [Dianthus

caryophyllus]

Seq. No. 40534

Seq. ID LIB3138-053-Q1-N1-E1

Method BLASTX
NCBI GI g2498731
BLAST score 223
E value 3.0e-18
Match length 69
% identity 61

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1

>gi_1362013_pir__S57611 zeta-crystallin homolog Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 40535

Seq. ID LIB3138-053-Q1-N1-E3

Method BLASTX
NCBI GI g1076510
BLAST score 380
E value 8.0e-37



Match length 72 % identity

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean

>gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus

vulgaris]

Seq. No.

40536 Seq. ID

LIB3138-053-Q1-N1-F5

Method BLASTX NCBI GI g731089 BLAST score 349 4.0e-33 E value Match length 125 54 % identity

NCBI Description D-MANNONATE OXIDOREDUCTASE (FRUCTURONATE REDUCTASE)

>gi_1363395_pir__S56548 D-mannonate oxidoreductase uxuB -

Escherichia coli >gi_537164 (U14003) D-mannonate

oxidoreductase [Escherichia coli] >gi 1790779 (AE000503)

D-mannonate oxidoreductase [Escherichia coli]

>gi_1841885_dbj_BAA02591_ (D13329) Mannonate oxidoreductase

[Escherichia coli]

40537 Seq. No.

Seq. ID LIB3138-053-Q1-N1-G7

Method BLASTX NCBI GI g20729 BLAST score 229 4.0e-19 E value 94 Match length 61 % identity

NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]

Seq. No.

40538

LIB3138-053-Q1-N1-H8 Seq. ID

Method BLASTN NCBI GI q210811 BLAST score 131 E value 2.0e-67 323 Match length % identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40539

Seq. ID LIB3138-054-Q1-N1-B12

Method BLASTN NCBI GI q210811 BLAST score 86 E value 1.0e-40 Match length 359 % identity

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40540

Seq. ID LIB3138-054-Q1-N1-B3

Method BLASTX

```
NCBI GI
                  q2244807
BLAST score
                  196
E value
                  4.0e-31
Match length
                  114
                  56
% identity
                 (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  40541
Seq. ID
                  LIB3138-054-Q1-N1-D1
Method
                  BLASTX
NCBI GI
                  g138364
BLAST score
                  457
E value
                  1.0e-45
Match length
                  131
                  69
% identity
NCBI Description
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi_75639 pir_ GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  40542
Seq. ID
                  LIB3138-054-Q1-N1-D8
Method
                  BLASTN
NCBI GI
                  q602564
BLAST score
                  114
                  2.0e-57
E value
Match length
                  230
                  87
% identity
NCBI Description C.paradisi (Macf) INO1 gene
                  40543
Seq. No.
Seq. ID
                  LIB3138-054-Q1-N1-E4
Method
                  BLASTX
NCBI GI
                  q1854443
BLAST score
                  205
                  3.0e-16
E value
Match length
                  118
                  39
% identity
NCBI Description (D83970) CPRD8 protein [Vigna unguiculata]
Seq. No.
                  40544
Seq. ID
                  LIB3138-054-Q1-N1-E7
Method
                  BLASTN
NCBI GI
                  q1173649
BLAST score
                  114
                  3.0e-57
E value
Match length
                  114
                  100
% identity
NCBI Description Glycine max lipoxygenase mRNA, partial cds, 3' end
                  40545
Seq. No.
Seq. ID
                  LIB3138-054-Q1-N1-F2
```

Method BLASTX NCBI GI q4097880 BLAST score 225 E value 4.0e-19 Match length 72



% identity 61

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40546

Seq. ID

LIB3138-054-Q1-N1-G10

Method NCBI GI BLASTN g4097879

BLAST score

g4097879 43

E value

6.0e-15 55

Match length % identity

NCBI Description

95
Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40547

Seq. ID

LIB3138-054-Q1-N1-G8

Method NCBI GI BLAST score BLASTN g210811 119

E value
Match length
% identity

3.0e-60 367 83

NCBI Description

Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

40548

Seq. ID

LIB3138-054-Q1-N1-G9

Method BLASTN
NCBI GI g4097879
BLAST score 51
E value 8.0e-20
Match length 95
% identity 88

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40549

Seq. ID

LIB3138-054-Q1-N1-H4

Method BLASTN
NCBI GI g4097879
BLAST score 56
E value 6.0e-23
Match length 80
% identity 93

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40550

Seq. ID

LIB3138-054-Q1-N1-H7

Method BLASTN
NCBI GI g210811
BLAST score 107
E value 4.0e-53
Match length 308
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

```
Seq. No.
                   40551
Seq. ID
                   LIB3138-055-Q1-N1-B1
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   191
                   1.0e-103
E value
Match length
                   343
% identity
                   89
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
Seq. No.
                   40552
Seq. ID
                   LIB3138-055-Q1-N1-D12
Method
                   BLASTX
NCBI GI
                   q3834324
BLAST score
                   192
E value
                   7.0e-15
Match length
                   78
% identity
                   46
                  (ACO05679) Similar to gb_X92762 tafazzins protein from Homo
NCBI Description
                   sapiens. [Arabidopsis thaliana]
Seq. No.
                   40553
Seq. ID
                   LIB3138-055-Q1-N1-F4
Method
                   BLASTX
NCBI GI
                   g3075398
BLAST score
                   152
E value
                   6.0e-10
Match length
                   67
% identity
                   39
NCBI Description
                  (AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.
                   40554
Seq. ID
                  LIB3138-055-Q1-N1-F7
Method
                  BLASTN
NCBI GI
                   g312988
BLAST score
                  81
                   1.0e-37
E value
Match length
                  88
% identity
                   99
NCBI Description
                  G.max mRNA for beta-tubulin, partial cds
Seq. No.
                   40555
                  LIB3138-055-Q1-N1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746063
BLAST score
                  182
                   2.0e-13
E value
```

Match length 49 % identity 65

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 40556

Seq. ID LIB3138-056-Q1-N1-A1

Method BLASTX NCBI GI g4097880



```
BLAST score
                  2.0e-63
E value
Match length
                  137
                  84
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  40557
Seq. No.
Seq. ID
                  LIB3138-056-Q1-N1-A2
Method
                  BLASTX
NCBI GI
                  g3033513
BLAST score
                  350
                  3.0e-33
E value
                  102
Match length
                  73
% identity
                  (AF041068) rubisco activase [Phaseolus vulgaris]
NCBI Description
                  40558
Seq. No.
Seq. ID
                  LIB3138-056-Q1-N1-A7
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  163
                  2.0e-86
E value
                  386
Match length
                  86
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  40559
Seq. No.
Seq. ID
                  LIB3138-056-Q1-N1-A9
Method
                  BLASTX
NCBI GI
                  g3805853
BLAST score
                  434
                  5.0e-43
E value
Match length
                  111
                  77
% identity
NCBI Description
                  (AL031986) putative protein [Arabidopsis thaliana]
                  40560
Seq. No.
Seq. ID
                  LIB3138-056-Q1-N1-B11
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  136
E value
                  2.0e-70
                  386
Match length
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  40561
Seq. No.
Seq. ID
                  LIB3138-056-Q1-N1-B5
                  BLASTN
Method
```

Method BLASTN
NCBI GI g1055367
BLAST score 258
E value 1.0e-143
Match length 398
% identity 91

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

% identity

NCBI Description



subunit mRNA, complete cds

```
40562
Seq. No.
                  LIB3138-056-Q1-N1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g138364
BLAST score
                  181
                  3.0e-25
E value
                  117
Match length
                  58
% identity
NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  40563
Seq. ID
                  LIB3138-056-Q1-N1-D10
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  177
E value
                  6.0e-95
Match length
                  389
% identity
                  86
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  40564
Seq. ID
                  LIB3138-056-Q1-N1-D3
                  BLASTN
Method
                  g1055367
NCBI GI
BLAST score
                  325
E value
                  0.0e+00
Match length
                  373
                  97
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                  40565
                  LIB3138-056-Q1-N1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350785
                  208
BLAST score
                  1.0e-16
E value
Match length
                  76
% identity
                  59
NCBI Description 60S RIBOSOMAL PROTEIN L18 (L14B)
                  40566
Seq. No.
                  LIB3138-056-Q1-N1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  245
                  6.0e-22
E value
Match length
                  88
```

[Arabidopsis thaliana]

(AF027174) cellulose synthase catalytic subunit



```
Seq. No.
                   40567
Seq. ID
                  LIB3138-056-Q1-N1-F1
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                   55
                  2.0e-22
E value
Match length
                  155
% identity
                  84
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40568
Seq. ID
                  LIB3138-056-Q1-N1-G5
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  82
E value
                  2.0e-38
Match length
                  178
% identity
                  87
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40569
Seq. ID
                  LIB3138-056-Q1-N1-H1
Method
                  BLASTX
NCBI GI
                  g3297819
BLAST score
                  174
E value
                  1.0e-12
Match length
                  99
% identity
                  43
NCBI Description
                  (AL031032) protein kinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  40570
Seq. ID
                  LIB3138-056-Q1-N1-H2
Method
                  BLASTX
NCBI GI
                  q4335722
BLAST score
                  177
                  7.0e-13
E value
Match length
                  99
% identity
                  42
NCBI Description
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  40571
Seq. ID
                  LIB3138-057-Q1-N1-A12
Method
                  BLASTX
NCBI GI
                  q3850778
BLAST score
                  168
```

E value 6.0e-12 Match length 58 % identity 57

NCBI Description (Y18346) gluaredoxin [Lycopersicon esculentum]

Seq. No.

40572

Seq. ID LIB3138-057-Q1-N1-A5

Method

BLASTN



NCBI GI g169036 BLAST score 87 E value 2.0e-41 Match length 253 % identity 88

NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No.

40573

Seq. ID

LIB3138-057-Q1-N1-C4

Method BLASTX
NCBI GI g135181
BLAST score 247
E value 3.0e-21
Match length 114
% identity 39

NCBI Description VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)

>gi 143797 (M16318) valyl-tRNA synthetase [Bacillus

stearothermophilus]

Seq. No.

40574

Seq. ID

LIB3138-057-Q1-N1-C9

Method BLASTX
NCBI GI g3367793
BLAST score 358
E value 4.0e-34
Match length 82
% identity 82

NCBI Description (AL031154) 40s ribosomal protein s27 type

[Schizosaccharomyces pombe]

Seq. No.

40575

Seq. ID

LIB3138-057-Q1-N1-F10

Method BLASTN
NCBI GI g4097879
BLAST score 169
E value 4.0e-90
Match length 353
% identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40576

Seq. ID

LIB3138-057-Q1-N1-F12

Method BLASTN
NCBI GI g4097879
BLAST score 72
E value 3.0e-32
Match length 199
% identity 88

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

40577

Seq. ID

LIB3138-057-Q1-N1-H4

Method BLASTN NCBI GI g210811 BLAST score 103



```
E value
                   9.0e-51
Match length
                   279
% identity
NCBI Description
```

Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

40578 Seq. No. Seq. ID

LIB3138-057-Q1-N1-H6

BLASTX Method g2651310 NCBI GI BLAST score 200 1.0e-15 E value 98 Match length 39 % identity

(AC002336) putative PTR2-B peptide transporter [Arabidopsis NCBI Description

thaliana]

Seq. No.

40579 Seq. ID LIB3138-059-Q1-N1-A11

Method BLASTX NCBI GI g2569955 390 BLAST score 6.0e-38 E value Match length 105 73 % identity

(X98860) isocitrate lyase [Coprinus cinereus] NCBI Description

40580 Seq. No.

Seq. ID LIB3138-059-Q1-N1-A2

BLASTX Method NCBI GI g2613143 BLAST score 203 3.0e-16 E value 52 Match length

67 % identity

(AF030548) tubulin [Oryza sativa] NCBI Description

40581 Seq. No.

Seq. ID LIB3138-059-Q1-N1-A3

BLASTN Method NCBI GI g3236477 BLAST score 69 E value 1.0e-30 Match length 197 % identity

Gossypium hirsutum 26S protease regulatory subunit (PRA2) NCBI Description

mRNA, partial cds

40582 Seq. No.

LIB3138-059-Q1-N1-A5 Seq. ID

Method BLASTX NCBI GI g229708 BLAST score 136 1.0e-08 E value Match length 46 % identity 57

NCBI Description Bean pod mottle virus



```
Seq. No.
                  40583
Seq. ID
                  LIB3138-059-Q1-N1-A6
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  130
                   5.0e-67
E value
Match length
                  242
% identity
                  88
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
                  40584
Seq. No.
Seq. ID
                  LIB3138-059-Q1-N1-B12
Method
                  BLASTN
```

NCBI GI g210811 BLAST score 234 E value 1.0e-129 Match length 384 % identity 90

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. Seq. ID LIB3138-059-Q1-N1-B9 Method BLASTN g256142 NCBI GI BLAST score 38 E value 3.0e-12 Match length 78 % identity 87

NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var

Prize, mRNA, 1450 nt]

40586 Seq. No. Seq. ID LIB3138-059-Q1-N1-E3 Method BLASTX

40585

NCBI GI q3522929 BLAST score 487 E value 2.0e-49 Match length 97 92 % identity

NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase

> [Arabidopsis thaliana] >gi 3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 40587

Seq. ID LIB3138-059-Q1-N1-F6

Method BLASTX NCBI GI g231660 BLAST score 186 E value 5.0e-14Match length 102 % identity 27

NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No. 40588

NCBI Description



```
Seq. ID
                  LIB3138-059-Q1-N1-G6
                  BLASTX
Method
NCBI GI
                  g138364
BLAST score
                  203
                  2.0e-16
E value
Match length
                  58
% identity
                  72
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  40589
Seq. ID
                  LIB3138-059-Q1-N1-G7
Method
                  BLASTN
NCBI GI
                  q210811
BLAST score
                  51
                  8.0e-20
E value
Match length
                  91
% identity
                  89
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40590
Seq. ID
                  LIB3138-059-Q1-N1-H9
Method
                  BLASTX
NCBI GI
                  g3643608
BLAST score
                  202
                  6.0e-16
E value
Match length
                  82
% identity
                  51
NCBI Description
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  40591
Seq. ID
                  LIB3138-060-Q1-N1-F6
Method
                  BLASTX
NCBI GI
                  g3024875
BLAST score
                  160
E value
                  2.0e-11
Match length
                  70
% identity
                  41
NCBI Description
                  HYPOTHETICAL 65.0 KD PROTEIN SLL0095
                  >gi_1208478_dbj_BAA10646_ (D64004) ABC1-like [Synechocystis
                  sp.]
Seq. No.
                  40592
Seq. ID
                  LIB3138-060-Q1-N1-G11
Method
                  BLASTX
NCBI GI
                  q138364
BLAST score
                  502
E value
                  4.0e-51
Match length
                  111
% identity
                  84
```

6361

(M62738) coat protein [Bean pod mottle virus]

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi 210812



```
40593
Seq. No.
Seq. ID
                  LIB3138-060-Q1-N1-G3
                  BLASTN
Method
NCBI GI
                  g1419348
                  84
BLAST score
                  1.0e-39
E value
                  200
Match length
% identity
                  85
                  V.vinifera mRNA for ferredoxin-dependent glutamate synthase
NCBI Description
                   (clone pGOGAT1)
                   40594
Seq. No.
                  LIB3138-060-Q1-N1-H2
Seq. ID
Method
                  BLASTN
                  g210811
NCBI GI
BLAST score
                  88
                  5.0e-42
E value
                  192
Match length
% identity
                  86
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   40595
Seq. No.
Seq. ID
                  LIB3138-060-Q1-N1-H7
                  BLASTN
Method
                   q4038468
NCBI GI
BLAST score
                   51
                   3.0e-20
E value
                   91
Match length
                   89
% identity
NCBI Description Porteresia coarctata histone H3 mRNA, complete cds
                   40596
Seq. No.
Seq. ID
                   LIB3138-061-Q1-N1-A8
                   BLASTX
Method
                   g138364
NCBI GI
                   525
BLAST score
                   9.0e-54
E value
                   116
Match length
                   84
% identity
                   GENOME POLYPROTEIN M_{\tilde{e}} (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   40597
Seq. No.
Seq. ID
                   LIB3138-061-Q1-N1-B12
                   BLASTX
Method
                   q2500465
NCBI GI
BLAST score
                   214
```

40S RIBOSOMAL PROTEIN S13 >gi 1742935 emb CAA64365

(X94704) 40S ribosomal protein S13 [Agaricus bisporus]

8.0e-18

52 73

E value Match length

% identity

NCBI Description



```
Seq. No.
Seq. ID
                   LIB3138-061-Q1-N1-C7
                   BLASTX
Method
NCBI GI
                   g1731071
BLAST score
                   181
E value
                   3.0e-13
Match length
                   111
                   37
% identity
                   HYPOTHETICAL 47.0 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION
NCBI Description
                   >gi_1303959_dbj_BAA12614_ (D84432) YqjH [Bacillus subtilis]
>gi_2634822_emb_CAB14319_ (Z99116) similar to DNA-damage
                   repair protein [Bacillus subtilis]
                   40599
Seq. No.
Seq. ID
                   LIB3138-061-Q1-N1-E11
Method
                   BLASTX
NCBI GI
                   g3445200
                   470
BLAST score
                   3.0e-47
E value
Match length
                   118
% identity
                   76
NCBI Description
                   (AC004786) putative squalene epoxidase [Arabidopsis
                   thaliana]
                   40600
Seq. No.
Seq. ID
                   LIB3138-061-Q1-N1-F11
Method
                   BLASTN
NCBI GI
                   g4097879
BLAST score
                   115
                   3.0e-58
E value
Match length
                   187
                   90
% identity
NCBI Description
                   Bean pod mottle virus complete segment RNA1 polyprotein
                   gene, complete cds
                   40601
Seq. No.
Seq. ID
                   LIB3138-061-Q1-N1-H11
Method
                   BLASTX
NCBI GI
                   q730463
BLAST score
                   331
                   7.0e-31
E value
Match length
                   99
                   62
% identity
                   60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
NCBI Description
                   >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                   (Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal
                   protein L37 [Saccharomyces cerevisiae]
                   >gi 1420537 emb CAA99454 (Z75142) ORF YOR234c
                   [Saccharomyces cerevisiae]
                   40602
Seq. No.
Seq. ID
                   LIB3138-062-Q1-N1-A11
```

Method BLASTX
NCBI GI g138364
BLAST score 158

E value 6.0e-11 Match length 93



% identity 46 NCBI Description GENO

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40603

Seq. ID LIB3138-062-Q1-N1-A3

Method BLASTN
NCBI GI g4097879
BLAST score 79

E value 2.0e-36

Match length 219 % identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40604

Seq. ID LIB3138-062-Q1-N1-A9

Method BLASTX
NCBI GI g2213598
BLAST score 213
E value 4.0e-17
Match length 81
% identity 49

NCBI Description (AC000348) T7N9.18 [Arabidopsis thaliana]

Seq. No. 40605

Seq. ID LIB3138-062-Q1-N1-B4

Method BLASTN
NCBI GI g4406529
BLAST score 67
E value 2.0e-29
Match length 143
% identity 87

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40606

Seq. ID LIB3138-062-Q1-N1-E2

Method BLASTX
NCBI GI g2347188
BLAST score 232
E value 2.0e-19
Match length 85
% identity 51

NCBI Description (AC002338) laccase isolog [Arabidopsis thaliana]

>gi_3150401 (AC004165) putative laccase [Arabidopsis

thalianal

Seq. No. 40607

Seq. ID LIB3138-062-Q1-N1-E6

Method BLASTX
NCBI GI g4097880
BLAST score 390
E value 5.0e-38
Match length 111



% identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No.

40608

Seq. ID

LIB3138-062-Q1-N1-G7

Method

BLASTX

NCBI GI

g2495499

BLAST score

415

E value

7.0e-41

Match length % identity

111 66

NCBI Description

HYPOTHETICAL 24.3 KD PROTEIN IN INTF-EAEH INTERGENIC REGION

>gi 1657487 (U73857) similar to A. nicotinovorans nicotine dehydrogenase [Escherichia coli] >gi 1786480 (AE000136) putative xanthine dehydrogenase (EC 1.1.1.20) [Escherichia

coli]

Seq. No.

40609

Seq. ID

LIB3138-062-Q1-N1-H10

Method NCBI GI BLASTX g2133240

BLAST score

145

E value

1.0e-09

Match length

44

% identity

61

NCBI Description

immunoreactive protein - Coccidioides immitis >gi 1161374

(U39835) immunoreactive spherule cell wall protein [Coccidioides immitis] >gi_1200180 (U32518) antigen 2 [Coccidioides immitis] >gi_1256444 (U51200) antigen 2 [Coccidioides immitis] >gi_2331289 (AF013256) proline rich antigen [Coccidioides immitis] >gi 1586922 prf 2205231A

immunoreactive protein [Coccidioides immitis]

Seq. No.

40610

Seq. ID

LIB3138-062-Q1-N1-H12

Method BLASTX NCBI GI g1326010 BLAST score 231 E value 3.0e-19 Match length 126

% identity

NCBI Description (Z47813) Sec7p [Saccharomyces cerevisiae]

Seq. No.

40611

40

Seq. ID

LIB3138-063-Q1-N1-A6

Method BLASTX NCBI GI q3023996 BLAST score 268 1.0e-23 E value 70 Match length 69 % identity

NCBI Description

ISOCITRATE DEHYDROGENASE (NADP), MITOCHONDRIAL PRECURSOR (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH)

(IDP) >gi_2564042_dbj_BAA22945_ (AB004556) mitochondrial NADP-linked isocitrate dehydrogenase [Candida tropicalis]

Seq. No.

40612



Seq. ID LIB3138-063-Q1-N1-C9

Method BLASTN
NCBI GÍ g210811
BLAST score 129
E value 3.0e-66
Match length 329
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40613

Seq. ID LIB3138-063-Q1-N1-D5

Method BLASTX
NCBI GI g138364
BLAST score 261
E value 3.0e-23
Match length 61
% identity 82

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40614

Seq. ID LIB3138-064-Q1-N1-B2

Method BLASTN
NCBI GI g4097879
BLAST score 107
E value 3.0e-53
Match length 231
% identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40615

Seq. ID LIB3138-064-Q1-N1-C11

Method BLASTN
NCBI GI g210811
BLAST score 129
E value 3.0e-66
Match length 387
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40616

Seq. ID LIB3138-064-Q1-N1-C8

Method BLASTX
NCBI GI g3367534
BLAST score 141
E value 2.0e-15
Match length 65
% identity 72

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis

thaliana]



```
Seq. No.
Seq. ID
                  LIB3138-064-Q1-N1-H1
Method
                  BLASTN
NCBI GI
                  q210811
BLAST score
                  89
E value
                  1.0e-42
Match length
                  268
% identity
                  84
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40618
Seq. ID
                  LIB3138-064-Q1-N1-H9
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  55
E value
                  2.0e-22
Match length
                  143
% identity
                  85
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40619
Seq. ID
                  LIB3138-065-Q1-N1-A3
Method
                  BLASTX
NCBI GI
                  g2997729
BLAST score
                  538
E value
                  3.0e-55
Match length
                  123
% identity
                  82
NCBI Description
                  (AF054511) ribosomal protein S7 [Yarrowia lipolytica]
Seq. No.
                  40620
Seq. ID
                  LIB3138-065-Q1-N1-A7
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  130
E value
                  5.0e-67
Match length
                  258
% identity
                  88
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  40621
Seq. ID
                  LIB3138-065-Q1-N1-B6
                  BLASTN
```

Seq. No.

Method NCBI GI q12147 BLAST score 48 E value 2.0e-18 Match length 108 % identity 86

NCBI Description Pea chloroplast genes for ATP synthetase subunits beta and

epsilon (atpB and atpE)

Seq. No. 40622

Seq. ID LIB3138-065-Q1-N1-C12

Method BLASTX

```
NCBI GI
                   q3758890
BLAST score
                   414
E value
                   1.0e-40
                   131
Match length
```

% identity NCBI Description (Y14317) catalase/peroxidase [Streptomyces reticuli]

40623 Seq. No. LIB3138-065-Q1-N1-C4 Seq. ID Method BLASTN NCBI GI g4097879 BLAST score 135 E value 8.0e-70 Match length 369 % identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

40624 Seq. No. LIB3138-065-Q1-N1-E11 Seq. ID Method BLASTN NCBI GI g4097879 BLAST score 155 E value 9.0e-82

57

Match length 410 85 % identity

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

40625 Seq. No.

LIB3138-065-Q1-N1-E4 Seq. ID

Method BLASTX NCBI GI q138364 BLAST score 369 1.0e-35 E value Match length 103 % identity 71

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

40626 Seq. No.

Seq. ID LIB3138-066-Q1-N1-C2

Method BLASTX NCBI GI q3876111 BLAST score 177 E value 7.0e-13 Match length 97 % identity 38

NCBI Description (Z54271) similar to signal recognition particle protein

(SRP54); cDNA EST EMBL: M88956 comes from this gene; cDNA EST EMBL: Z14505 comes from this gene; cDNA EST EMBL: Z14541 comes from this gene; cDNA EST EMBL: 214549 comes from t...

>gi_3876124_emb_CAA92301_ (Z68161) similar to signal

recognition particle protein (SRP54); cDNA EST EMBL:M88956 comes from this gene; cDNA EST EMBL: 214505 comes from this



gene; cDNA EST EMBL:Z14541 comes from this gene; cDNA EST EMBL:Z14549 comes from t

 Seq. No.
 40627

 Seq. ID
 LIB3138-066-Q1-N1-D1

 Method
 BLASTN

 NCBI GI
 g531828

 BLAST score
 51

 E value
 9.0e-20

Match length 215 % identity 81

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 40628

Seq. ID LIB3138-066-Q1-N1-D3

Method BLASTX
NCBI GI g3600054
BLAST score 388
E value 1.0e-37
Match length 133

% identity 58

NCBI Description (AF080120) No definition line found [Arabidopsis thaliana]

Seq. No. 40629

Seq. ID LIB3138-066-Q1-N1-G12

Method BLASTN
NCBI GI g210811
BLAST score 136
E value 2.0e-70
Match length 356
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40630

Seq. ID LIB3138-066-Q1-N1-H12

Method BLASTN
NCBI GI g210811
BLAST score 91
E value 1.0e-43
Match length 226
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40631

Seq. ID LIB3138-066-Q1-N1-H2

Method BLASTN
NCBI GI g4097879
BLAST score 80
E value 4.0e-37
Match length 228
% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40632

6369



LIB3138-066-Q1-N1-H3 Seq. ID Method BLASTX g4097880 NCBI GI BLAST score 230 1.0e-19 E value 63 Match length 76 % identity (U70866) polyprotein [Bean pod mottle virus] NCBI Description Seq. No. 40633 Seq. ID LIB3138-069-P1-N1-A4 Method BLASTN NCBI GI q210811 BLAST score 137 E value 5.0e-71 352 Match length 86 % identity Bean pod mottle virus coat protein gene, complete cds, NCBI Description complete middle component (M) RNA Seq. No. 40634 Seq. ID LIB3138-069-P1-N1-A7 BLASTN Method NCBI GI q4097879 BLAST score 87 3.0e-41 E value Match length 274 % identity 84 Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description gene, complete cds Seq. No. 40635 Seq. ID LIB3138-069-P1-N1-B5 Method BLASTN NCBI GI q4406529 BLAST score 190 E value 1.0e-102 Match length 377 88 % identity Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene NCBI Description encoding chloroplast protein, complete cds Seq. No. 40636 LIB3138-069-P1-N1-C4 Seq. ID Method BLASTX NCBI GI g2414666 BLAST score 197 E value 2.0e-15 Match length 111 % identity 43

NCBI Description (299262) pyridoxal reductase. [Schizosaccharomyces pombe]

Seq. No.

40637

Seq. ID LIB3138-069-P1-N1-G10

Method BLASTX NCBI GI g1150375 BLAST score 160



E value Match length 91 21 % identity

(X89811) ssrp2 [Drosophila melanogaster] NCBI Description

Seq. No.

% identity

40638

Seq. ID LIB3138-069-P1-N1-G5

BLASTN Method NCBI GI g1055367 BLAST score 143 1.0e-74 E value 275 Match length 88

Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description

subunit mRNA, complete cds

40639 Seq. No.

Seq. ID LIB3138-069-P1-N1-H7

BLASTX Method g229708 NCBI GI BLAST score 221 2.0e-18 E value 81 Match length 53 % identity

NCBI Description Bean pod mottle virus

Seq. No. 40640

Seq. ID LIB3138-069-P1-N1-H8

BLASTX Method g4097880 NCBI GI BLAST score 230 E value 5.0e-19 Match length 79 % identity 65

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No.

40641

Seq. ID LIB3138-070-P1-N1-A3

Method BLASTX NCBI GI g138364 BLAST score 188 1.0e-14 E value Match length 62 60 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

40642 Seq. No.

Seq. ID LIB3138-070-P1-N1-A6

Method BLASTN NCBI GI q210811 BLAST score 118 E value 1.0e-59 Match length 290 % identity 86



NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.

40643

Seq. ID

LIB3138-070-P1-N1-B3

Method NCBI GI BLASTX

NCBI GI BLAST score g138364 576

E value Match length

1.0e-59 128

% identity

85

NCBI Description

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No.

40644

Seq. ID

LIB3138-070-P1-N1-B8

Method NCBI GI BLAST score BLASTN g210811 108

E value Match length

9.0e-54 312

84

% identity NCBI Description

Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

40645

Seq. ID

LIB3138-070-P1-N1-C1

Method BLASTX
NCBI GI g2828147
BLAST score 232
E value 1.0e-19
Match length 72

Match length % identity

NCBI Description (AF042384) BC-2 protein [Homo sapiens]

Seq. No.

40646

62

Seq. ID

LIB3138-070-P1-N1-C10

Method BLASTX
NCBI GI g1352009
BLAST score 213
E value 1.0e-17
Match length 54
% identity 78

NCBI Description

ATP SYNTHASE A CHAIN (PROTEIN 6) >gi_67916_pir__PWKQ6 H+-transporting ATP synthase (EC 3.6.1.34) protein 6 - fungus (Cochliobolus heterostrophus) mitochondrion (SGC3) >qi 12870 emb CAA31791 (X13439) ATPase subunit 6 (AA

1-257) [Cochliobolus heterostrophus]

Seq. No.

40647

Seq. ID

LIB3138-070-P1-N1-C5

Method BLASTN
NCBI GI g210811
BLAST score 142
E value 4.0e-74



Match length % identity 89

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

40648

Seq. ID

LIB3138-070-P1-N1-D8

Method NCBI GI BLASTX

BLAST score

g3915601 266

E value

2.0e-23

Match length

111

% identity

50

NCBI Description

ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD

SUBUNIT) (A1 38 KD SUBUNIT) (RF-C 38 KD SUBUNIT) (RFC38) >gi_1498259 (L07541) replication factor C, 38-kDa subunit

[Homo sapiens] >gi_4506489_ref_NP_002906.1_pRFC3

replication factor C (activator 1) 3 (38kD)

Seq. No.

40649

Seq. ID

LIB3138-070-P1-N1-D9

Method BLASTN NCBI GI g210811 BLAST score 179 E value

4.0e-96 355

Match length % identity

88

NCBI Description

Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. Seq. ID

40650

LIB3138-070-P1-N1-E1

Method BLASTX NCBI GI q4097880 BLAST score 186 E value 5.0e-14 Match length 96

% identity 44

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40651

Seq. ID

LIB3138-070-P1-N1-G3

Method BLASTN NCBI GI q210811 BLAST score 134 E value 3.0e-69 Match length 330 % identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

40652

Seq. ID

LIB3138-070-P1-N1-H2

Method BLASTN NCBI GI g210811 BLAST score 34 E value 1.0e-09



Match length 70 % identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40653

Seq. ID LIB3138-070-P1-N1-H8

Method BLASTX
NCBI GI g4097880
BLAST score 357
E value 3.0e-34
Match length 98
% identity 74

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 40654

Seq. ID LIB3138-071-P1-N1-B1

Method BLASTN
NCBI GI g210811
BLAST score 114
E value 3.0e-57
Match length 317
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40655

Seq. ID LIB3138-071-P1-N1-B11

Method BLASTN
NCBI GI g4406529
BLAST score 111
E value 2.0e-55
Match length 332
% identity 84

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40656

Seq. ID LIB3138-071-P1-N1-C11

Method BLASTN
NCBI GI g210811
BLAST score 135
E value 7.0e-70
Match length 363
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40657

Seq. ID LIB3138-071-P1-N1-D11

Method BLASTX
NCBI GI g138364
BLAST score 416
E value 7.0e-41
Match length 96
% identity 78

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

50



PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 40658 Seq. ID LIB3138-071-P1-N1-F2

Method BLASTN
NCBI GI g18551
BLAST score 88
E value 4.0e-42
Match length 126

% identity 98
NCBI Description Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding

protein

Seq. No. 40659

Seq. ID LIB3138-071-P1-N1-F6

Method BLASTN
NCBI GI g170087
BLAST score 254
E value 1.0e-141
Match length 309
% identity 96

NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)

Seq. No. 40660

Seq. ID LIB3138-071-P1-N1-F8

Method BLASTX
NCBI GI g138364
BLAST score 369
E value 2.0e-35
Match length 114
% identity 71

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40661

Seq. ID LIB3138-072-P1-N1-A11

Method BLASTX
NCBI GI g138364
BLAST score 155
E value 3.0e-13
Match length 73
% identity 63

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40662

Seq. ID LIB3138-072-P1-N1-A3

Method BLASTN
NCBI GI g609224
BLAST score 120
E value 7.0e-61



Match length 259 % identity 87

NCBI Description P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB

Pisum sativum S-adenosylmethionine synthase mRNA, complete

cds

Seq. No. 40663

Seq. ID LIB3138-072-P1-N1-A5

Method BLASTN
NCBI GI g210811
BLAST score 65
E value 2.0e-28

E value 2.0e-2 Match length 145 % identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40664

Seq. ID LIB3138-072-P1-N1-D7

Method BLASTX
NCBI GI g1527217
BLAST score 146
E value 2.0e-12
Match length 78
% identity 44

NCBI Description (U68217) ferritin [Brassica napus]

Seq. No. 40665

Seq. ID LIB3138-072-P1-N1-D8

Method BLASTN
NCBI GI 94097879
BLAST score 47
E value 2.0e-17
Match length 83

% identity 89

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40666

Seq. ID LIB3138-072-P1-N1-E4

Method BLASTN
NCBI GI g170087
BLAST score 208
E value 1.0e-113
Match length 273
% identity 93

NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)

Seq. No. 40667

Seq. ID LIB3138-072-P1-N1-E9

Method BLASTN
NCBI GI 94406529
BLAST score 89
E value 2.0e-42
Match length 237
% identity 85

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

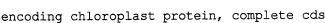
E value

Match length % identity

60

62 NCBI Description Bean pod mottle virus





```
40668
Seq. No.
Seq. ID
                  LIB3138-072-P1-N1-F1
                  BLASTN
Method
                  g210811
NCBI GI
BLAST score
                  212
                  1.0e-116
E value
                  403
Match length
                  88
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  40669
Seq. No.
Seq. ID
                  LIB3138-072-P1-N1-F11
                  {\tt BLASTX}
Method
                  g138364
NCBI GI
                  179
BLAST score
                  2.0e-13
E value
Match length
                  41
% identity
                  88
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
                  40670
Seq. No.
                  LIB3138-072-P1-N1-F3
Seq. ID
                  BLASTX
Method
                  g2262105
NCBI GI
BLAST score
                  261
                  1.0e-22
E value
                  100
Match length
                  52
% identity
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                  40671
Seq. No.
Seq. ID
                  LIB3138-072-P1-N1-F8
                  BLASTX
Method
NCBI GI
                  g2655169
BLAST score
                  221
E value
                  5.0e-18
                  65
Match length
                   65
% identity
                  (AF025809) glyceraldehyde-3-phosphate dehydrogenase-2
NCBI Description
                   [Drosophila pseudoobscura]
                   40672
Seq. No.
Seq. ID
                  LIB3138-072-P1-N1-G7
Method
                  BLASTX
                  q229707
NCBI GI
BLAST score
                   201
                   3.0e-16
```



```
Seq. No.
                  LIB3138-073-P1-N1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1502421
BLAST score
                  172
                  3.0e-12
E value
                  72
Match length
% identity
                  49
                   (U59433) 3-ketoacyl-acyl carrier protein reductase
NCBI Description
                   [Bacillus subtilis]
Seq. No.
                   40674
                  LIB3138-073-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3600059
BLAST score
                  150
E value
                   4.0e-10
Match length
                  50
% identity
                   60
                   (AF080120) contains similarity to WB domains, G-beta
NCBI Description
                  repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
                 [Arabidopsis thaliana]
                   40675
Seq. No.
                  LIB3138-073-P1-N1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706130
BLAST score
                  293
                   1.0e-26
E value
                   74
Match length
% identity
                   76
                  CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052
NCBI Description
                   calcium-dependent protein kinase homolog - carrot
                   >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein
                   kinase [Daucus carota]
                   40676
Seq. No.
Seq. ID
                   LIB3138-073-P1-N1-D6
Method
                  BLASTN
                   g210811
NCBI GI
BLAST score
                   38
                   4.0e-12
E value
Match length
                   78
                   88
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   40677
Seq. No.
                   LIB3138-073-P1-N1-E4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4097879
BLAST score
                   52
                   3.0e-20
E value
Match length
                   136
```

Bean pod mottle virus complete segment RNA1 polyprotein

93

gene, complete cds

% identity

NCBI Description



```
40678
Seq. No.
Seq. ID
                   LIB3138-073-P1-N1-E8
Method
                   BLASTX
NCBI GI
                   g4097880
BLAST score
                   142
E value
                   4.0e-09
                   66
Match length
                   45
% identity
NCBI Description
                   (U70866) polyprotein [Bean pod mottle virus]
                   40679
Seq. No.
Seq. ID
                   LIB3138-073-P1-N1-F4
                   BLASTN
Method
NCBI GI
                   g4097879
BLAST score
                   129
                   2.0e-66
E value
                   229
Match length
                   89
% identity
                   Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   40680
Seq. No.
Seq. ID
                   LIB3138-073-P1-N1-G3
                   BLASTN
Method
                   g210811
NCBI GI
                   40
BLAST score
                   2.0e-13
E value
Match length
                   115
                   84
% identity
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
                   40681
Seq. No.
                   LIB3138-073-P1-N1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g138364
                   347
BLAST score
                   3.0e-33
E value
Match length
                   82
 % identity
                   78
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                   40682
Seq. ID
                   LIB3138-073-P1-N1-H12
                   BLASTX
Method
```

Method BLASTX
NCBI GI g1353352
BLAST score 198
E value 2.0e-15
Match length 48
% identity 79

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

reinhardtii]

Method

NCBI GI

BLASTN

g210811



```
Seq. No.
                   40683
                   LIB3138-073-P1-N1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4097880
BLAST score
                   216
E value
                   9.0e-18
Match length
                   77
% identity
                   61
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   40684
Seq. ID
                   LIB3138-073-P1-N1-H3
Method
                   BLASTN
NCBI GI
                   q210811
BLAST score
                   123
                   9.0e-63
E value
Match length
                   271
% identity
                   86
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
Seq. No.
                   40685
Seq. ID
                   LIB3138-074-P1-N1-A5
Method
                   BLASTX
NCBI GI
                   g229708
BLAST score
                   176
                   8.0e-13
E value
Match length
                   75
% identity
                   51
NCBI Description Bean pod mottle virus
Seq. No.
                   40686
                   LIB3138-074-P1-N1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   134
E value
                   4.0e-69
Match length
                   327
                   87
% identity
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
                   40687
Seq. No.
Seq. ID
                  LIB3138-074-P1-N1-C11
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   216
E value
                   1.0e-118
Match length
                   400
% identity
                   89
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
Seq. No.
                   40688
Seq. ID
                   LIB3138-074-P1-N1-F7
```

6380



BLAST score 121 E value 1.0e-61 Match length 269 % identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40689

Seq. ID LIB3138-074-P1-N1-G5

Method BLASTN
NCBI GI g4097879
BLAST score 60
E value 4.0e-25

E value 4.0e-25 Match length 156 % identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40690

Seq. ID LIB3138-075-P1-N1-B10

Method BLASTX
NCBI GI g2462760
BLAST score 157
E value 1.0e-10
Match length 56
% identity 48

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 40691

Seq. ID LIB3138-075-P1-N1-B5

Method BLASTX
NCBI GI g138364
BLAST score 200
E value 4.0e-16
Match length 58
% identity 71

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40692

Seq. ID LIB3138-075-P1-N1-F1

Method BLASTN
NCBI GI g210811
BLAST score 63
E value 6.0e-27
Match length 231
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40693

Seq. ID LIB3138-075-P1-N1-H11

Method BLASTN NCBI GI g4097879

BLAST score 67



```
2.0e-29
E value
                  139
Match length
                  87
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  40694
Seq. No.
                  LIB3138-075-P1-N1-H12
Seq. ID
                  BLASTX
Method
                  g3121844
NCBI GI
                  193
BLAST score
                  7.0e-15
E value
                  102
Match length
                   41
% identity
                  PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE
NCBI Description
                   SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE)
                   (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE
                   CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)
                   >gi 1652668 dbj BAA17588_ (D90907) phosphatidate
                   cytidylyltransferase [Synechocystis sp.]
Seq. No.
                   40695
                   LIB3138-079-P1-N1-A1
Seq. ID
                   BLASTX
Method
                   g3298443
NCBI GI
                   204
BLAST score
                   1.0e-16
E value
Match length
                   51
                   78
% identity
                   (AB010880) chloroplast ribosomal protein L17 [Nicotiana
NCBI Description
                   tabacum]
                   40696
Seq. No.
                   LIB3138-079-P1-N1-B7
Seq. ID
                   BLASTX
Method
                   g2208899
NCBI GI
BLAST score
                   163
                   2.0e-11
E value
                   103
Match length
                   33
% identity
                  (AB004795) dipeptidyl aminopeptidase [Pseudomonas sp.]
NCBI Description
                   40697
Seq. No.
Seq. ID
                   LIB3138-079-P1-N1-B8
                   BLASTN
Method
```

NCBI GI g4325340
BLAST score 99
E value 2.0e-48
Match length 242
% identity 87

NCBI Description Arabidopsis thaliana BAC T1J1

Seq. No. 40698

Seq. ID LIB3138-079-P1-N1-C4

Method BLASTN
NCBI GI g4097879
BLAST score 145



E value 8.0e-76 Match length 273 % identity 88

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40699

Seq. ID LIB3138-079-P1-N1-D1

Method BLASTN
NCBI GI g1022364
BLAST score 209
E value 1.0e-114
Match length 328
% identity 92

NCBI Description V.faba mRNA for sucrose phosphate synthase

Seq. No. 40700

Seq. ID LIB3138-079-P1-N1-D2

Method BLASTX
NCBI GI g4105798
BLAST score 196
E value 4.0e-15
Match length 54
% identity 59

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 40701

Seq. ID LIB3138-079-P1-N1-E10

Method BLASTX
NCBI GI g2956770
BLAST score 203
E value 5.0e-16
Match length 94
% identity 48

NCBI Description (AL022103) putative protein transport protein

[Schizosaccharomyces pombe]

Seq. No. 40702

Seq. ID LIB3138-079-P1-N1-G12

Method BLASTN
NCBI GI g210811
BLAST score 119
E value 2.0e-60
Match length 279
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40703

Seq. ID LIB3138-079-P1-N1-G7

Method BLASTX
NCBI GI g138364
BLAST score 435
E value 3.0e-43
Match length 115
% identity 72

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT



PROTEIN VP23) >qi 75639 pir GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

40704 Seq. No. Seq. ID LIB3138-079-P1-N1-H2 Method BLASTN g210811 NCBI GI BLAST score 95

E value 6.0e-46 344 Match length 86 % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

40705 Seq. No.

Seq. ID LIB3138-080-P1-N1-A6

BLASTX Method NCBI GI g4097880 BLAST score 347 E value 5.0e-33 96 Match length

72 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

40706 Seq. No.

LIB3138-080-P1-N1-C9 Seq. ID

Method BLASTX g3152584 NCBI GI BLAST score 153 4.0e-10 E value Match length 44

70 % identity

(AC002986) YUP8H12R.31 [Arabidopsis thaliana] NCBI Description

40707 Seq. No.

LIB3138-080-P1-N1-E8 Seq. ID

BLASTN Method g862479 NCBI GI 36 BLAST score E value 6.0e-11 60 Match length % identity 90

Glycine max valosin-containing protein mRNA, complete cds NCBI Description

40708 Seq. No.

Seq. ID LIB3138-080-P1-N1-G3

BLASTX Method NCBI GI q4097880 BLAST score 170 1.0e-17 E value Match length 98 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No. 40709

Seq. ID LIB3138-081-P1-N1-A3

6384



```
BLASTN
Method
                  g4097879
NCBI GI
                  153
BLAST score
                  1.0e-80
E value
Match length
                  364
                  85
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  40710
Seq. No.
Seq. ID
                  LIB3138-081-P1-N1-A7
Method
                  BLASTN
NCBI GI
                  g2894303
                  83
BLAST score
                  6.0e-39
E value
                  193
Match length
% identity
                  25
NCBI Description Nicotiana tabacum TUQG2 gene, complete CDS
                  40711
Seq. No.
Seq. ID
                  LIB3138-081-P1-N1-B7
Method
                  BLASTN
                  g296336
NCBI GI
                  118
BLAST score
                  1.0e-59
E value
                  295
Match length
% identity
                  89
NCBI Description A.nidulans gene for core histone for H3
                  40712
Seq. No.
                  LIB3138-081-P1-N1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g138364
                  255
BLAST score
                  2.0e-22
E value
Match length
                  81
                  64
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle vīrus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                  40713
Seq. No.
                  LIB3138-081-P1-N1-E2
```

Seq. ID Method BLASTX

NCBI GI g113603 BLAST score 320 1.0e-29 E value 70 Match length 81 % identity

THIOL PROTEASE ALEURAIN PRECURSOR >gi 19021 emb CAA28804 NCBI Description

(X05167) aleurain [Hordeum vulgare]

40714 Seq. No.

Seq. ID LIB3138-081-P1-N1-H2

Method BLASTN NCBI GI g12139



BLAST score E value 1.0e-109 Match length 313 % identity 91

NCBI Description Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three

CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No. 40715

Seq. ID LIB3138-082-P1-N1-B11

Method BLASTX NCBI GI g3123310 BLAST score 225 E value 1.0e-18 Match length 116 % identity 40

NCBI Description PUTATIVE FLAVOPROTEIN C26F1.14C

40716 Seq. No.

Seq. ID LIB3138-082-P1-N1-C12

Method BLASTX NCBI GI q134822 BLAST score 390 E value 6.0e-38 Match length 85 % identity 86

NCBI Description GTP-BINDING NUCLEAR PROTEIN SPI1 >gi 101078 pir A40039

spil hypothetical protein - fission yeast

(Schizosaccharomyces pombe) >gi_299321_bbs_128166 GTPase=spil gene product [Schizosaccharomyces pombe, Peptide, 216 aa] >gi 4490658 emb CAB38683.1 (AL035675) gtp-binding nuclear protein spil. [Schizosaccharomyces

pombe]

Seq. No. 40717

Seq. ID LIB3138-082-P1-N1-C7

Method BLASTN NCBI GI g4097879 BLAST score 46 E value 8.0e-17

Match length 110 % identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

40718

Seq. No. Seq. ID LIB3138-082-P1-N1-F6

Method BLASTN NCBI GI g170083 BLAST score 297 E value 1.0e-166 Match length: 373 % identity 97

Soybean (clone E15) urease (ure) gene, exons 2,3 and 4 and NCBI Description

partial cds

Seq. No. 40719



```
LIB3138-082-P1-N1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3434975
                  250
BLAST score
                  2.0e-21
E value
                  67
Match length
                  66
% identity
                   (AB008107) ethylene responsive element binding factor 5
NCBI Description
                   [Arabidopsis thaliana]
                  40720
Seq. No.
                  LIB3138-082-P1-N1-G2
Seq. ID
                  BLASTN
Method
                  g4406529
NCBI GI
BLAST score
                  120
                  7.0e-61
E value
                  299
Match length
                  85
% identity
                  Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
NCBI Description
                  encoding chloroplast protein, complete cds
                   40721
Seq. No.
                  LIB3138-082-P1-N1-H11
Seq. ID
                  BLASTN
Method
                   g3128141
NCBI GI
BLAST score
                   38
                   5.0e-12
E value
                   106
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQD22, complete sequence [Arabidopsis thaliana]
                   40722
Seq. No.
Seq. ID
                  LIB3138-082-P1-N1-H4
                   BLASTX
Method
NCBI GI
                   q138364
                   350
BLAST score
                   2.0e-33
E value
                   95
Match length
                   74
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi 75639_pir GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                   40723
Seq. No.
Seq. ID
                   LIB3138-083-P1-N1-B12
                   BLASTX
Method
                   g229707
NCBI GI
BLAST score
                   464
                   1.0e-46
E value
Match length
                   107
```

79 % identity

NCBI Description Bean pod mottle virus

40724 Seq. No.

Seq. ID LIB3138-083-P1-N1-B8



```
BLASTX
Method
                  g1706110
NCBI GI
                  467
BLAST score
                  5.0e-47
E value
                  100
Match length
                  87
% identity
                  NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR
NCBI Description
                  (CTPT) >gi 1143713 (U13632) non-green plastid
                  phosphate/triose-phosphate translocator precursor [Brassica
                  oleracea]
                  40725
Seq. No.
                  LIB3138-083-P1-N1-D1
Seq. ID
                  BLASTN
Method
                  g3510343
NCBI GI
                  53
BLAST score
E value
                  6.0e-21
Match length
                  117
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  40726
Seq. ID
                  LIB3138-083-P1-N1-E3
                  BLASTN
Method
                  g1732468
NCBI GI
                   73
BLAST score
                  8.0e-33
E value
                  251
Match length
                  89
% identity
NCBI Description Soybean mRNA for Mg chelatase subunit (46 kD), complete cds
                   40727
Seq. No.
Seq. ID
                  LIB3138-083-P1-N1-G3
                  BLASTX
Method
                   g4097880
NCBI GI
BLAST score
                   252
                   3.0e-22
E value
                   73
Match length
                   68
% identity
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   40728
Seq. No.
Seq. ID
                  LIB3138-083-P1-N1-H4
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   62
E value
                   3.0e-26
Match length
                   110
                   89
% identity
NCBI Description Tobacco chloroplast genome DNA
```

Seq. No.

40729

Seq. ID LIB3138-084-P1-N1-A10

Method BLASTX NCBI GI g3294467 BLAST score 249



E value 1.0e-27
Match length 84
% identity 80

NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]

Seq. No. 40730

Seq. ID LIB3138-084-P1-N1-A6

Method BLASTN
NCBI GI g210811
BLAST score 159
E value 4.0e-84
Match length 335
% identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40731

Seq. ID LIB3138-084-P1-N1-B3

Method BLASTN
NCBI GI g210811
BLAST score 133
E value 1.0e-68
Match length 305
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40732

Seq. ID LIB3138-084-P1-N1-B6

Method BLASTN
NCBI GI g210811
BLAST score 117
E value 5.0e-59
Match length 329
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40733

Seq. ID LIB3138-084-P1-N1-C10

Method BLASTX
NCBI GI g3006191
BLAST score 473
E value 1.0e-47
Match length 111
% identity 81

NCBI Description (AL022304) 40s ribosomal protein s16. [Schizosaccharomyces

pombe]

Seq. No. 40734

Seq. ID LIB3138-084-P1-N1-D1

Method BLASTX
NCBI GI g138364
BLAST score 331
E value 4.0e-52
Match length 138
% identity 78

6389



NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

3

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40735

Seq. ID LIB3138-084-P1-N1-D3

Method BLASTN
NCBI GI g210811
BLAST score 140
E value 8.0e-73
Match length 260
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40736

Seq. ID LIB3138-084-P1-N1-D5

Method BLASTN
NCBI GI g4097879
BLAST score 92
E value 3.0e-44
Match length 299

% identity 84
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40737

Seq. ID LIB3138-084-P1-N1-D7

Method BLASTN
NCBI GI g210811
BLAST score 124
E value 3.0e-63
Match length 364
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40738

Seq. ID LIB3138-084-P1-N1-D8

Method BLASTX
NCBI GI g4097880
BLAST score 227
E value 6.0e-19
Match length 103
% identity 51

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

40739

Seq. ID LIB3138-084-P1-N1-E10

Method BLASTX
NCBI GI g3818624
BLAST score 389
E value 7.0e-38
Match length 101
% identity 72

NCBI Description (AF095912) actin related protein 2; ARP2 [Arabidopsis



thaliana]

```
40740
Seq. No.
Seq. ID
                  LIB3138-084-P1-N1-E12
                  BLASTN
Method
                  g402752
NCBI GI
                  246
BLAST score
                  1.0e-136
E value
                   336
Match length
                   96
% identity
NCBI Description
                  G.max gene fusA
                   40741
Seq. No.
                   LIB3138-084-P1-N1-E2
Seq. ID
                   BLASTX
Method
                   g3776557
NCBI GI
BLAST score
                   305
                   5.0e-28
E value
                   100
Match length
                   54
% identity
                   (AC005388) Contains similarity to gi 2924495 hypothetical
NCBI Description
                   protein Rv1920 from Mycobacterium tuberculosis genome
                   gb AL022020. [Arabidopsis thaliana]
                   40742
Seq. No.
                   LIB3138-084-P1-N1-E6
Seq. ID
                   BLASTX
Method
                   g3582335
NCBI GI
                   182
BLAST score
                   2.0e-13
E value
                   33
Match length
                   91
% identity
                   (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
                   40743
Seq. No.
Seq. ID
                   LIB3138-084-P1-N1-E9
                   BLASTN
Method
                   g4097879
NCBI GI
BLAST score
                   36
                   9.0e-11
E value
Match length
                   48
                   94
% identity
                   Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   40744
Seq. No.
Seq. ID
                   LIB3138-084-P1-N1-F12
                   BLASTN
Method
                   g984307
NCBI GI
BLAST score
                   164
                   3.0e-87
E value
Match length
                   221
                   93
% identity
                   Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                   cds, beta-carboxyltransferase (accD), photosystem I
```

component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

NCBI Description



precurso

40745 Seq. No. Seq. ID LIB3138-084-P1-N1-F8 BLASTX Method g138364 NCBI GI 551 BLAST score 8.0e-57 E value 121 Match length 87 % identity GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi 75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus] 40746 Seq. No. Seq. ID LIB3138-084-P1-N1-G1 Method BLASTX g2443753 NCBI GI 226 BLAST score 1.0e-18 E value Match length 74 % identity (AF020346) pyridoxal kinase [Rattus norvegicus] NCBI Description 40747 Seq. No. LIB3138-084-P1-N1-G12 Seq. ID Method BLASTX g2760330 NCBI GI 390 BLAST score 8.0e-38 E value 101 Match length % identity 69 (AC002130) F1N21.15 [Arabidopsis thaliana] NCBI Description 40748 Seq. No. LIB3138-085-P1-N1-D11 Seq. ID BLASTN Method g408793 NCBI GI 90 BLAST score 3.0e-43E value 186 Match length % identity 86 Glycine soja chloroplast 3-omega faty acid desaturase NCBI Description (Fad3) mRNA, complete cds 40749 Seq. No. LIB3138-085-P1-N1-F6 Seq. ID BLASTN Method NCBI GI g4240030 BLAST score 44 1.0e-15 E value Match length 168 82 % identity

(Pspzf), partial cds

Pisum sativum mRNA for DNA binding zinc finger protein



```
Seq. No.
Seq. ID
                  LIB3138-085-P1-N1-H12
                  BLASTN
Method
NCBI GI
                  g210811
                  49
BLAST score
                  6.0e-19
E value
                  100
Match length
                  89
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  40751
Seq. No.
                  LIB3138-085-P1-N1-H4
Seq. ID
                  BLASTN
Method
                  g4097879
NCBI GI
                  58
BLAST score
                  4.0e-24
E value
                  90
Match length
                  91
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  40752
                  LIB3138-086-P1-N1-A11
Seq. ID
                  BLASTX
Method
                  q2462832
NCBI GI
                  205
BLAST score
                  3.0e-16
E value
                  57
Match length
                  65
% identity
                  (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  40753
                  LIB3138-087-P1-N1-A1
Seq. ID
                  BLASTX
Method
                  q138364
NCBI GI
BLAST score
                  201
                  3.0e-16
E value
                  52
Match length
                  79
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   40754
Seq. No.
Seq. ID
                  LIB3138-087-P1-N1-B6
Method
                   BLASTN
NCBI GI
                   q210811
BLAST score
                   90
```

4.0e-43 E value 246 Match length 84 % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

40755 Seq. No.



```
LIB3138-087-P1-N1-D1
Seq. ID
                  BLASTN
Method
                  g467614
NCBI GI
                  368
BLAST score
                  0.0e + 00
E value
                  415
Match length
% identity
                  97
NCBI Description A.alternata AltA2 mRNA for aldehyde dehydrogenase
                  40756
Seq. No.
                  LIB3138-087-P1-N1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g138364
                  336
BLAST score
                  8.0e-32
E value
                  91
Match length
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle vīrus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                   40757
                  LIB3138-087-P1-N1-D8
Seq. ID
                  BLASTN
Method
                   q4097879
NCBI GI
                   96
BLAST score
                   1.0e-46
E value
Match length
                   240
                   85
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                   gene, complete cds
                   40758
Seq. No.
Seq. ID
                   LIB3138-087-P1-N1-E1
Method
                   BLASTN
                   q210811
NCBI GI
BLAST score
                   118
E value
                   1.0e-59
                   270
Match length
% identity
                   86
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   40759
Seq. No.
Seq. ID
                   LIB3138-087-P1-N1-E9
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   104
                   2.0e-51
E value
                   184
Match length
                   89
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
```

Seq. No. 40760

Seq. ID LIB3138-088-P1-N1-B10



```
Method
                  BLASTX
NCBI GI
                  g1708462
BLAST score
                  212
E value
                   4.0e-17
Match length
                   65
                  62
% identity
NCBI Description
                  IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi 902791
                   (U23796) ILL2 [Arabidopsis thaliana]
Seq. No.
                  40761
Seq. ID
                  LIB3138-088-P1-N1-C3
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  133
E value
                  1.0e-68
Match length
                  305
% identity
                  86
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40762
Seq. ID
                  LIB3138-088-P1-N1-C6
Method
                  BLASTX
NCBI GI
                  g2979559
BLAST score
                  232
E value
                  7.0e-20
                  59
Match length
                  78
% identity
NCBI Description
                  (AC003680) putative DNA binding protein [Arabidopsis
                  thaliana]
                  40763
Seq. No.
                  LIB3138-088-P1-N1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g309673
BLAST score
                  144
E value
                  5.0e-10
Match length
                  62
% identity
                  68
NCBI Description
                  (L19651) light harvesting protein [Pisum sativum]
Seq. No.
                  40764
Seq. ID
                  LIB3138~088-P1-N1-D5
Method
                  BLASTN
                  g210811
NCBI GI
BLAST score
                  49
E value
                  1.0e-18
Match length
                  124
                  86
% identity
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40765
```

Seq. ID LIB3138-088-P1-N1-E11

Method BLASTN NCBI GI g210811 BLAST score 202



E value 1.0e-110
Match length 362
% identity 89

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40766

Seq. ID LIB3138-088-P1-N1-E12

Method BLASTX
NCBI GI g138364
BLAST score 250
E value 8.0e-26
Match length 106
% identity 66

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40767

Seq. ID LIB3138-088-P1-N1-E2

Method BLASTN
NCBI GI g210811
BLAST score 107
E value 3.0e-53
Match length 231
% identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40768

Seq. ID LIB3138-088-P1-N1-E6

Method BLASTN
NCBI GI g210811
BLAST score 156
E value 2.0e-82
Match length 300
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40769

Seq. ID LIB3138-088-P1-N1-F10

Method BLASTN
NCBI GI g4406529
BLAST score 66
E value 8.0e-29
Match length 182
% identity 85

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40770

Seq. ID LIB3138-088-P1-N1-F3

Method BLASTX NCBI GI g4097880 BLAST score 158

E value

Match length

% identity

8.0e-67

351

84



```
E value
                   2.0e-12
Match length
                   63
% identity
                   57
NCBI Description
                   (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                   40771
                   LIB3138-088-P1-N1-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4406529
BLAST score
                   69
                   2.0e-30
E value
Match length
                   173
% identity
                   88
NCBI Description
                   Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
                   encoding chloroplast protein, complete cds
Seq. No.
                   40772
Seq. ID
                   LIB3138-088-P1-N1-G12
Method
                   BLASTN
NCBI GI
                   g4538949
BLAST score
                   54
E value
                   5.0e-22
Match length
                   82
% identity
                   91
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24
                   (ESSA project)
Seq. No.
                   40773
Seq. ID
                   LIB3138-088-P1-N1-G3
Method
                   BLASTN
NCBI GI
                   g3900935
BLAST score
                   53
E value
                   5.0e-21
Match length
                   93
% identity
                   89
                   Cicer arietinum mRNA for glucan endo-beta-1,3-glucosidase,
NCBI Description
                   acidic isoform
Seq. No.
                   40774
Seq. ID
                   LIB3138-088-P1-N1-H2
Method
                   BLASTN
NCBI GI
                   g4097879
BLAST score
                   41
E value
                   8.0e-14
Match length
                   93
% identity
                   86
NCBI Description
                  Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
Seq. No.
                   40775
Seq. ID
                  LIB3138-090-P1-N1-A11
Method
                  BLASTN
NCBI GI
                  g4406529
BLAST score
                  130
```





Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene NCBI Description encoding chloroplast protein, complete cds

Seq. No. 40776

Seq. ID LIB3138-090-P1-N1-A4

Method BLASTN NCBI GI g169127 BLAST score 57 E value 2.0e-23 232 Match length % identity 82

NCBI Description Pisum sativum (clone pCLp) nuclear encoded precursor to

chloroplast protein mRNA, complete cds

Seq. No. 40777

Seq. ID LIB3138-090-P1-N1-D3

Method BLASTN NCBI GI q4097879 BLAST score 80 E value 5.0e-37 Match length 196

% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40778

Seq. ID LIB3138-090-P1-N1-D4

Method BLASTX NCBI GI q138364 BLAST score 351 E value 3.0e-33 Match length 121 % identity 60

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40779

Seq. ID LIB3138-090-P1-N1-E1

Method BLASTX NCBI GI q68200 BLAST score 238 E value 5.0e-20 Match length 80 % identity 65

fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description

chloroplast - spinach >gi 22633 emb CAA47293 (X66814)

fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 40780

Seq. ID LIB3138-090-P1-N1-E10

Method BLASTX NCBI GI g1130682 BLAST score 305 E value 5.0e-28 Match length 107



```
% identity
NCBI Description
                  (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]
Seq. No.
                  40781
Seq. ID
                  LIB3138-090-P1-N1-F10
Method
                  BLASTN
                  q4406529
NCBI GI
BLAST score
                  70
E value
                  2.0e-31
                  118
Match length
```

% identity 90 NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene encoding chloroplast protein, complete cds

Seq. No. 40782 Seq. ID LIB3138-090-P1-N1-F12 Method BLASTX NCBI GI g138364 BLAST score 237 E value 2.0e-20 69 Match length

% identity 71 GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639 pir GNWXG7 genome polyprotein M -

bean pod mottle vīrus (straīn Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

40783 Seq. No.

Seq. ID LIB3138-090-P1-N1-F2

Method BLASTX NCBI GI q4097880 BLAST score 412 E value 1.0e-40 Match length 110 % identity

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 40784

Seq. ID LIB3138-090-P1-N1-F6

Method BLASTX NCBI GI g4559382 BLAST score 146 3.0e-09 E value Match length 47 % identity

NCBI Description (AC006526) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 40785

Seq. ID LIB3138-090-P1-N1-G12

Method BLASTN NCBI GI g4097879 BLAST score 163 E value 2.0e-86 Match length 403 % identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein



gene, complete cds

```
Seq. No.
                  40786
                  LIB3138-090-P1-N1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  91
E value
                  1.0e-43
                  259
Match length
% identity
                  84
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  40787
                  LIB3138-090-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115797
BLAST score
                  437
E value
                  3.0e-43
Match length
                  113
% identity
                  74
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
NCBI Description
                  (CAB-215) (LHCP) >gi_100026_pir__S16592 chlorophyll
                  a/b-binding protein - garden pea >gi 20658 emb_CAA40365
                  (X57082) chlorophyll a/b-binding protein [Pisum sativum]
                  40788
Seq. No.
Seq. ID
                  LIB3138-090-P1-N1-G8
                  BLASTN
Method
NCBI GI
                  q210811
BLAST score
                  207
                  1.0e-113
E value
                  403
Match length
                  88
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  40789
Seq. No.
                  LIB3138-090-P1-N1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097880
BLAST score
                  261
E value
                  9.0e-23
                  114
Match length
% identity
                  46
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  40790
Seq. No.
Seq. ID
                  LIB3138-090-P1-N1-H3
Method
                  BLASTN
NCBI GI
                  g2773269
BLAST score
                  70
                  4.0e-31
E value
Match length
                  134
% identity
                  89
                  Glycine max ferredoxin-dependent glutamate synthase (glu)
NCBI Description
```

mRNA, partial cds

Seq. No.

Seq. ID

40796

LIB3138-092-Q1-N1-A12

```
Seq. No.
                  40791
Seq. ID
                  LIB3138-091-Q1-N1-A7
Method
                  BLASTN
NCBI GI
                  g2687725
BLAST score
                  53
E value
                  6.0e-21
Match length
                  57
% identity
                  98
                  Glycine max mRNA for putative 2-hydroxydihydrodaidzein
NCBI Description
                  reductase
                  40792
Seq. No.
Seq. ID
                  LIB3138-091-Q1-N1-B12
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  111
E value
                  1.0e-55
                  349
Match length
% identity
                  83
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40793
Seq. ID
                  LIB3138-091-Q1-N1-G6
Method
                  BLASTX
                  g100196
NCBI GI
BLAST score
                  457
E value
                  1.0e-45
Match length
                  93
% identity
                  88
NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato
                  40794
Seq. No.
Seq. ID
                  LIB3138-091-Q1-N1-H11
Method
                  BLASTN
NCBI GI
                  q210811
BLAST score
                  155
E value
                  1.0e-81
Match length
                  361
% identity
                  86
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40795
Seq. ID
                  LIB3138-091-Q1-N1-H4
Method
                  BLASTN
NCBI GI
                  g1055367
BLAST score
                  364
E value
                  0.0e + 00
Match length
                  390
% identity
                  98
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
```

6401



Method BLASTX NCBI GI q2497199 BLAST score 214 3.0e-17 E value Match length 112 % identity 42

NCBI Description HYPOTHETICAL 50.5 KD PROTEIN IN RNA1-RNT1 INTERGENIC REGION >gi 1362402 pir S57605 probable membrane protein YMR238w -

yeast (Saccharomyces cerevisiae) >gi_887619_emb_CAA90209

(Z49939) unknown [Saccharomyces cerevisiae]

Seq. No.

40797

Seq. ID LIB3138-092-Q1-N1-B11

Method BLASTX NCBI GI q418149 BLAST score 208 E value 1.0e-16 Match length 121 % identity 43

NCBI Description PROBABLE UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE

(UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP)

>gi_320115_pir__S30007 probable UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - yeast (Saccharomyces cerevisiae) >gi_4794_emb_CAA49303_ (X69584) YKL248

[Saccharomyces cerevisiae] >gi 486040 emb CAA81872 (Z28035) ORF YKL035w [Saccharomyces cerevisiae] >gi_1585157_prf__2124302A UDP-glucose pyrophosphorylase

[Saccharomyces cerevisiae]

Seq. No. 40798

Seq. ID LIB3138-092-Q1-N1-B2

Method BLASTX NCBI GI q452683 BLAST score 351 E value 3.0e-33 Match length 128

% identity 55

NCBI Description (X77312) pyruvate decarboxylase [Saccharomyces cerevisiae]

Seq. No. 40799

Seq. ID LIB3138-092-Q1-N1-C2

Method BLASTX NCBI GI g115471 BLAST score 216 2.0e-17 E value Match length 99 % identity 52

NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE

DEHYDRATASE) >gi_100078 pir_ S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea >gi 20673 emb CAA36792 (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]

Seq. No. 40800

LIB3138-092-Q1-N1-C7 Seq. ID

Method BLASTX NCBI GI g2497175 BLAST score 255



E value 4.0e-22 Match length 72 % identity 61

NCBI Description HYPOTHETICAL 31.1 KD PROTEIN IN SIP18-SPT21 INTERGENIC

REGION >gi_1078525_pir__S55125 hypothetical protein YMR178w - yeast (Saccharomyces cerevisiae) >gi_854448_emb_CAA89911_

(Z49808) unknown [Saccharomyces cerevisiae]

Seq. No. 40801

Seq. ID LIB3138-092-Q1-N1-C8

Method BLASTX
NCBI GI g2388943
BLAST score 410
E value 3.0e-40
Match length 102

% identity 75

NCBI Description (Z98978) SPAC27E2.03c, putative gtp-binding protein,

len:392a a, similar eg. to YBR025C, YBN5 YEAST, P38219, hypothetica l 44.2 kd protein, (394aa), fasta scores, opt:1664, E():0, (63.7% identity in 391 aa overlap), also

sim

Seq. No. 40802

Seq. ID LIB3138-092-Q1-N1-E12

Method BLASTN
NCBI GI g3087
BLAST score 135
E value 7.0e-70
Match length 355
% identity 27

NCBI Description Neurospora crassa ubiquitin gene

Seq. No. 40803

Seq. ID LIB3138-092-Q1-N1-E5 Method BLASTN

Method BLASTN
NCBI GI g3687388
BLAST score 73
E value 7.0e-33
Match length 255
% identity 86

NCBI Description Lycopersicon esculentum mRNA for putative cullin protein

Seq. No.

40804

Seq. ID LIB3138-092-Q1-N1-H12

Method BLASTX
NCBI GI g117290
BLAST score 405
E value 1.0e-39
Match length 122
% identity 69

NCBI Description CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)

(P36) (E30) >gi_100071_pir__S23774 triose

phosphate/3-phosphoglycerate/phosphate translocator
precursor - garden pea >gi_20691_emb_CAA38451_ (X54639)

chloroplast import receptor p36 [Pisum sativum]

>gi_20853_emb_CAA48210_ (X68077) phosphate translocator
[Pisum sativum] >gi_228551_prf _1805409A phosphate



translocator [Pisum sativum] Seq. No. 40805 Seq. ID LIB3138-092-Q1-N1-H5 Method BLASTX NCBI GI q138364 BLAST score 371 E value 9.0e-36 Match length 110 % identity 71 NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus] Seq. No. 40806 LIB3138-093-Q1-N1-D10 Seq. ID Method BLASTX NCBI GI g3298542 BLAST score 320 E value 1.0e-29 Match length 129 % identity 45 NCBI Description (AC004681) putative cellulose synthase [Arabidopsis thaliana] Seq. No. 40807 Seq. ID LIB3138-093-Q1-N1-D3 Method BLASTX NCBI GI g2343157 BLAST score 174 E value 2.0e-12 Match length 122 % identity 36 NCBI Description (AF009746) peroxisomal membrane protein 69 [Homo sapiens] >gi 2706518 emb CAA74699 (Y14318) peroxisomal ABC-transporter [Homo sapiens] Seq. No. 40808 Seq. ID LIB3138-093-Q1-N1-E2 Method BLASTN NCBI GI g4097879 BLAST score 147 E value 5.0e-77 Match length 341 % identity 86 NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds Seq. No. 40809 LIB3138-093-Q1-N1-F3 Seq. ID Method

Method BLASTX
NCBI GI g4154817
BLAST score 477
E value 5.0e-48
Match length 126
% identity 67

% identity

NCBI Description

52





```
NCBI Description
                   (AE001466) putative [Helicobacter pylori J99]
Seq. No.
                   40810
Seq. ID
                   LIB3138-093-Q1-N1-F6
Method
                   BLASTX
NCBI GI
                   q1787692
BLAST score
                   163
E value
                   3.0e-11
Match length
                   83
% identity
                   47
NCBI Description
                  (AE000239) orf, hypothetical protein [Escherichia coli]
Seq. No.
                   40811
Seq. ID
                   LIB3138-093-Q1-N1-F9
Method
                   BLASTX
NCBI GI
                   g1703215
BLAST score
                   143
E value
                   5.0e-09
Match length
                   90
% identity
                   32
                  GENRAL ALPHA-GLUCOSIDE PERMEASE >gi_2119801_pir__S64624
NCBI Description
                   alpha-glucoside transport protein - yeast (Saccharomyces
                   cerevisiae) >gi 1323529 emb_CAA97322_ (Z73074) ORF YGR289c
                   [Saccharomyces cerevisiae]
Seq. No.
                   40812
Seq. ID
                  LIB3138-093-Q1-N1-G1
Method
                   BLASTN
NCBI GI
                  q4097879
BLAST score
                   64
E value
                   1.0e-27
Match length
                   186
% identity
                   85
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  40813
Seq. ID
                  LIB3138-093-Q1-N1-H10
Method
                  BLASTN
NCBI GI
                  g531832
BLAST score
                  51
E value
                  9.0e-20
Match length
                  191
% identity
                  82
NCBI Description
                  Cloning vector pSport2, complete sequence
Seq. No.
                  40814
Seq. ID
                  LIB3138-093-Q1-N1-H11
Method
                  BLASTX
NCBI GI
                  g3810866
BLAST score
                  357
E value
                  6.0e-34
Match length
                  123
```

6405

[Schizosaccharomyces pombe]

(AL032681) putative hydroxyacylglutathione hydrolase



```
Seq. No.
Seq. ID
                   LIB3138-093-Q1-N1-H6
Method
                   BLASTX
NCBI GI
                   g1161575
BLAST score
                   349
E value
                   4.0e-33
Match length
                   103
% identity
                   69
NCBI Description (X94947) homeobox [Lycopersicon esculentum]
Seq. No.
                   40816
Seq. ID
                  LIB3138-094-Q1-N1-B10
Method
                  BLASTN
NCBI GI
                   g210811
BLAST score
                   38
E value
                   3.0e-12
Match length
                  157
% identity
                  83
NCBI Description
                  Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  40817
Seq. ID
                  LIB3138-094-Q1-N1-B7
Method
                  BLASTX
NCBI GI
                  q4105782
BLAST score
                  175
                  1.0e-12
E value
Match length
                  50
% identity
                  76
NCBI Description
                  (AF049922) PGP169-12 [Petunia x hybrida]
Seq. No.
                  40818
                  LIB3138-094-Q1-N1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q138364
BLAST score
                  351
E value
                  2.0e-33
Match length
                  115
% identity
                  67
NCBI Description
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle vīrus (straīn Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  40819
Seq. ID
                  LIB3138-094-Q1-N1-C8
Method
                  BLASTN
                  g210811
```

NCBI GI BLAST score 133 E value 1.0e-68 Match length 337 % identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40820

Seq. ID LIB3138-094-Q1-N1-D10



Method BLASTX
NCBI GI g3047123
BLAST score 518
E value 7.0e-53
Match length 132
% identity 68

NCBI Description (AF058919) similar to the family of glycosyl hydrolases

[Arabidopsis thaliana]

Seq. No. 40821

Seq. ID LIB3138-094-Q1-N1-D7

Method BLASTX
NCBI GI g3688173
BLAST score 430
E value 1.0e-42
Match length 122
% identity 61

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 40822

Seq. ID LIB3138-094-Q1-N1-E10

Method BLASTX
NCBI GI g3123217
BLAST score 595
E value 7.0e-62
Match length 132
% identity 77

NCBI Description GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)

>gi_2388925_emb CAB11660 (Z98977) glutamine synthetase

[Schizosaccharomyces pombe]

Seq. No. 40823

Seq. ID LIB3138-094-Q1-N1-F7

Method BLASTX
NCBI GI g138364
BLAST score 255
E value 9.0e-23
Match length 115
% identity 56

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40824

Seq. ID LIB3138-094-Q1-N1-F9

Method BLASTN
NCBI GI g4097879
BLAST score 131
E value 2.0e-67
Match length 243
% identity 89

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40825

Seq. ID LIB3138-095-Q1-N1-A5



Method BLASTX
NCBI GI g1657617
BLAST score 206
E value 7.0e-17
Match length 60
% identity 76

NCBI Description (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236)

putative nuclear DNA-binding protein G2p [Arabidopsis

thaliana]

Seq. No. 40826

Seq. ID LIB3138-095-Q1-N1-B5

Method BLASTN
NCBI GI g1079735
BLAST score 110
E value 7.0e-55
Match length 320
% identity 91

NCBI Description Glycine soja ribulose 1,5-bisphosphate carboxylase small

subunit precursor (rbcS) gene, nuclear gene encoding

chloroplast protein, complete cds

Seq. No. 40827

Seq. ID LIB3138-095-Q1-N1-D1

Method BLASTX
NCBI GI g138364
BLAST score 402
E value 3.0e-39
Match length 130
% identity 66

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40828

Seq. ID LIB3138-095-Q1-N1-D3

Method BLASTN
NCBI GI g210811
BLAST score 44
E value 8.0e-16
Match length 84
% identity 90

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40829

Seq. ID LIB3138-095-Q1-N1-D6

Method BLASTX
NCBI GI g1946367
BLAST score 168
E value 7.0e-12
Match length 86
% identity 44

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 40830



```
LIB3138-095-Q1-N1-E3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4097879
BLAST score
                  68
E value
                  9.0e-30
Match length
                  273
                  86
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  40831
Seq. No.
                  LIB3138-095-Q1-N1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  123
                  1.0e-62
E value
Match length
                  271
% identity
                  86
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  40832
Seq. ID
                  LIB3138-095-Q1-N1-F5
Method
                  BLASTX
NCBI GI
                  g3292817
BLAST score
                  290
                  4.0e-26
E value
Match length
                  100
% identity
                  60
                  (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  40833
                  LIB3138-095-Q1-N1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3292817
BLAST score
                  213
                  4.0e-17
E value
                  56
Match length
                  71
% identity
                  (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   40834
Seq. ID
                  LIB3138-095-Q1-N1-F7
Method
                  BLASTX
NCBI GI
                  g2829870
BLAST score
                  186
                  4.0e-14
E value
```

Match length 67 % identity 54

(AC002396) Hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 40835

LIB3138-095-Q1-N1-G1 Seq. ID

Method BLASTN NCBI GI q210811 BLAST score 114 E value 3.0e-57



Match length 298 % identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40836

Seq. ID LIB3138-095-Q1-N1-G3

Method BLASTN
NCBI GI g210811
BLAST score 63
E value 6.0e-27
Match length 127
% identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40837

Seq. ID LIB3138-095-Q1-N1-G4

Method BLASTN
NCBI GI g4097879
BLAST score 36
E value 4.0e-11
Match length 56
% identity 91

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40838

Seq. ID LIB3138-095-Q1-N1-H8

Method BLASTX
NCBI GI g229708
BLAST score 172
E value 2.0e-12
Match length 100
% identity 42

NCBI Description Bean pod mottle virus

Seq. No. 40839

Seq. ID LIB3138-096-Q1-N1-A11

Method BLASTN
NCBI GI g210811
BLAST score 214
E value 1.0e-117
Match length 374
% identity 89

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40840

Seq. ID LIB3138-096-Q1-N1-D12

Method BLASTX
NCBI GI g2754849
BLAST score 347
E value 7.0e-33
Match length 74
% identity 91

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase

% identity

NCBI Description

61

thaliana]



[Fritillaria agrestis]

```
Seq. No.
                  40841
Seq. ID
                  LIB3138-096-Q1-N1-D9
Method
                  BLASTX
NCBI GI
                  q3116132
BLAST score
                  326
                  2.0e-30
E value
Match length
                  125
                  53
% identity
                  (AL023288) ribosomal protein [Schizosaccharomyces pombe]
NCBI Description
                  >gi 3201578 dbj BAA28752 (AB015169) ribosomal protein L19
                  homolog [Schizosaccharomyces pombe]
                  40842
Seq. No.
                  LIB3138-096-Q1-N1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1170659
BLAST score
                  208
E value
                  4.0e-19
                  115
Match length
                  49
% identity
                  KINESIN-LIKE PROTEIN KIF4 >gi 1083417 pir A54803
NCBI Description
                  microtubule-associated motor KIF4 - mouse
                  >gi_563773_dbj_BAA02167_ (D12646) KIF4 [Mus musculus]
                  40843
Seq. No.
                  LIB3138-096-Q1-N1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160161
BLAST score
                  176
                   9.0e-13
E value
                  124
Match length
                   7
% identity
NCBI Description
                  (AC000132) F21M12.7 gene product [Arabidopsis thaliana]
                   40844
Seq. No.
Seq. ID
                  LIB3138-096-Q1-N1-E6
Method
                   BLASTN
NCBI GI
                   g4097879
BLAST score
                  160
E value
                   9.0e-85
Match length
                   348
                  87
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                   40845
                  LIB3138-096-Q1-N1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3643598
BLAST score
                   290
                   3.0e-26
E value
Match length
                  120
```

6411

(AC005395) putative poly(A) polymerase [Arabidopsis



```
40846
Seq. No.
Seq. ID
                  LIB3138-097-Q1-N1-A11
Method
                  BLASTX
NCBI GI
                  g1001311
BLAST score
                  426
                  5.0e-42
E value
                  133
Match length
                  61
% identity
                 (D64006) hypothetical protein [Synechocystis sp.]
NCBI Description
                  40847
Seq. No.
Seq. ID
                  LIB3138-097-Q1-N1-A3
                  BLASTX
Method
NCBI GI
                  g2498731
BLAST score
                  343
                  2.0e-32
E value
                  124
Match length
                  56
% identity
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi 1362013 pir S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi 886428 emb CAA89838 (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
                  40848
Seq. No.
Seq. ID
                  LIB3138-097-Q1-N1-B1
Method
                  BLASTX
NCBI GI
                  g123537
BLAST score
                  155
                  2.0e-10
E value
Match length
                  70
% identity
                  49
                  12 KD HEAT SHOCK PROTEIN (GLUCOSE AND LIPID-REGULATED
NCBI Description
                  PROTEIN) >gi 72231 pir HHBY12 heat shock protein 12 -
                  yeast (Saccharomyces cerevisiae) >gi 3800 emb CAA39306_
                  (X55785) hsp12 [Saccharomyces cerevisiae] >gi 171607
                  (M60827) 15 kD glucose and lipid regulated protein
                  [Saccharomyces cerevisiae] >gi_559934_emb_CAA86349
                  (Z46255) hsp12, glp1, len: 109, CAI: 0.65, HS12_YEAST
                  P22943 12 KD HEAT SHOCK PROTEIN [Saccharomyces cerevisiae]
                  >gi 836740 dbj BAA09224_ (D50617) 12KD heat shock protein
                  [Saccharomyces cerevisiae] >gi 1100790 dbj BAA08003_
                  (D44596) 15kD glucose and lipid regulated protein
                  [Saccharomyces cerevisiae] >gi 1742028 dbj BAA14033_
                  (D89864) Sc-Hsp12p [Saccharomyces pastorianus]
Seq. No.
                  40849
                  LIB3138-097-Q1-N1-B7
Seq. ID
                  BLASTX
Method
```

NCBI GI g4097880
BLAST score 596
E value 6.0e-62
Match length 139
% identity 83

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 40850



```
LIB3138-097-Q1-N1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q229707
BLAST score
                  428
                  3.0e-42
E value
Match length
                  133
% identity
                  65
                  Bean pod mottle virus
NCBI Description
Seq. No.
                  40851
                  LIB3138-097-Q1-N1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  149
E value
                   3.0e-78
Match length
                  377
                  85
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   40852
Seq. No.
Seq. ID
                  LIB3138-097-Q1-N1-E3
                   BLASTX
Method
NCBI GI
                  g4314400
BLAST score
                   250
                   2.0e-21
E value
Match length
                  134
                   21
% identity
                  (AC006232) putative selenium-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   40853
Seq. ID
                  LIB3138-097-Q1-N1-E5
Method
                  BLASTX
NCBI GI
                  q229707
BLAST score
                  169
E value
                   2.0e-12
Match length
                   41
% identity
                   80
NCBI Description Bean pod mottle virus
Seq. No.
                   40854
                  LIB3138-097-Q1-N1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                   q1055367
BLAST score
                   119
                   3.0e-60
E value
                   375
Match length
% identity
                   84
NCBI Description
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
```

Seq. No. 40855

LIB3138-097-Q1-N1-F12 Seq. ID

Method BLASTN g1055367 NCBI GI 90 BLAST score



E value 4.0e-43 Match length 162 % identity 90

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 40856

Seq. ID LIB3138-097-Q1-N1-G2

Method BLASTX
NCBI GI g3136024
BLAST score 255
E value 5.0e-22
Match length 83
% identity 64

NCBI Description (AL023587) 40s ribosomal protein [Schizosaccharomyces

pombe]

Seq. No. 40857

Seq. ID LIB3138-097-Q1-N1-H1

Method BLASTN
NCBI GI g210811
BLAST score 85
E value 6.0e-40
Match length 214
% identity 89

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 40858

Seq. ID LIB3138-097-Q1-N1-H12

Method BLASTN
NCBI GI g3449321
BLAST score 36
E value 9.0e-11
Match length 116
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG10, complete sequence [Arabidopsis thaliana]

Seq. No. 40859

Seq. ID LIB3138-098-P1-N1-A10

Method BLASTN
NCBI GI g201821
BLAST score 277
E value 1.0e-154
Match length 404
% identity 92

NCBI Description Mouse binding protein for T-cell receptor (TCR-ATF1) mRNA,

complete cds

Seq. No. 40860

Seq. ID LIB3138-098-P1-N1-A12

Method BLASTN
NCBI GI g3721859
BLAST score 160
E value 1.0e-84
Match length 408



% identity

NCBI Description Mus musculus mRNA for oncostatin M receptor beta, complete

cds

Seq. No. 40861

Seq. ID LIB3138-098-P1-N1-C12

BLASTN Method NCBI GI g1050755 BLAST score 166 1.0e-88 E value Match length 170 99 % identity

NCBI Description R.norvegicus mRNA for ubiquitin and ribosomal protein S27a

40862 Seq. No.

Seq. ID LIB3138-098-P1-N1-C9

Method BLASTN NCBI GI g1228140 BLAST score 363 0.0e+00E value 379 Match length % identity 99

NCBI Description Rattus norvegicus macrophage inflammatory protein-2

precursor, mRNA, complete cds

40863 Seq. No.

Seq. ID LIB3138-098-P1-N1-D2

Method BLASTN NCBI GI g55881 BLAST score 315 1.0e-177 E value Match length 323

% identity 99

NCBI Description Rat mRNA for preprocathepsin D (EC 3.4.23.5)

40864 Seq. No.

Seq. ID LIB3138-098-P1-N1-D8

BLASTN Method g205869 NCBI GI BLAST score 381 0.0e + 00E value Match length 416 97 % identity

NCBI Description Rat ornithine aminotransferase mRNA, complete cds

40865 Seq. No.

Seq. ID LIB3138-098-P1-N1-F6

Method BLASTN q1279978 NCBI GI BLAST score 32 1.0e-08 E value Match length 32 % identity 100

Rattus norvegicus estrogen-responsive uterine mRNA, partial NCBI Description

sequence

Seq. No. 40866



```
LIB3138-098-P1-N1-G9
Seq. ID
                  BLASTN
Method
                  g1304167
NCBI GI
                  149
BLAST score
                  3.0e-78
E value
                  371
Match length
                  86
% identity
                  Mouse seizure-related mRNA, partial cds
NCBI Description
                  40867
Seq. No.
                  LIB3138-098-P1-N1-H10
Seq. ID
                  BLASTN
Method
                  q205631
NCBI GI
                  73
BLAST score
                  3.0e-33
E value
                  89
Match length
% identity
                  96
                  Rattus norvegicus Na, K-ATPase alpha-1 subunit mRNA,
NCBI Description
                  complete cds
                   40868
Seq. No.
Seq. ID
                  LIB3138-098-P1-N1-H8
Method
                  BLASTN
                  g50488
NCBI GI
                   65
BLAST score
                   4.0e-28
E value
                   241
Match length
                   82
% identity
                  Mouse COL1A2 mRNA for pro-alpha-2(I) collagen
NCBI Description
                   40869
Seq. No.
                   LIB3138-099-Q1-N1-A2
Seq. ID
                   BLASTN
Method
                   g802104
NCBI GI
                   224
BLAST score
                   1.0e-123
E value
                   248
Match length
                   98
% identity
                  PP1M M110=protein phosphatase 1M 110 kda regulatory subunit
NCBI Description
                   [rats, aorta, mRNA, 3300 nt]
Seq. No.
                   40870
Seq. ID
                   LIB3138-099-Q1-N1-A3
                   BLASTN
Method
NCBI GI
                   q2708306
                   49
BLAST score
                   1.0e-18
E value
                   77
Match length
                   91
% identity
                   Homo sapiens U4/U6 small nuclear ribonucleoprotein hPrp3
NCBI Description
                   mRNA, complete cds
                   40871
Seq. No.
Seq. ID
                   LIB3138-099-Q1-N1-A9
```

BLASTN

g4092758 103

Method NCBI GI

BLAST score



```
1.0e-50
E value
Match length
                   115
                   97
 % identity
                   Homo sapiens alphaE-catenin (CTNNA1) gene, exon
 NCBI Description
                   40872
 Seq. No.
                   LIB3138-099-Q1-N1-C3
 Seq. ID
 Method
                   BLASTN
                   g37243
 NCBI GI
                   327
 BLAST score
 E value
                   0.0e+00
 Match length
                   379
 % identity
                   97
                   Human fetal lung plasminogen activator (t-PA) mRNA (EC
 NCBI Description
                   3.4.21.31)
                    40873
 Seq. No.
 Seq. ID
                   LIB3138-099-Q1-N1-D2
                   BLASTN
 Method
                    g34757
 NCBI GI
                    404
 BLAST score
                    0.0e+00
 E value
 Match length
                    407
 % identity
                    100
                   Human mRNA for enkephalinase (EC 3.4.24.11)
 NCBI Description
                    >gi_589230_gb_I08056_ Sequence 2 from Patent EP
                    40874
 Seq. No.
                    LIB3138-099-Q1-N1-D3
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g632081
 BLAST score
                    143
 E value
                    8.0e-09
 Match length
                    62
 % identity
                    48
                    hypothetical protein 4 - Xanthobacter sp
 NCBI Description
                    >gi 581833_emb_CAA56244_ (X79863) orf4 [Xanthobacter sp.
                    Py2]
                    40875
 Seq. No.
                    LIB3138-099-Q1-N1-D4
 Seq. ID
                    BLASTN
 Method
                    g340306
 NCBI GI
                    298
 BLAST score
                    1.0e-167
 E value
                    371
 Match length
                    95
 % identity
                    Human cell adhesion protein (vitronectin) receptor alpha
 NCBI Description
                    subunit mRNA, complete cds.
                    >gi_4504762_ref_NM_002210.1_ITGAV_ Homo sapiens integrin,
                    alpha V (vitronectin receptor, alpha polypeptide, antigen
                    CD51) (ITGAV) mRNA
```

Seq. No. 40876

Seq. ID LIB3138-099-Q1-N1-D6

Method BLASTN NCBI GI g31164



```
BLAST score
                  0.0e + 00
E value
                  410
Match length
                  98
% identity
                  Human ENO2 gene for neuron specific (gamma) enolase
NCBI Description
                  40877
Seq. No.
                  LIB3138-099-Q1-N1-E1
Seq. ID
                  BLASTN
Method
                  q3482960
NCBI GI
BLAST score
                  332
                  0.0e+00
E value
Match length
                   364
                   98
% identity
                  Homo sapiens chromosome 17, clone HCIT524C5, complete
NCBI Description
                   sequence [Homo sapiens]
                   40878
Seq. No.
                   LIB3138-099-Q1-N1-F2
Seq. ID
                   BLASTN
Method
                   q1217667
NCBI GI
                   352
BLAST score
                   0.0e + 00
E value
Match length
                   379
% identity
                   ArgRS=arginyl-tRNA synthetase [human, ataxia-telangiectasia
NCBI Description
                   patients, EBV-lymphoblastoid cells, mRNA, 2120 nt]
                   >gi 4506428 ref NM 002887.1_RARS_ Homo sapiens arginyl-tRNA
                   synthetase (RARS) mRNA
                   40879
Seq. No.
                   LIB3138-099-Q1-N1-F3
Seq. ID
                   BLASTN
Method
NCBI GI
                   q434752
                   331
BLAST score
                   0.0e+00
E value
Match length
                   347
                   99
% identity
NCBI Description Human mRNA for KIAA0030 gene, partial cds
                   40880
Seq. No.
                   LIB3138-099-Q1-N1-G1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g238266
 BLAST score
                   36
                   6.0e-11
E value
Match length
                   70
                   96
 % identity
                   NMDA receptor glutamate-binding subunit [rats, mRNA, 1742
 NCBI Description
                    40881
 Seq. No.
                   LIB3138-099-Q1-N1-G2
 Seq. ID
```

BLASTN Method g3387928 NCBI GI 284 BLAST score 1.0e-159 E value



Match length 305 % identity 99

NCBI Description Homo sapiens clone 24703 beta-tubulin mRNA, complete cds

Seq. No. 40882

Seq. ID LIB3138-099-Q1-N1-G4

Method BLASTN
NCBI GI g2906225
BLAST score 161
E value 2.0e-85
Match length 399
% identity 87

NCBI Description Homo sapiens origin recognition complex subunit 4 (ORC4L)

mRNA, complete cds

Seq. No. 40883

Seq. ID LIB3138-099-Q1-N1-G5

Method BLASTN
NCBI GI g4503524
BLAST score 323
E value 0.0e+00
Match length 379
% identity 97

NCBI Description Homo sapiens eukaryotic translation initiation factor 3,

subunit 8 (110kD) (EIF3S8) mRNA, and translated products,

complete sequence

Seq. No. 40884

Seq. ID LIB3138-099-Q1-N1-G6

Method BLASTN
NCBI GI g2809323
BLAST score 272
E value 1.0e-151
Match length 306
% identity 97

NCBI Description Homo sapiens calumenin mRNA, complete cds

Seq. No. 40885

Seq. ID LIB3138-099-Q1-N1-H10

Method BLASTN
NCBI GI g337488
BLAST score 371
E value 0.0e+00
Match length 407
% identity 98

NCBI Description Human replication protein A 70kDa subunit mRNA complete

cds. >qi 4506582 ref NM 002945.1 RPA1 Homo sapiens

replication protein A1 (70kD) (RPA1) mRNA

Seq. No. 40886

Seq. ID LIB3138-099-Q1-N1-H12

Method BLASTN
NCBI GI g184134
BLAST score 375
E value 0.0e+00
Match length 387
% identity 99



NCBI Description Human HLA-E class I mRNA

Seq. No. 40887

Seq. ID LIB3138-099-Q1-N1-H4

Method BLASTN
NCBI GI g31190
BLAST score 409
E value 0.0e+00
Match length 409
% identity 100

NCBI Description H.sapiens mRNA for epican

Seq. No. 40888

Seq. ID LIB3138-099-Q1-N1-H6

Method BLASTN
NCBI GI g511636
BLAST score 223
E value 1.0e-122
Match length 306
% identity 93

NCBI Description Human Ca2-activated neutral protease large subunit (CANP)

mRNA, complete cds. >gi_4502562_ref_NM_001748.1_CAPN2_ Homo

sapiens calpain, large polypeptide L2 (CAPN2) mRNA

Seq. No. 40889

Seq. ID LIB3138-100-Q1-N1-C1

Method BLASTX
NCBI GI g3643090
BLAST score 437
E value 2.0e-43
Match length 106
% identity 75

NCBI Description (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

Seq. No. 40890

Seq. ID LIB3138-100-Q1-N1-D10

Method BLASTX
NCBI GI g431162
BLAST score 200
E value 9.0e-16
Match length 104
% identity 43

NCBI Description (D21822) ORF [Lilium longiflorum]

Seq. No. 40891

Seq. ID LIB3138-100-Q1-N1-D2

Method BLASTN
NCBI GI g1053215
BLAST score 281
E value 1.0e-157
Match length 325
% identity 97

NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA,

nuclear gene encoding chloroplast protein, complete cds

Seq. No. 40892



```
LIB3138-100-Q1-N1-F10
Seq. ID
                  BLASTX
Method
                  g138364
NCBI GI
                  353
BLAST score
                  8.0e-34
E value
                  88
Match length
                  80
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                  40893
Seq. No.
                  LIB3138-100-Q1-N1-H1
Seq. ID
Method
                  BLASTN
                  g4406529
NCBI GI
                  39
BLAST score
                  7.0e-13
E value
                   63
Match length
                   90
% identity
                  Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
NCBI Description
                   encoding chloroplast protein, complete cds
                   40894
Seq. No.
                   LIB3138-100-Q1-N1-H10
Seq. ID
                   BLASTX
Method
                   g84163
NCBI GI
                   338
BLAST score
                   3.0e - 32
E value
                   82
Match length
                   80
% identity
                  myosin calcium-binding light chain - slime mold (Physarum
NCBI Description
                   polycephalum)
                   40895
Seq. No.
                   LIB3138-100-Q1-N1-H5
Seq. ID
                   BLASTX
Method
                   q138364
NCBI GI
                   420
BLAST score
                   1.0e-41
E value
Match length
                   100
                   77
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   40896
Seq. No.
                   LIB3138-101-Q1-N1-A11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q115709
                   388
BLAST score
                   1.0e-37
E value
```

142 Match length 52 % identity

NCBI Description CATALASE A >gi_66302_pir__CSBYP catalase (EC 1.11.1.6),

peroxisomal - yeast (Saccharomyces cerevisiae)

```
>gi_3605_emb_CAA31443_ (X13028) catalase A (AA 1-515)
[Saccharomyces cerevisiae] >gi_1136211_emb_CAA92713_
(Z68329) unknown [Saccharomyces cerevisiae]
>gi_1226032_emb_CAA94095_ (Z70202) Ctalp [Saccharomyces cerevisiae]
```

Seq. No. 40897 LIB3138-101-Q1-N1-C3 Seq. ID Method BLASTX NCBI GI q138364 BLAST score 208 E value 7.0e-17 Match length 79 % identity 53

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

 Seq. No.
 40898

 Seq. ID
 LIB3138-101-Q1-N1-D10

 Method
 BLASTN

 NCBI GI
 g4097879

 BLAST score
 143

 E value
 1.0e-74

E value 1.0e
Match length 422
% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40899

Seq. ID LIB3138-101-Q1-N1-G10

Method BLASTN
NCBI GI 94097879
BLAST score 140
E value 7.0e-73
Match length 324
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40900

Seq. ID LIB3138-101-Q1-N1-H10

Method BLASTX
NCBI GI g138364
BLAST score 296
E value 3.0e-52
Match length 153
% identity 76

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40901

Seq. ID LIB3138-101-Q1-N1-H11

Method BLASTN



q210811 NCBI GI 201 BLAST score 1.0e-109 E value 455 Match length % identity Bean pod mottle virus coat protein gene, complete cds, NCBI Description complete middle component (M) RNA 40902 Seq. No. LIB3138-102-Q1-N1-C4 Seq. ID BLASTX Method

Method BLASIX
NCBI GI g138364
BLAST score 138
E value 7.0e-17
Match length 102
% identity 54

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40903

Seq. ID LIB3138-102-Q1-N1-C9

Method BLASTX
NCBI GI g138364
BLAST score 159
E value 2.0e-15
Match length 98
% identity 53

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40904

Seq. ID LIB3138-102-Q1-N1-D8

Method BLASTX
NCBI GI g138364
BLAST score 196
E value 1.0e-15
Match length 63
% identity 63

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 40905

Seq. ID LIB3138-102-Q1-N1-E12

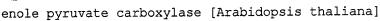
Method BLASTX
NCBI GI g3264805
BLAST score 326
E value 2.0e-30
Match length 75
% identity 83

NCBI Description (AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho

Method

NCBI GI





```
40906
Seq. No.
Seq. ID
                  LIB3138-102-Q1-N1-E4
Method
                  BLASTN
NCBI GI
                  g2731815
BLAST score
                  37
                  2.0e-11
E value
                  41
Match length
                  98
% identity
NCBI Description Glycine max nitrate reductase (BCNR-A) mRNA, partial cds
Seq. No.
                   40907
                  LIB3138-102-Q1-N1-F1
Seq. ID
                  BLASTN
Method
                   a2660685
NCBI GI
                   205
BLAST score
E value
                   1.0e-111
                   392
Match length
                   88
% identity
                  Filobasidiella neoformans translation elongation factor
NCBI Description
                  EF1-alpha (CnTEF1) mRNA, complete cds
Seq. No.
                   40908
                   LIB3138-102-Q1-N1-F2
Seq. ID
                   BLASTX
Method
                   q4099833
NCBI GI
                   471
BLAST score
E value
                   3.0e-47
                   130
Match length
% identity
                  (U90265) bifunctional nuclease [Zinnia elegans]
NCBI Description
Seq. No.
                   40909
                   LIB3138-102-Q1-N1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4097880
                   392
BLAST score
E value
                   4.0e-38
Match length
                   115
% identity
                   70
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   40910
                   LIB3138-103-Q1-N1-E10
Seq. ID
Method
                   BLASTX
                   g3292824
NCBI GI
BLAST score
                   271
                   2.0e-24
E value
                   77
Match length
                   69
% identity
                   (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                   40911
Seq. No.
                   LIB3138-103-Q1-N1-G6
Seq. ID
                   BLASTN
```

g4097879



BLAST score 66 E value 1.0e-28 Match length 138 % identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40912

Seq. ID LIB3138-104-Q1-N1-B7

Method BLASTX
NCBI GI g2677828
BLAST score 141
E value 5.0e-09
Match length 36
% identity 75

NCBI Description (U93166) cysteine protease [Prunus armeniaca]

Seq. No. 40913

Seq. ID LIB3138-104-Q1-N1-C11

Method BLASTX
NCBI GI g4558679
BLAST score 382
E value 6.0e-37
Match length 124
% identity 58

NCBI Description (AC006586) 40S Ribosomal protein S16 [Arabidopsis thaliana]

Seq. No. 40914

Seq. ID LIB3138-104-Q1-N1-D8

Method BLASTN
NCBI GI g2934883
BLAST score 81
E value 1.0e-37
Match length 81
% identity 100

NCBI Description Glycine max TGACG-motif binding protein (STF1) mRNA,

complete cds

Seq. No. 40915

Seq. ID LIB3138-104-Q1-N1-E2

Method BLASTN
NCBI GI g403328
BLAST score 49
E value 1.0e-18
Match length 97
% identity 88

NCBI Description T.repens TrMT1B mRNA for metallothionein-like protein

Seq. No. 40916

Seq. ID LIB3138-104-Q1-N1-G9

Method BLASTN
NCBI GI g4097879
BLAST score 172
E value 6.0e-92
Match length 360
% identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

Seq. ID



gene, complete cds

```
40917
Seq. No.
Seq. ID
                  LIB3138-104-Q1-N1-H9
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  163
E value
                  1.0e-24
                  125
Match length
% identity
                   61
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  40918
Seq. No.
Seq. ID
                  LIB3138-105-Q1-N1-A12
Method
                  BLASTN
                   q210811
NCBI GI
BLAST score
                   254
                  1.0e-141
E value
Match length
                   470
% identity
                   89
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   40919
Seq. No.
Seq. ID
                  LIB3138-105-Q1-N1-A4
Method
                  BLASTN
                   g210811
NCBI GI
BLAST score
                   235
                   1.0e-129
E value
                   442
Match length
                  89
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   40920
Seq. ID
                  LIB3138-105-Q1-N1-B2
                  BLASTX
Method
NCBI GI
                   q4220520
BLAST score
                   176
                   8.0e-13
E value
                   93
Match length
                   44
% identity
                  (AL035356) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   40921
Seq. ID
                   LIB3138-105-Q1-N1-C6
Method
                  BLASTX
NCBI GI
                   g173408
BLAST score
                   380
                   9.0e-37
E value
Match length
                   124
                   65
% identity
NCBI Description
                   (M60208) mitochondrial heat shock protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   40922
```

7

6426

LIB3138-105-Q1-N1-C7

% identity

36



```
BLASTN
  Method
  NCBI GI
                    g170073
  BLAST score
                    68
                    3.0e-30
  E value
                    165
  Match length
  % identity
                    86
                    Soybean calmodulin (SCaM-3) mRNA, complete cds
  NCBI Description
Seq. No.
                    40923
                    LIB3138-105-Q1-N1-C8
  Seq. ID
                    BLASTN
  Method
  NCBI GI
                    g531828
  BLAST score
                    33
                     4.0e-09
  E value
                     61
  Match length
                    89
  % identity
                    Cloning vector pSport1, complete cds
  NCBI Description
                     40924
  Seq. No.
  Seq. ID
                    LIB3138-105-Q1-N1-D11
  Method
                    BLASTX
  NCBI GI
                    g3540204
  BLAST score
                     252
                    1.0e-21
  E value
                     60
  Match length
                     72
  % identity
                    (AC004260) Hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                     40925
  Seq. No.
  Seq. ID
                    LIB3138-105-Q1-N1-D12
                    BLASTN
  Method
  NCBI GI
                     g1262439
                     78
  BLAST score
                     5.0e-36
  E value
                     206
  Match length
                     85
  % identity
  NCBI Description Glycine max lipoxygenase (vlxC) mRNA, complete cds
                     40926
  Seq. No.
  Seq. ID
                    LIB3138-105-Q1-N1-F1
  Method
                     BLASTN
  NCBI GI
                     g4097879
  BLAST score
                     77
  E value
                     2.0e-35
  Match length
                     229
                     83
  % identity
                    Bean pod mottle virus complete segment RNA1 polyprotein
  NCBI Description
                     gene, complete cds
  Seq. No.
                     40927
  Seq. ID
                     LIB3138-105-Q1-N1-G3
  Method
                     BLASTX
  NCBI GI
                     g138364
  BLAST score
                     186
  E value
                     3.0e-14
  Match length
                     86
```



```
GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  40928
                  LIB3138-105-Q1-N1-H1
Seq. ID
Method
                BLASTN
                  g1055367
NCBI GI
BLAST score
                  181
                  2.0e-97
E value
```

% identity 95 Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description subunit mRNA, complete cds

40929 Seq. No. Seq. ID LIB3138-105-Q1-N1-H7 Method BLASTX NCBI GI g4558558 BLAST score 319 E value 1.0e-29

225

Match length 97 % identity 57

Match length

(AC007138) putative polygalacturonidase [Arabidopsis NCBI Description thaliana]

Seq. No. 40930

LIB3138-106-Q1-N1-E12 Seq. ID

Method BLASTN NCBI GI g4406529 BLAST score 72 E value 1.0e-32 Match length 144

88 % identity

Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene NCBI Description

encoding chloroplast protein, complete cds

Seq. No. 40931

LIB3138-106-Q1-N1-E9 Seq. ID

BLASTX Method g2651308 NCBI GI BLAST score 176 9.0e-13 E value 65 Match length 62 % identity

(AC002336) putative myosin heavy chain [Arabidopsis NCBI Description

thaliana]

40932 Seq. No.

Seq. ID LIB3138-106-Q1-N1-F5

BLASTX Method NCBI GI g3721926 BLAST score 192 3.0e-15 E value 76 Match length 63 % identity

6428



```
NCBI Description (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
                  40933
Seq. No.
                  LIB3138-106-Q1-N1-G4
Seq. ID
Method
                  BLASTX
                  g100226
NCBI GI
BLAST score
                  179
                  3.0e-13
E value
                  109
Match length
                  45
% identity
                  hypothetical protein - tomato >gi_19275_emb_CAA78112_
NCBI Description
                   (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi 445619_prf 1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                  40934
Seq. No.
                  LIB3138-119-Q1-N1-A11
Seq. ID
                  BLASTX
Method
                  g3006140
NCBI GI
                   251
BLAST score
                   6.0e-27
E value
                   111
Match length
                   55
% identity
                   (AL022299) ribosomal protein [Schizosaccharomyces pombe]
NCBI Description
                   >gi_3123705_emb_CAA04548_ (AJ001133) ribosomal protein L7
                   [Schizosaccharomyces pombe]
                   40935
Seq. No.
                   LIB3138-119-Q1-N1-A4
Seq. ID
                   BLASTN
Method
                   g2244901
NCBI GI
                   46
BLAST score
E value
                   7.0e-17
Match length
                   78
                   90
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   40936
Seq. No.
                   LIB3138-119-Q1-N1-C5
Seq. ID
Method
                   BLASTN
                   g210811
NCBI GI
BLAST score
                   175
E value
                   1.0e-93
Match length
                   322
                   89
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   40937
Seq. No.
                   LIB3138-119-Q1-N1-C8
Seq. ID
                   BLASTX
Method
                   g3832512
NCBI GI
                   446
BLAST score
                   3.0e-44
E value
```

152

64

Match length

% identity

```
(AF097922) granule-bound glycogen (starch) synthase
NCBI Description
                  [Astragalus membranaceus]
                  40938
Seq. No.
                  LIB3138-119-Q1-N1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3766376
                  276
BLAST score
                  9.0e-25
E value
                  85
Match length
% identity
                  (AL031907) putative 60s acidic ribosomal protein p0
NCBI Description
                  [Schizosaccharomyces pombe]
                  40939
Seq. No.
                  LIB3138-119-Q1-N1-D6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g210811
                  86
BLAST score
                  1.0e-40
E value
Match length
                  150
                  90
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  40940
Seq. No.
                  LIB3138-119-Q1-N1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3914605
                  159
BLAST score
                   6.0e-11
E value
Match length
                  106
                   41
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE
NCBI Description
                   PRECURSOR (RUBISCO ACTIVASE) >gi_541930_pir__S39551
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase -
                   apple tree >gi 415852 emb CAA79857 (Z21794)
                   ribulose-1,5-bisphosphate carboxylase/oxygenase activase
                   [Malus domestica]
                   40941
Seq. No.
                   LIB3138-119-Q1-N1-G6
```

Seq. ID

Method BLASTX NCBI GI g3658 274 BLAST score 2.0e-24 E value Match length 109 % identity 55

NCBI Description (X07238) delta-P8 [Saccharomyces cerevisiae]

40942 Seq. No.

LIB3138-119-Q1-N1-H1 Seq. ID

BLASTN Method g4097879 NCBI GI 138 BLAST score 1.0e-71 E value 333 Match length



```
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  40943
Seq. No.
                  LIB3138-119-Q1-N1-H11
Seq. ID
Method
                  BLASTX
                  g4097880
NCBI GI
BLAST score
                  146
                   4.0e-17
E value
Match length
                   95
% identity
                   56
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
                   40944
Seq. No.
                   LIB3138-119-Q1-N1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4097880
                   172
BLAST score
                   7.0e-13
E value
                   62
Match length
                   61
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   40945
Seq. No.
                   LIB3138-119-Q1-N1-H4
Seq. ID
                   BLASTN
Method
                   q2370311
NCBI GI
BLAST score
                   33
                   3.0e-09
E value
                   93
Match length
                   84
% identity
NCBI Description Medicago sativa mRNA for DnaJ-like protein
                   40946
Seq. No.
                   LIB3138-120-Q1-N1-B5
Seq. ID
Method
                   BLASTX
                   q4138583
NCBI GI
BLAST score
                   183
                   2.0e-20
E value
                   74
Match length
                   73
% identity
                   (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
NCBI Description
                   40947
 Seq. No.
                   LIB3138-120-Q1-N1-C5
 Seq. ID
Method
                   BLASTN
                   g4097879
 NCBI GI
 BLAST score
                   93
                   8.0e-45
E value
```

203 Match length 90 % identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

40948 Seq. No.

LIB3138-120-Q1-N1-F11 Seq. ID



```
BLASTN
Method
                  q1079735
NCBI GI
BLAST score
                  118
                  5.0e-60
E value
                  194
Match length
% identity
                  90
                  Glycine soja ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit precursor (rbcS) gene, nuclear gene encoding
                  chloroplast protein, complete cds
                  40949
Seq. No.
Seq. ID
                  LIB3138-120-Q1-N1-H12
Method
                  BLASTX
                  q1019946
NCBI GI
                  190
BLAST score
                  1.0e-14
E value
Match length
                  100
% identity
                   45
                  (U37060) ascorbate peroxidase [Gossypium hirsutum]
NCBI Description
                   40950
Seq. No.
Seq. ID
                  LIB3138-121-Q1-N1-B3
Method
                  BLASTN
NCBI GI
                   g1431621
BLAST score
                   154
                   4.0e-81
E value
Match length
                   300
                   92
% identity
                  T.repens mRNA for protein kinase
NCBI Description
                   40951
Seq. No.
Seq. ID
                   LIB3138-121-Q1-N1-C2
Method
                   BLASTX
                   q4097880
NCBI GI
BLAST score
                   223
                   3.0e-18
E value
                   90
Match length
                   56
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   40952
Seq. No.
Seq. ID
                   LIB3138-121-Q1-N1-C7
                   BLASTX
Method
                   g2330797
NCBI GI
BLAST score
                   282
                   3.0e-25
E value
                   130
Match length
                   47
% identity
                  (Z98601) zinc finger protein [Schizosaccharomyces pombe]
NCBI Description
                   40953
Seq. No.
```

LIB3138-121-Q1-N1-E4 Seq. ID

Method BLASTX NCBI GI g4097880 BLAST score 153 1.0e-10 E value Match length 52



% identity (U70866) polyprotein [Bean pod mottle virus] NCBI Description Seq. No. 40954 LIB3138-121-Q1-N1-F4 Seq. ID Method BLASTN NCBI GI q4097879 BLAST score 155 E value 8.0e-82 Match length 323 % identity 87 Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description gene, complete cds 40955 Seq. No. Seq. ID LIB3138-121-Q1-N1-G5 Method BLASTN NCBI GI q210811 BLAST score 69 9.0e-31 E value 183 Match length 87 % identity Bean pod mottle virus coat protein gene, complete cds, NCBI Description complete middle component (M) RNA 40956 Seq. No. LIB3138-121-Q1-N1-H11 Seq. ID Method BLASTX NCBI GI q3925277 BLAST score 210 E value 7.0e-17 Match length 83 % identity 47 (AL032643) similar to Uncharacterized protein family NCBI Description UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans] Seq. No. 40957 LIB3138-122-Q1-N1-D4 Seq. ID BLASTN Method g210811 NCBI GI BLAST score 51 1.0e-19 E value 163 Match length 88 % identity Bean pod mottle virus coat protein gene, complete cds, NCBI Description complete middle component (M) RNA 40958 Seq. No. Seq. ID LIB3138-122-Q1-N1-D6

Method BLASTN
NCBI GI g210811
BLAST score 35
E value 3.0e-10
Match length 86
% identity 91



```
NCBI Description

Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No.

40959

Seq. ID

LIB3138-122-Q1-N1-E8

Method

BLASTN

NCBI GI

4406529
```

NCBI GI g4406529 BLAST score 117 E value 4.0e-59 Match length 296 % identity 85

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 40960 Seq. ID LIB3138-122-Q1-N1-G2

Method BLASTN
NCBI GI g4097879
BLAST score 181
E value 3.0e-97
Match length 455
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 40961

Seq. ID LIB3138-122-Q1-N1-H10

Method BLASTX
NCBI GI g2492515
BLAST score 244
E value 8.0e-21
Match length 109
% identity 49

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR

>gi_2129924_pir__S58298 ATPase - pepper (fragment)

>gi_929013_emb_CAA62084_ (X90472) ATPase [Capsicum annuum]

Seq. No. 40962

Seq. ID LIB3138-123-Q1-N1-A10

Method BLASTX
NCBI GI g229707
BLAST score 161
E value 3.0e-11
Match length 91
% identity 41

NCBI Description Bean pod mottle virus

Seq. No. 40963

Seq. ID LIB3138-123-Q1-N1-A2

Method BLASTX
NCBI GI g4566614
BLAST score 230
E value 7.0e-40
Match length 93
% identity 89

NCBI Description (AF112887) actin depolymerizing factor [Populus alba x

Populus tremula]



```
Seq. No.
                  40964
                  LIB3138-123-Q1-N1-A3
Seq. ID
Method
                  BLASTX
                  g3878443
NCBI GI
                  141
BLAST score
E value
                  1.0e-08
Match length
                  114
                  35
% identity
                  (Z81568) similar to UTP--GLUCOSE-1-PHOSPHATE
NCBI Description
                  URIDYLYLTRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP); cDNA EST EMBL:D36116 comes from
                  this gene [Caenorhabditis elegans]
                  40965
Seq. No.
                  LIB3138-123-Q1-N1-B10
Seq. ID
                  BLASTN
Method
                  g3550981
NCBI GI
BLAST score
                   33
                  5.0e-09
E value
                  69
Match length
                   87
% identity
NCBI Description Arabidopsis thaliana mutM homologue gene, complete cds
Seq. No.
                   40966
                  LIB3138-123-Q1-N1-C8
Seq. ID
Method
                  BLASTN
                   q1055367
NCBI GI
BLAST score
                   230
                   1.0e-126
E value
Match length
                   305
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   40967
Seq. ID
                   LIB3138-123-Q1-N1-D7
Method
                   BLASTX
NCBI GI
                   g229708
BLAST score
                   338
                   7.0e-32
E value
Match length
                   93
% identity
                   71
NCBI Description Bean pod mottle virus
                   40968
Seq. No.
                   LIB3138-123-Q1-N1-E10
Seq. ID
Method
                   BLASTX
                   g4204695
NCBI GI
BLAST score
                   264
```

4.0e-23 E value 77 Match length 69 % identity

(AF117062) putative inositol polyphosphate 5-phosphatase NCBI Description

At5P1 [Arabidopsis thaliana]

Seq. No. 40969



```
LIB3138-123-Q1-N1-E7
Seq. ID
Method
                  BLASTN
                  g210811
NCBI GI
                  53
BLAST score
                  3.0e-21
E value
Match length
                  85
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   40970
Seq. No.
                  LIB3138-123-Q1-N1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g132845
BLAST score
                   344
                   2.0e-32
E value
                   121
Match length
                   58
% identity
                   60S RIBOSOMAL PROTEIN L27A (L29) (CRP1)
NCBI Description
                   >gi_71193_pir__R6NC7A ribosomal protein L27a.e - Neurospora
                   crassa >gi_2991_emb_CAA29635_ (X06320) put. ribosomal
                   protein [Neurospora crassa] >gi_2993_emb_CAA31630_ (X13254)
                   put. ribosomal protein (AA 1-149) [Neurospora crassa]
Seq. No.
                   40971
                   LIB3138-123-Q1-N1-H10
Seq. ID
                   BLASTX
Method
                   q3831457
NCBI GI
BLAST score
                   166
                   1.0e-11
E value
Match length
                   90
                   41
% identity
                   (AC005700) putative ion channel protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   40972
                   LIB3138-123-Q1-N1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3063459
BLAST score
                   454
E value
                   2.0e-45
                   105
Match length
                   76
% identity
                   (AC003981) F22013.21 [Arabidopsis thaliana]
NCBI Description
                   40973
Seq. No.
                   LIB3138-124-Q1-N1-A10
Seq. ID
Method
                   BLASTX
                   g1709191
NCBI GI
BLAST score
                   337
                   1.0e-31
E value
```

93 Match length 76 % identity

MAJOR VAULT PROTEIN BETA (MVP-BETA) >gi 1362213_pir A57241 NCBI Description

major vault protein B - slime mold (Dictyostelium

discoideum) >gi_887422_emb CAA85473_ (Z37109) major vault

protein B [Dictyostelium discoideum]

NCBI Description

papaya]



```
Seq. No.
                  40974
                  LIB3138-124-Q1-N1-A5
Seq. ID
                  BLASTX
Method
                  q1168347
NCBI GI
                  162
BLAST score
                  3.0e-11
E value
Match length
                  112
% identity
                  ALCOHOL DEHYDROGENASE (ADH-T) >gi_282375_pir__A42654
NCBI Description
                   alcohol dehydrogenase (EC 1.1.1.1), thermostable - Bacillus
                   stearothermophilus >gi_216230_dbj_BAA14411 (D90421)
                   alcohol dehydrogenase [Bacillus stearothermophilus]
                   40975
Seq. No.
                  LIB3138-124-Q1-N1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2341042
                   375
BLAST score
                   3.0e-36
E value
                   88
Match length
                   80
% identity
                  (AC000104) F19P19.26 [Arabidopsis thaliana]
NCBI Description
                   40976
Seq. No.
                   LIB3138-124-Q1-N1-C12
Seq. ID
                   BLASTX
Method
                   a115471
NCBI GI
BLAST score
                   344
                   1.0e-32
E value
                   121
Match length
% identity
                   CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE
NCBI Description
                   DEHYDRATASE) >gi_100078_pir S10200 carbonate dehydratase
                   (EC 4.2.1.1) precursor - garden pea >gi_20673_emb_CAA36792
                   (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]
                   40977
Seq. No.
Seq. ID
                   LIB3138-124-Q1-N1-F2
Method
                   BLASTX
                   q1935914
NCBI GI
                   227
BLAST score
                   8.0e-19
E value
                   52
Match length
 % identity
                   (U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]
NCBI Description
                   40978
 Seq. No.
                   LIB3138-124-Q1-N1-G10
 Seq. ID
                   BLASTX
Method
                   q3342798
 NCBI GI
                   174
 BLAST score
                   5.0e-13
 E value
 Match length
                   72
 % identity
                   57
```

(AF061240) glutamine cyclotransferase precursor [Carica



```
40979
Seq. No.
Seq. ID
                  LIB3138-124-Q1-N1-H10
Method
                  BLASTX
NCBI GI
                  g4097880
                  248
BLAST score
                  2.0e-21
E value
Match length
                  80
                  64
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  40980
Seq. No.
                  LIB3138-124-Q1-N1-H11
Seq. ID
                  BLASTX
Method
                  g1931654
NCBI GI
BLAST score
                  311
                  1.0e-28
E value
                  71
Match length
                  76
% identity
                   (U95973) BRCA1-associated RING domain protein isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   40981
Seq. ID
                  LIB3138-125-Q1-N1-B5
                  BLASTX
Method
                  q543905
NCBI GI
BLAST score
                  107
                  2.0e-11
E value
                  108
Match length
                   47
% identity
                  BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
NCBI Description
                  brassinosteroid-regulated protein [Glycine max]
                   40982
Seq. No.
Seq. ID
                  LIB3138-125-Q1-N1-C1
                  BLASTX
Method
                  g3560228
NCBI GI
                  274
BLAST score
                   3.0e-24
E value
                   92
Match length
                   59
% identity
                   (AL031530) putative nadh-cytochrome b5 reductase
NCBI Description
                   [Schizosaccharomyces pombe]
                   40983
Seq. No.
Seq. ID
                  LIB3138-125-Q1-N1-E4
                  BLASTX
Method
                   g138364
NCBI GI
BLAST score
                   416
                   4.0e-41
E value
Match length
                   102
                   78
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
```

(M62738) coat protein [Bean pod mottle virus]

bean pod mottle virus (strain Kentucky G7) >gi 210812



```
Seq. No.
                  LIB3138-125-Q1-N1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g229707
BLAST score
                  550
E value
                  1.0e-56
Match length
                  117
                  85
% identity
NCBI Description Bean pod mottle virus
Seq. No.
                  40985
Seq. ID
                  LIB3138-125-Q1-N1-G2
Method
                  BLASTX
NCBI GI
                  q3080398
BLAST score
                   159
E value
                  8.0e-11
Match length
                  86
% identity
                   43
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   40986
Seq. ID
                  LIB3138-125-Q1-N1-H2
Method
                  BLASTX
NCBI GI
                   q1488043
BLAST score
                   155
E value
                   7.0e-11
Match length
                   63
                   46
% identity
                  (U63784) PAPS-reductase-like protein [Catharanthus roseus]
NCBI Description
Seq. No.
                   40987
                   LIB3138-125-Q1-N1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2970050
BLAST score
                   86
                   1.0e-40
E value
                   202
Match length
                   86
% identity
NCBI Description Vigna radiata mRNA for ARG10, complete cds
                   40988
Seq. No.
Seq. ID
                   LIB3138-126-Q1-N1-A1
                   BLASTX
Method.
NCBI GI
                   q729773
BLAST score
                   444
E value
                   3.0e-44
Match length
                   123
                   75
% identity
                   HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK
NCBI Description
                   TRANSCRIPTION FACTOR 1) (HSTF 1) >gi 429155 emb CAA53761_
                   (X76167) heat shock factor [Arabidopsis thaliana]
                   40989
Seq. No.
```

Seq. ID LIB3138-126-Q1-N1-A4

Method BLASTX NCBI GI g2104961 BLAST score 377

% identity

NCBI Description

22



```
E value
                    2.0e-36
 Match length
                    117
 % identity
                    63
                   (U96967) alcohol oxidase [Pichia pastoris]
 NCBI Description
 Seq. No.
                   40990
 Seq. ID
                   LIB3138-126-Q1-N1-B6
 Method
                   BLASTX
 NCBI GI
                   g2865171
 BLAST score
                   429
                   2.0e-42
 E value
 Match length
                   115
 % identity
                   69
 NCBI Description
                   (AB010901) ribosomal protein L21 homolog
                   [Schizosaccharomyces pombe]
 Seq. No.
                   40991
                   LIB3138-126-Q1-N1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2181190
BLAST score
                   428
                   2.0e-42
E value
Match length
                   119
% identity
                   69
NCBI Description
                   (Y12531) serine/threonine kinase [Brassica oleracea]
Seq. No.
                   40992
Seq. ID
                   LIB3138-126-Q1-N1-D1
Method
                   BLASTN
NCBI GI
                   q531828
BLAST score
                   62
                   2.0e-26
E value
Match length
                   231
% identity
                   82
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                   40993
Seq. ID
                   LIB3138-126-Q1-N1-D5
Method
                   BLASTX
NCBI GI
                   g102012
BLAST score
                   224
E value
                   2.0e-18
Match length
                   75
% identity
                   59
NCBI Description
                   ecp2 protein - fungus (Cladosporium fulvum)
                   >gi_2561_emb_CAA78401_ (Z14024) ecp2 [Cladosporium fulvum]
Seq. No.
                   40994
Seq. ID
                  LIB3138-126-Q1-N1-F4
Method
                  BLASTX
NCBI GI
                  g2832642
BLAST score
                  161
E value
                  5.0e-11
Match length
                  90
```

(AL021710) putative protein [Arabidopsis thaliana]



```
40995
Seq. No.
                  LIB3138-126-Q1-N1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4097880
                   251
BLAST score
                   6.0e-35
E value
Match length
                   121
                   68
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   40996
Seq. No.
Seq. ID
                   LIB3138-126-Q1-N1-F9
Method
                   BLASTN
                   q18551
NCBI GI
                   359
BLAST score
E value
                   0.0e + 00
Match length
                   368
                   99
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
                   40997
Seq. No.
                   LIB3138-126-Q1-N1-G10
Seq. ID
Method
                   BLASTN
                   q4406529
NCBI GI
BLAST score
                   63
                   6.0e-27
E value
                   248
Match length
% identity
                   Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
NCBI Description
                   encoding chloroplast protein, complete cds
                   40998
Seq. No.
                   LIB3138-127-Q1-N1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3702338
BLAST score
                   541
                   1.0e-55
E value
                   116
Match length
% identity
                   84
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                   40999
Seq. No.
                   LIB3138-127-Q1-N1-C11
Seq. ID
Method
                   BLASTX
                   g3549664
NCBI GI
BLAST score
                   166
E value
                   1.0e-11
                   45
Match length
                   62
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                   41000
Seq. No.
                   LIB3138-128-Q1-N1-E11
Seq. ID
Method
                   BLASTX
```

g4490330

128

NCBI GI

BLAST score



```
6.0e-14
E value
                  116
Match length
                  47
% identity
                  (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  41001
Seq. No.
Seq. ID
                  LIB3138-128-Q1-N1-F3
Method
                  BLASTX
NCBI GI
                  g229708
BLAST score
                  446
E value
                  1.0e-44
Match length
                  103
                   79
% identity
NCBI Description Bean pod mottle virus
                  41002
Seq. No.
Seq. ID
                  LIB3138-128-Q1-N1-G3
Method
                  BLASTN
NCBI GI
                  q169036
BLAST score
                   101
                  1.0e-49
E value
Match length
                  168
% identity
                   90
NCBI Description Pisum sativum L. aldolase gene, 3' end cds
                   41003
Seq. No.
                   LIB3138-128-Q1-N1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g229708
BLAST score
                   193
E value
                   6.0e-15
Match length
                   94
% identity
                   45
NCBI Description Bean pod mottle virus
                   41004
Seq. No.
Seq. ID
                   LIB3138-128-Q1-N1-H12
Method
                   BLASTX
                   q3935170
NCBI GI
BLAST score
                   432
                   7.0e-43
E value
                   104
Match length
% identity
                   74
                   (AC004557) F17L21.13 [Arabidopsis thaliana]
NCBI Description
                   41005
Seq. No.
                   LIB3138-128-Q1-N1-H5
Seq. ID
                   BLASTN
Method
                   q169036
NCBI GI
```

72 BLAST score 2.0e-32 E value 124 Match length 90 % identity

NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No.

41006

6442

Seq. ID Method



```
LIB3138-129-Q1-N1-A1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4097879
BLAST score
                   137
                   4.0e-71
E value
                   269
Match length
                   88
% identity
                   Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41007
Seq. No.
Seq. ID
                   LIB3138-129-Q1-N1-C11
                   BLASTX
Method
NCBI GI
                   g2347143
BLAST score
                   335
                   1.0e-31
E value
                   86
Match length
                   67
% identity
                  (U48234) spU2AF23 [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                   41008
                   LIB3138-129-Q1-N1-C2
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   90
Match length
                   87
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41009
Seq. No.
                   LIB3138-129-Q1-N1-D4
Seq. ID
Method
                   BLASTX
                   a539016
NCBI GI
BLAST score
                   146
                   3.0e-09
E value
                   40
Match length
% identity
                   reverse transcriptase (copia-like retrotransposon) Ta7 -
NCBI Description
                   Arabidopsis thaliana (fragment)
Seq. No.
                   41010
                   LIB3138-129-Q1-N1-E4
Seq. ID
                   BLASTN
Method
NCBI GI
                   q20728
BLAST score
                   98
                   8.0e-48
E value
                   273
Match length
                   89
% identity
                   Pea chloroplast GAPA mRNA encoding
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A
                   (EC 1.2.1.13)
Seq. No.
                   41011
```

LIB3138-129-Q1-N1-F8

BLASTX



NCBI GI g2132987
BLAST score 246
E value 5.0e-21
Match length 107
% identity 36

NCBI Description probable membrane protein YPL134c - yeast (Saccharomyces cerevisiae) >gi 1244780 (U43703) Lpillp [Saccharomyces

cerevisiae]

Seq. No. 41012

Seq. ID LIB3138-129-Q1-N1-G12

Method BLASTN
NCBI GI g667048
BLAST score 66
E value 6.0e-29
Match length 106
% identity 91

NCBI Description P.vulgaris mRNA for protein phosphatase 1 (PP1)

Seq. No. 41013

Seq. ID LIB3138-130-Q1-N1-A8

Method BLASTX
NCBI GI g136057
BLAST score 298
E value 3.0e-27
Match length 88
% identity 67

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi 99499 pir A32187 (S)-tetrahydroberberine oxidase -

Coptis japonica >gi_556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 41014

Seq. ID LIB3138-130-Q1-N1-B1

Method BLASTN
NCBI GI g210811
BLAST score 122
E value 4.0e-62
Match length 334
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41015

Seq. ID LIB3138-130-Q1-N1-C11

Method BLASTN
NCBI GI g169036
BLAST score 81
E value 1.0e-37
Match length 113
% identity 93

NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No. 41016

Seq. ID LIB3138-130-Q1-N1-D7

Method BLASTX NCBI GI g4097880

NCBI GI BLAST score

E value

Match length

138

66

7.0e-09



```
BLAST score
                  4.0e-43
E value
                  107
Match length
                  78
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  41017
Seq. No. -
                  LIB3138-130-Q1-N1-F12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q12147
                  233
BLAST score
                  1.0e-128
E value
                  325
Match length
                  93
% identity
                  Pea chloroplast genes for ATP synthetase subunits beta and
NCBI Description
                   epsilon (atpB and atpE)
                   41018
Seq. No.
                  LIB3138-130-Q1-N1-F7
Seq. ID
                  BLASTX
Method
                   q125578
NCBI GI
BLAST score
                   193
                   6.0e-15
E value
                   96
Match length
                   47
% identity
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi 167266 (M73707) phosphoribulokinase
                   [Mesembryanthemum crystallinum]
                   41019
Seq. No.
                   LIB3138-130-Q1-N1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4097880
BLAST score
                   462
                   2.0e-46
E value
                   118
Match length
                   77
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41020
Seq. No.
Seq. ID
                   LIB3139-001-Q1-N1-A4
Method
                   BLASTX
                   g2853078
NCBI GI
BLAST score
                   220
                   6.0e-18
E value
                   120
Match length
                   43
% identity
                   (AL021768) TMV resistance protein N-like [Arabidopsis
NCBI Description
                   thalianal
                   41021
Seq. No.
Seq. ID
                   LIB3139-001-Q1-N1-B11
Method
                   BLASTX
                   g3212869
```

6445



```
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  41022
Seq. No.
                  LIB3139-001-Q1-N1-B2
Seq. ID
Method
                  BLASTX
                  g4204289
NCBI GI
                  198
BLAST score
                  2.0e-15
E value
Match length
                  95
% identity
                  55
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  41023
                  LIB3139-001-Q1-N1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170065
BLAST score
                  184
E value
                  3.0e-99
                  244
Match length
                  18
% identity
NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP2)
                  gene, complete cds
                  41024
Seq. No.
                  LIB3139-001-Q1-N1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493129
BLAST score
                  136
                  1.0e-08
E value
Match length
                  57
                  58
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                  SUBUNIT) >qi 459198 (U07052) vacuolar H+-ATPase subunit B
                   [Gossypium hirsutum]
                  41025
Seq. No.
                  LIB3139-001-Q1-N1-D12
Seq. ID
                  BLASTN
Method
                  g210811
NCBI GI
                  137
BLAST score
                  5.0e-71
E value
Match length
                  360
                   87
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   41026
Seq. No.
Seq. ID
                  LIB3139-001-Q1-N1-E1
                  BLASTX
Method
                   g2827702
NCBI GI
BLAST score
                   289
                   5.0e-26
E value
                   55
Match length
```

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

89

% identity



```
41027
Seq. No.
                   LIB3139-001-Q1-N1-G2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g20901
BLAST score
                   100
                   6.0e-49
E value
Match length
                   152
                   91
% identity
NCBI Description Pisum sativum mRNA for manganese superoxide dismutase
Seq. No.
                   41028
                   LIB3139-002-Q1-N1-A1
Seq. ID
                   BLASTX
Method
                   q1706329
NCBI GI
                    645
BLAST score
                    1.0e-67
E value
Match length
                    142
% identity
                   PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
NCBI Description
                    >gi_2146788_pir__S65471 pyruvate decarboxylase (EC 4.1.1.1)
(clone PDC2) - Garden pea (fragment)
                    >gi 1177605_emb_CAA91445_ (Z66544) pyruvate decarboxylase
                    [Pisum sativum]
Seq. No.
                    41029
                    LIB3139-002-Q1-N1-A2
Seq. ID
                    BLASTN
Method
NCBI GI
                    g1763062
                    66
BLAST score
                    6.0e-29
E value
                    98
Match length
                    92
 % identity
                    Glycine max putative transcription factor SCOF-1 (scof-1)
NCBI Description
                    mRNA, complete cds
                    41030
 Seq. No.
                    LIB3139-002-Q1-N1-C10
 Seq. ID
 Method
                    BLASTN
                    g20556
 NCBI GI
 BLAST score
                    114
                    3.0e-57
 E value
                    322
 Match length
                    86
 % identity
 NCBI Description Petunia hsp70 gene
 Seq. No.
                    41031
                    LIB3139-002-Q1-N1-C3
 Seq. ID
                    BLASTX
 Method
                    g4097880
 NCBI GI
                    297
 BLAST score
                    9.0e-42
 E value
                    121
 Match length
                    64
 % identity
                    (U70866) polyprotein [Bean pod mottle virus]
```

41032 Seq. No.

NCBI Description

Method NCBI GI



```
LIB3139-002-Q1-N1-C7
Seq. ID
                  BLASTX
Method
                  g4417287
NCBI GI
                  307
BLAST score
                  3.0e-28
E value
Match length
                  95
% identity
                  61
                  (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
                  41033
Seq. No.
                  LIB3139-002-Q1-N1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2911797
                  149
BLAST score
                  5.0e-10
E value
                   64
Match length
% identity
                   (AF008183) 4-coumarate:CoA ligase 2 [Populus balsamifera
NCBI Description
                   subsp. trichocarpa X Populus deltoides]
                   41034
Seq. No.
                   LIB3139-002-Q1-N1-H12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q434905
                   63
BLAST score
                   7.0e-27
E value
                   209
Match length
                   87
% identity
                  A.thaliana (Columbia) gene for S18 ribosomal protein
NCBI Description
                   (1471bp)
                   41035
Seq. No.
                   LIB3139-003-P1-N1-C1
Seq. ID
Method
                   BLASTX
                   g2088647
NCBI GI
                   242
BLAST score
                   1.0e-20
E value
                   99
Match length
                   57
% identity
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   41036
Seq. No.
                   LIB3139-003-P1-N1-C5
Seq. ID
                   BLASTX
Method
                   g3114968
NCBI GI
                   178
BLAST score
                   3.0e-13
E value
                   86
Match length
                   43
% identity
                   (Y14997) prolidase [Suberites domuncula]
NCBI Description
                   41037
Seq. No.
                   LIB3139-003-P1-N1-D10
Seq. ID
                   BLASTX
```

g4539314



```
BLAST score
                  5.0e-17
E value
                  110
Match length
                  42
% identity
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]
                  41038
Seq. No.
                  LIB3139-003-P1-N1-D8
Seq. ID
                  BLASTX
Method
                  q283362
NCBI GI
BLAST score
                   308
                   2.0e-28
E value
Match length
                  111
% identity
                   51
NCBI Description tyrosine--tRNA ligase (EC 6.1.1.1) precursor, mitochondrial
                   - Podospora anserina
                   41039
Seq. No.
                   LIB3139-003-P1-N1-E2
Seq. ID
                   BLASTX
Method
                   g3935157
NCBI GI
                   263
BLAST score
                   4.0e-23
E value
Match length
                   82
% identity
                   54
NCBI Description (AC005106) T25N20.21 [Arabidopsis thaliana]
                   41040
Seq. No.
                   LIB3139-003-P1-N1-F2
Seq. ID
                   BLASTX
Method
                   q163575
NCBI GI
                   148
BLAST score
E value
                   1.0e-09
Match length
                   75
                   25
% identity
NCBI Description (M62429) polyubiquitin [Bos taurus]
                   41041
Seq. No.
                   LIB3139-003-P1-N1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1362060
                   177
BLAST score
                   5.0e-13
E value
Match length
                   63
% identity
NCBI Description dehydroquinase-shikimate dehydrogenase - garden pea
                   41042
Seq. No.
Seq. ID
                   LIB3139-003-P1-N1-F6
Method
                   BLASTN
NCBI GI
                   g403326
BLAST score
                   44.
                   1.0e-15
E value
Match length
                   120
```

NCBI Description T.repens TrMT1A mRNA for metallothionein-like protein

84

% identity

Seq. ID

Method



```
Seq. No.
                  LIB3139-003-P1-N1-F7
Seq. ID
                  BLASTN
Method
                  g210811
NCBI GI
                  129
BLAST score
                  2.0e-66
E value
                  269
Match length
                  90
% identity
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  41044
                  LIB3139-004-P1-N1-A10
Seq. ID
Method
                  BLASTX
                  g229707
NCBI GI
                  230
BLAST score
E value
                  3.0e-19
                  97
Match length
% identity
                  48
NCBI Description Bean pod mottle virus
Seq. No.
                  41045
                  LIB3139-004-P1-N1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541943
                  242
BLAST score
                  3.0e-23
E value
Match length
                  73
                  73
% identity
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
Seq. No.
                   41046
                  LIB3139-004-P1-N1-E5
Seq. ID
Method
                  BLASTN
                  q4097879
NCBI GI
BLAST score
                   33
                   5.0e-09
E value
                   100
Match length
                   91
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41047
Seq. No.
Seq. ID
                   LIB3139-004-P1-N1-F8
                   BLASTN
Method
                   g4097879
NCBI GI
BLAST score
                   90
                   5.0e-43
E value
                   238
Match length
                   84
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41048
Seq. No.
```

LIB3139-005-P1-N1-A1

BLASTX



```
a3522933
NCBI GI
BLAST score
                  371
                  1.0e-35
E value
Match length
                  82
                  79
% identity
                  (AC004411) putative anion exchange protein 3 [Arabidopsis
NCBI Description
                  thaliana]
                  41049
Seq. No.
                  LIB3139-005-P1-N1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432832
BLAST score
                  154
E value
                  1.0e-10
                  75
Match length
                  55
% identity
NCBI Description (AC006283) similar to protein Htf9C [Arabidopsis thaliana]
                  41050
Seq. No.
                  LIB3139-005-P1-N1-C6
Seq. ID
                  BLASTX
Method
                  g2961348
NCBI GI
                   245
BLAST score
                   6.0e-21
E value
Match length
                   116
                   44
% identity
                  (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
                   41051
Seq. No.
                   LIB3139-005-P1-N1-H8
Seq. ID
                   BLASTX
Method
                   q138364
NCBI GI
                   315
BLAST score
E value
                   5.0e-37
Match length
                   89
                   87
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle vīrus (straīn Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41052
Seq. No.
                   LIB3139-006-P1-N1-A7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2598656
                   53
BLAST score
                   3.0e-21
E value
                   113
Match length
% identity
NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
                   41053
Seq. No.
                   LIB3139-006-P1-N1-A8
Seq. ID
```

BLASTX Method NCBI GI q3860273 306 BLAST score 4.0e-28 E value



Match length % identity 53

(AC005824) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi_4314398_gb_AAD15608_ (AC006232) hypothetical protein

[Arabidopsis thaliana]

41054 Seq. No.

Seq. ID LIB3139-006-P1-N1-B8

Method BLASTN NCBI GI g642129 BLAST score 78 E value 5.0e-36

Match length 146 % identity 88

NCBI Description Arabidopsis thaliana AME1 mRNA for protein kinase, complete

Seq. No.

41055

Seq. ID LIB3139-006-P1-N1-B9

Method BLASTX NCBI GI g4097880 BLAST score 339 E value 6.0e-32 Match length 118 % identity 58

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 41056

Seq. ID LIB3139-006-P1-N1-C11

Method BLASTX NCBI GI g138364 BLAST score 213 2.0e-17 E value Match length 97

% identity 54

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir_ GNWXG7 genome polyprotein M -

bean pod mottle vīrus (straīn Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 41057

Seq. ID LIB3139-006-P1-N1-E11

Method BLASTN NCBI GI g4097879 BLAST score 87

E value 3.0e-41 Match length 267 % identity 83

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

Seq. No. 41058

Seq. ID LIB3139-006-P1-N1-E5

Method BLASTX NCBI GI g3935181 BLAST score 240 E value 2.0e-20



Match length 74 % identity

(AC004557) F17L21.24 [Arabidopsis thaliana] NCBI Description

Seq. No.

41059

Seq. ID

LIB3139-006-P1-N1-F7

Method NCBI GI BLASTX g4097880

BLAST score E value

402 2.0e-39

Match length % identity

116 72

NCBI Description

(U70866) polyprotein [Bean pod mottle virus]

Seq. No.

41060

Seq. ID

LIB3139-006-P1-N1-G9

Method NCBI GI BLASTN g2606080

BLAST score E value

66 5.0e-29

Match length % identity

166 85

NCBI Description Glycine max sucrose synthase (SS) mRNA, complete cds

Seq. No.

41061

Seq. ID

LIB3139-007-P1-N1-A11

Method NCBI GI BLAST score BLASTX g3176669 198

E value Match length

2.0e-15 68

% identity NCBI Description

47 (AC004393) End is cut off. [Arabidopsis thaliana]

Seq. No.

41062

Seq. ID

LIB3139-007-P1-N1-A4

Method NCBI GI BLASTX q2827143

BLAST score E value

304

Match length

6.0e-28

% identity

105 63

NCBI Description

(AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No.

41063

Seq. ID

LIB3139-007-P1-N1-C8 BLASTN

Method NCBI GI

q210811

BLAST score E value

116 1.0e-58

Match length % identity NCBI Description

274 Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No.

41064

```
LIB3139-007-P1-N1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q538502
                  254
BLAST score
                  5.0e-22
E value
                  74
Match length
% identity
NCBI Description (L36231) peroxidase [Stylosanthes humilis]
                  41065
Seq. No.
                  LIB3139-007-P1-N1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953458
                  242
BLAST score
E value
                  1.0e-20
Match length
                  51
% identity
NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]
                  41066
Seq. No.
                  LIB3139-007-P1-N1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4455330
BLAST score
                  220
                  5.0e-18
E value
                  76
Match length
% identity
NCBI Description (AL035525) contains EST gb:T44002 [Arabidopsis thaliana]
                   41067
Seq. No.
                  LIB3139-007-P1-N1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1675195
BLAST score
                   54
                   1.0e-21
E value
Match length
                   98
% identity
                   89
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                   complete cds
                   41068
Seq. No.
                   LIB3139-007-P1-N1-H6
Seq. ID
Method.
                   BLASTN
                   g19511
NCBI GI
                   101
BLAST score
                   1.0e-49
E value
Match length
                   253
% identity
                   85
NCBI Description L.polyphyllus mRNA for ribosomal protein S16
```

41069 Seq. No. Seq. ID LIB3139-008-P1-N1-C1 BLASTX Method

g4325371 NCBI GI 201 BLAST score 9.0e-16 E value 55 Match length



% identity 71
NCBI Description (AF128396) contains similarity to Medicago truncatula N7
protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No. 41070

Seq. ID LIB3139-008-P1-N1-C7

Method BLASTX
NCBI GI g4510376
BLAST score 231
E value 3.0e-19
Match length 77
% identity 58

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 41071

Seq. ID LIB3139-008-P1-N1-D2

Method BLASTX
NCBI GI g4097880
BLAST score 220
E value 5.0e-18
Match length 76
% identity 61

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 41072

Seq. ID LIB3139-008-P1-N1-E4

Method BLASTX
NCBI GI g3738301
BLAST score 235
E value 9.0e-20
Match length 99
% identity 45

NCBI Description (AC005309) putative zinc-finger protein [Arabidopsis thaliana] >gi_4249397 (AC006072) putative zinc-finger

protein (B-box zinc finger domain) [Arabidopsis thaliana]

Seq. No. 41073

Seq. ID LIB3139-008-P1-N1-F11

Method BLASTX
NCBI GI g2960358
BLAST score 207
E value 4.0e-22
Match length 107
% identity 55

NCBI Description (AJ224895) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa] >gi 2960360_emb_CAA12200_

(AJ224896) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa] >gi_3550590_emb_CAA11495_ (AJ223620) caffeoyl CoA 3-O-methyltransferase [Populus

balsamifera subsp. trichocarpa]

Seq. No. 41074

Seq. ID LIB3139-008-P1-N1-G11

MethodBLASTNNCBI GIg210811BLAST score173E value1.0e-92



```
Match length
                  89
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                  41075
                  LIB3139-008-P1-N1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1778095
BLAST score
                  268
E value
                  1.0e-23
Match length
                  89
% identity
                  (U64903) putative sugar transporter; member of major
NCBI Description
                  facilitative superfamily; integral membrane protein [Beta
                  vulgaris]
Seq. No.
                  41076
                  LIB3139-009-P1-N1-C4
Seq. ID
Method
                  BLASTN
                  q18745
NCBI GI
                  57
BLAST score
E value
                  9.0e-24
Match length
                  88
                  92
% identity
                  Soybean sc514 gene for lipoxygenase
NCBI Description
                   41077
Seq. No.
                  LIB3139-009-P1-N1-D9
Seq. ID
Method
                  BLASTX
                   g2578440
NCBI GI
BLAST score
                   301
E value
                   2.0e-27
Match length
                   119
% identity
                   46
                  (X67425) pectinesterase [Pisum sativum]
NCBI Description
                   41078
Seq. No.
                   LIB3139-009-P1-N1-E4
Seq. ID
                   BLASTX
Method
                   g2911075
NCBI GI
                   265
BLAST score
                   3.0e-23
E value
Match length
                   86
% identity
                   58
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41079
                   LIB3139-009-P1-N1-F12
Seq. ID
Method
                   BLASTN
```

Method BLASTN
NCBI GI 94218522
BLAST score 174
E value 4.0e-93
Match length 327
% identity 90

NCBI Description Pisum sativum mRNA for PPF-1 protein



```
41080
Seq. No.
                  LIB3139-009-P1-N1-F7
Seq. ID
                  BLASTN
Method
                  g210811
NCBI GI
                  40
BLAST score
E value
                  3.0e-13
                  60
Match length
% identity
                  92
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                   41081
                  LIB3139-010-P1-N1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                   103
E value
                   1.0e-50
Match length
                   251
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
Seq. No.
                   41082
                   LIB3139-010-P1-N1-H10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2738981
BLAST score
                   85
E value
                   4.0e-40
Match length
                   149
% identity
                   89
                  Glycine max cytochrome P450 monooxygenase CYP71A10
NCBI Description
                   (CYP71A10) mRNA, complete cds
                   41083
Seq. No.
Seq. ID
                   LIB3139-010-P1-N1-H8
Method
                   BLASTN
                   q210811
NCBI GI
                   147
BLAST score
                   5.0e-77
E value
                   271
Match length
                   89
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41084
Seq. No.
                   LIB3139-011-P1-N1-C4
Seq. ID
                   BLASTX
Method
                   g2642165
NCBI GI
BLAST score
                   247
                   9.0e-33
E value
```

119 Match length 59 % identity

(AC003000) hypothetical protein [Arabidopsis thaliana] NCBI Description

41085 Seq. No.

Seq. ID LIB3139-011-P1-N1-D4

Method BLASTN



```
q4097879
NCBI GI
                  168
BLAST score
                  1.0e-89
E value
Match length
                  344
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  41086
Seq. ID
                  LIB3139-011-P1-N1-E5
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  170
E value
                  9.0e-91
Match length
                  358
                  87
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
Seq. No.
                  41087
                  LIB3139-011-P1-N1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3702342
BLAST score
                  160
E value
                  6.0e-11
Match length
                  120
% identity
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
                  41088
Seq. No.
                  LIB3139-011-P1-N1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4097880
                  215
BLAST score
E value
                  1.0e-24
                  120
Match length
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
                  41089
Seq. No.
                  LIB3139-011-P1-N1-H10
Seq. ID
                  BLASTN
Method
                  g4097879
NCBI GI
                  151
BLAST score
                  2.0e-79
E value
Match length
                  335
                  86
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  41090
Seq. No.
Seq. ID
                  LIB3139-012-P1-N1-A2
```

Method BLASTX
NCBI GI g3925703
BLAST score 237
E value 1.0e-30
Match length 126

NCBI Description



```
% identity
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
                   41091
Seq. No.
                   LIB3139-012-P1-N1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1781326
BLAST score
                   347
E value
                   7.0e-33
Match length
                   103
% identity
NCBI Description (Y10464) peroxidase [Spinacia oleracea]
                   41092
Seq. No.
                   LIB3139-012-P1-N1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3023436
BLAST score
                   189
                   2.0e-14
E value
Match length
                   81
% identity
                   49
                   CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA
NCBI Description
                   3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT) >gi 857578
                   (U27116) caffeoyl-CoA 3-O-methyltransferase [Populus
                   tremuloides]
Seq. No.
                   41093
                   LIB3139-012-P1-N1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4154281
BLAST score
                   178
                   3.0e-13
E value
                   73
Match length
 % identity
                   51
NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
Seq. No.
                   41094
Seq. ID
                   LIB3139-013-P1-N1-A11
Method
                   BLASTX
NCBI GI
                   q4104931
BLAST score
                   219
E value
                   2.0e-20
Match length
                   100
 % identity
                   49
NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana]
 Seq. No.
                   41095
 Seq. ID
                   LIB3139-013-P1-N1-A3
 Method
                   BLASTX
 NCBI GI
                   g1072188
 BLAST score
                   306
                   4.0e-28
 E value
                   89
Match length
                   69
 % identity
```

(SP:P38992) [Caenorhabditis elegans]

(U40941) weak similarity to the S. cerevisiae SUR2 protein

Seq. No.

Seq. ID

Method

41101

BLASTN

LIB3139-014-P1-N1-D9



```
Seq. No.
                   41096
                  LIB3139-013-P1-N1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4138178
BLAST score
                  71
                  1.0e-31
E value
Match length
                  155
                  86
% identity
NCBI Description Malus domestica mRNA for elongation factor 1 alpha subunit
Seq. No.
Seq. ID
                  LIB3139-013-P1-N1-E12
Method
                  BLASTN
                  q408793
NCBI GI
BLAST score
                   189
E value
                  1.0e-102
                   344
Match length
% identity
                  Glycine soja chloroplast 3-omega faty acid desaturase
NCBI Description
                   (Fad3) mRNA, complete cds
                   41098
Seq. No.
Seq. ID
                   LIB3139-013-P1-N1-G12
Method
                  BLASTX
                  q4406778
NCBI GI
BLAST score
                   228
E value
                   6.0e-19
                   120
Match length
% identity
                   (AC006532) putative brassinosteroid insensitive protein
NCBI Description
                   [Arabidopsis thaliana]
                   41099
Seq. No.
Seq. ID
                   LIB3139-013-P1-N1-H11
Method
                   BLASTN
NCBI GI
                   q609224
BLAST score
                   91
E value
                   1.0e-43
Match length
                   259
% identity
                   84
                   P.sativum mRNA for SAMS-2 >gi 609558 gb L36681 PEADENSYNB
NCBI Description
                   Pisum sativum S-adenosylmethionine synthase mRNA, complete
                   cds
Seq. No.
                   41100
                   LIB3139-014-P1-N1-A8
Seq. ID
Method
                   BLASTX
                   g4097880
NCBI GI
BLAST score
                   415
                   7.0e-41
E value
                   106
Match length
                   76
% identity
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
```

6460



```
NCBI GI
                  q4388705
BLAST score
                  35
                  3.0e-10
E value
                  183
Match length
% identity
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  41102
Seq. No.
                  LIB3139-014-P1-N1-E6
Seq. ID .
Method
                  BLASTX
NCBI GI
                  q4097880
BLAST score
                  327
                  2.0e-30
E value
                  121
Match length
                  59
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                  41103
                  LIB3139-014-P1-N1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2598656
BLAST score
                  141
E value
                  2.0e-73
Match length
                  285
% identity
                  87
NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
                   41104
Seq. No.
                  LIB3139-014-P1-N1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                   q479144
BLAST score
                   208
E value
                   1.0e-113
Match length
                   293
% identity
                   95
NCBI Description G.max mRNA for ATP synthase subunit
Seq. No.
                   41105
                   LIB3139-014-P1-N1-F7
Seq. ID
Method
                   BLASTN
                   g210811
NCBI GI
BLAST score
                   132
E value
                   4.0e-68
Match length
                   332
                   85
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   41106
                   LIB3139-014-P1-N1-G4
Seq. ID
                   BLASTX
Method
                   g1403675
NCBI GI
                   309
BLAST score
                   2.0e-28
E value
                   106
Match length
```

6461

60

% identity



88

% identity

NCBI Description

```
NCBI Description (U41323) beta-1,3-glucanase [Glycine max]
                  41107
Seq. No.
                  LIB3139-015-P1-N1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4097879
                  127
BLAST score
                   5.0e-65
E value
                   239
Match length
                   88
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41108
Seq. No.
                   LIB3139-015-P1-N1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g138364
BLAST score
                   461
                   3.0e-46
E value
                   110
Match length
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi 75639 pir__GNWXG7 genome polyprotein M -
                   bean pod mottle vīrus (straīn Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41109
Seq. No.
                   LIB3139-015-P1-N1-H10
Seq. ID
Method
                   BLASTX
                   g4097880
NCBI GI
                   190
BLAST score
                   6.0e-15
E value
Match length
                   45
% identity
                   82
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41110
Seq. No.
                   LIB3139-016-P1-N1-B6
Seq. ID
Method
                   BLASTN
                   g1518539
NCBI GI
                   329
BLAST score
                   0.0e+00
E value
                   349
Match length
                   99
% identity
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
Seq. No.
                   41111
                   LIB3139-016-P1-N1-D11
Seq. ID
                   BLASTN
Method
                   q210811
NCBI GI
                   136
BLAST score
                   1.0e-70
E value
                   272
Match length
```

6462

complete middle component (M) RNA

Bean pod mottle virus coat protein gene, complete cds,

Seq. No.

Seq. ID

41117

LIB3139-016-P1-N1-H6



```
Seq. No.
                    41112
 Seq. ID
                   LIB3139-016-P1-N1-E5
 Method
                   BLASTX
 NCBI GI
                   g4467359
 BLAST score
                   260
 E value
                   1.0e-22
 Match length
                   66
 % identity
                   77
                   (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
 NCBI Description
                   thaliana]
 Seq. No.
                   41113
 Seq. ID
                   LIB3139-016-P1-N1-F12
Method
                   BLASTN
NCBI GI
                   g303900
BLAST score
                   87
E value
                   3.0e-41
Match length
                   335
 % identity
                   50
NCBI Description Soybean gene for ubiquitin, complete cds
Seq. No.
                   41114
Seq. ID
                   LIB3139-016-P1-N1-F9
Method
                   BLASTX
NCBI GI
                   q2764524
BLAST score
                   200
E value
                   1.0e-15
Match length
                   59
% identity
                   68
NCBI Description
                  (AJ000520) Rieske iron-sulfur protein Tic55 [Pisum sativum]
Seq. No.
                   41115
Seq. ID
                   LIB3139-016-P1-N1-G1
Method
                   BLASTX
NCBI GI
                   q138364
BLAST score
                   206
E value
                   2.0e-16
Match length
                   96
% identity
                   52
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle vīrus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  41116
Seq. ID
                  LIB3139-016-P1-N1-G8
Method
                  BLASTX
NCBI GI
                  g1781299
BLAST score
                  231
E value
                  3.0e-19
Match length
                  66
% identity
                  73
NCBI Description
                  (Y09506) transformer-SR ribonucleoprotein [Nicotiana
                  tabacum]
```

6463



BLASTX Method NCBI GI g229707 BLAST score 227 1.0e-18 E value Match length 64 67 % identity

NCBI Description Bean pod mottle virus

Seq. No.

41118

Seq. ID

LIB3139-017-P1-N1-E6

Method BLASTX NCBI GI g3860274 BLAST score 227 E value 8.0e-19 Match length 74 % identity 66

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

>gi_4314397_gb AAD15607 (AC006232) putative zinc finger

protein [Arabidopsis thaliana]

Seq. No. 41119

Seq. ID LIB3139-017-P1-N1-G8

Method BLASTN NCBI GI g210811

BLAST score 43

4.0e-15 E value 202 Match length 86 % identity

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41120

Seq. ID LIB3139-017-P1-N1-H5

Method BLASTN NCBI GI g2304954 57 BLAST score E value 2.0e-23

Match length 97 % identity 90

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No. 41121

Seq. ID LIB3139-017-P1-N1-H9

Method BLASTX NCBI GI g2979554 BLAST score 494 4.0e-50 E value Match length 125 % identity 63

NCBI Description (AC003680) CDC4 like protein [Arabidopsis thaliana]

Seq. No. 41122

Seq. ID LIB3139-018-P1-N1-A6

Method BLASTX NCBI GI q4097880 BLAST score 285 E value 5.0e-26



```
Match length
% identity
                  79
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                  41123
                  LIB3139-018-P1-N1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q414833
BLAST score
                  45
                  3.0e-16
E value
Match length
                  73
                  97
% identity
NCBI Description
                  Glycine max (Rab7p) mRNA, complete cds
Seq. No.
                  41124
Seq. ID
                  LIB3139-018-P1-N1-D11
Method
                  BLASTX
                  g138364
NCBI GI
BLAST score
                  243
                  2.0e-36
E value
Match length
                  115
% identity
                  71
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  41125
Seq. ID
                  LIB3139-018-P1-N1-E3
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                   98
                   6.0e-48
E value
Match length
                  266
                  85
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  41126
Seq. ID
                  LIB3139-018-P1-N1-E4
Method
                  BLASTX
NCBI GI
                  q3075391
BLAST score
                  120
E value
                  8.0e-10
Match length
                  55
                   69
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41127
                  LIB3139-018-P1-N1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q138364
BLAST score
                  180
E value
                  8.0e-14
Match length
                   63
% identity
                   62
```

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

```
PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
                  41128
Seq. No.
                  LIB3139-018-P1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q229708
BLAST score
                  150
                  8.0e-10
E value
Match length
                  45
                  69
% identity
NCBI Description
                  Bean pod mottle virus
Seq. No.
                  41129
Seq. ID
                  LIB3139-018-P1-N1-H10
Method
                  BLASTN
NCBI GI
                  g1370151
BLAST score
                  100
E value
                  5.0e-49
Match length
                  188
                  88
% identity
                  L.japonicus mRNA for small GTP-binding protein, RAB11F
NCBI Description
Seq. No.
                  41130
Seq. ID
                  LIB3139-018-P1-N1-H12
Method
                  BLASTX
NCBI GI
                  g2624883
BLAST score
                  210
E value
                  9.0e-17
                  85
Match length
                  45
% identity
                  Chain A, Recombinant Rat Liver 3-Alpha-Hydroxysteroid
NCBI Description
                  Dehydrogenase (3-Alpha-Hsd) Complexed With Nadp And
                  Testosterone >gi_2624884_pdb_1AFS_B Chain B, Recombinant
                  Rat Liver 3-Alpha-Hydroxysteroid Dehydrogenase
                   (3-Alpha-Hsd) Complexed With Nadp And Testosterone
                  41131
Seq. No.
Seq. ID
                  LIB3139-018-P1-N1-H5
Method
                  BLASTX
                  g4097880
NCBI GI
BLAST score
                  282
                  2.0e-25
E value
                  89
Match length
                  66
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                  41132
                  LIB3139-018-P1-N1-H8
Seq. ID
```

Method BLASTX
NCBI GI g1708313
BLAST score 287
E value 6.0e-26

Match length 114 % identity 56

NCBI Description HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396_bbs_163637

(S77849) heat-shock Protein=HSP81-3 [Arabidopsis thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis thaliana]

Seq. No. 41133

Seq. ID LIB3139-020-P1-N1-B3

Method BLASTN
NCBI GI g4097879
BLAST score 120
E value 7.0e-61
Match length 343
% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41134

Seq. ID LIB3139-020-P1-N1-D12

Method BLASTX
NCBI GI g2652938
BLAST score 360
E value 2.0e-34
Match length 98
% identity 45

NCBI Description (Z47554) orf [Zea mays]

Seq. No. 41135

Seq. ID LIB3139-020-P1-N1-D6

Method BLASTN
NCBI GI g2317899
BLAST score 106
E value 1.0e-52
Match length 318
% identity 84

NCBI Description Glycine max Sali3-2 mRNA, complete cds

Seq. No. 41136

Seq. ID LIB3139-020-P1-N1-E1

Method BLASTN
NCBI GI g4097879
BLAST score 107
E value 4.0e-53
Match length 327
% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

41137

Seq. ID LIB3139-020-P1-N1-H5

Method BLASTX
NCBI GI g4097880
BLAST score 174
E value 9.0e-14
Match length 53
% identity 70

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

41138

```
LIB3139-021-P1-N1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g549063
BLAST score
                   210
                   6.0e-17
E value
                   77
Match length
                   56
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   41139
Seq. No.
Seq. ID
                   LIB3139-021-P1-N1-D2
                   BLASTX
Method
NCBI GI
                   g1421730
                   205
BLAST score
                   2.0e-16
E value
                   62
Match length
                   55
% identity
NCBI Description
                   (U43082) RF2 [Zea mays]
Seq. No.
                   41140
Seq. ID
                   LIB3139-021-P1-N1-E10
                   BLASTX
Method
NCBI GI
                   q4416307
BLAST score
                   142
                   8.0e-09
E value
                   100
Match length
                   31
% identity
                   (AF105716) hypothetical protein [Zea mays]
NCBI Description
                    41141
Seq. No.
Seq. ID
                   LIB3139-022-P1-N1-B5
Method
                   BLASTX
NCBI GI
                    g2281090
BLAST score
                    194
E value
                    6.0e-15
Match length
                    48
                    73
% identity
                   (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    41142
Seq. No.
                   LIB3139-022-P1-N1-F1
Seq. ID
Method
                   BLASTX
                    g2980770
NCBI GI
BLAST score
                    318
E value
                    2.0e-29
Match length
                    90
% identity
                    68
                   (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                    41143
Seq. No.
```

LIB3139-022-P1-N1-G1 Seq. ID

Method BLASTN NCBI GI q4097879 BLAST score 151



E value 2.0e-79 Match length 351 % identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

Seq. No. 41144

LIB3139-022-P1-N1-G6 Seq. ID

Method BLASTN NCBI GI q210811 BLAST score 111 E value 1.0e-55 Match length 323 84 % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

Seq. No. 41145

LIB3139-023-P1-N1-C7 Seq. ID

Method BLASTN g4097879 NCBI GI 139 BLAST score E value 3.0e-72 Match length 355 % identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

Seq. No. 41146

LIB3139-023-P1-N1-D11 Seq. ID

Method BLASTX NCBI GI g4097880 BLAST score 164 E value 5.0e-25 Match length 83

% identity 76

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No.

LIB3139-023-P1-N1-D5 Seq. ID

41147

Method BLASTX g1717755 NCBI GI 205 BLAST score E value 3.0e-16 106 Match length % identity 42

TROPINONE REDUCTASE HOMOLOG (P29X) >gi 539028 pir__C48674 NCBI Description

tropinone reductase homolog - jimsonweed >gi_424158 (L20475) 29kDa protein; high homology to aa sequence of

tropinone reductases [Datura stramonium]

41148 Seq. No.

Seq. ID LIB3139-023-P1-N1-E10

BLASTX Method g3242785 NCBI GI 186 BLAST score E value 2.0e-17



```
Match length
% identity
                   69
NCBI Description
                   (AF055355) respiratory burst oxidase protein C [Arabidopsis
                   thaliana]
Seq. No.
                   41149
Seq. ID
                   LIB3139-023-P1-N1-G10
Method
                   BLASTX
NCBI GI
                   g138364
BLAST score
                   367
E value
                   3.0e-35
Match length
                   109
% identity
                   70
NCBI Description
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                   PROTEIN VP23) >gi 75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                   41150
Seq. ID
                  LIB3139-023-P1-N1-G4
Method
                  BLASTX
NCBI GI
                  g2708743
BLAST score
                  178
E value
                   4.0e-13
Match length
                   95
% identity
                   35
                   (AC003952) putative Tal-1-like reverse transcriptase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  41151
Seq. ID
                  LIB3139-023-P1-N1-H10
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  138
E value
                  1.0e-09
Match length
                  76
% identity
                  53
NCBI Description
                 (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  41152
                  LIB3139-023-P1-N1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2618684
BLAST score
                  161
E value
                  4.0e-11
Match length
                  110
% identity
                  40
NCBI Description
                  (AC002510) putative
                  UDP-N-acetylglucosamine--dolichyl-phosphate
                  N-acetylglucosaminephosphotransferase [Arabidopsis
```

thaliana] >gi_3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate

N-acetylglucosaminephosphotransferase [Arabidopsis

thaliana 1

Seq. No. 41153

Seq. ID LIB3139-023-P1-N1-H4

```
BLASTX
Method
NCBI GI
                  q4432857
BLAST score
                  170
                   4.0e-12
E value
                  102
Match length
% identity
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
                   41154
Seq. No.
                  LIB3139-024-P1-N1-C11
Seq. ID
```

Method BLASTN NCBI GI q206371 BLAST score 99 E value 2.0e-48 274 Match length 98 % identity

NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks

Seq. No. 41155 LIB3139-024-P1-N1-E11 Seq. ID BLASTN Method g206371 NCBI GI BLAST score 103 E value 1.0e-50 299 Match length

% identity NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks

41156 Seq. No. LIB3139-024-P1-N1-F4 Seq. ID BLASTX Method

98

q3641252 NCBI GI 191 BLAST score E value 1.0e-14 91 Match length % identity 32

(AF053127) leucine-rich receptor-like protein kinase [Malus NCBI Description

domestica]

Seq. No. 41157

LIB3139-024-P1-N1-G4 Seq. ID

Method BLASTX NCBI GI g4097880 BLAST score 407 E value 6.0e-40 114 Match length % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No. 41158

LIB3139-024-P1-N1-H2 Seq. ID

Method BLASTX g466172 NCBI GI 153 BLAST score 3.0e-10 E value 75 Match length 43 % identity

6471



NCBI Description GTP-BINDING PROTEIN YPTM2 >gi_283056_pir__B38202 ypt family - maize >gi 287835_emb_CAA44919_ (X63278) yptm2 [Zea mays]

Seq. No. 41159

Seq. ID LIB3139-025-P1-N1-A9

Method BLASTN
NCBI GI g467616
BLAST score 93
E value 8.0e-45
Match length 201
% identity 87

NCBI Description A.alternata AltA6 ribosomal protein mRNA for minor allergen

Seq. No. 41160

Seq. ID LIB3139-025-P1-N1-C11

Method BLASTX
NCBI GI g1418990
BLAST score 276
E value 1.0e-25
Match length 118
% identity 50

NCBI Description (Z75524) unknown [Lycopersicon esculentum]

Seq. No. 41161

Seq. ID LIB3139-025-P1-N1-C2

Method BLASTX
NCBI GI g3355480
BLAST score 270
E value 1.0e-23
Match length 91
% identity 56

NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis

thaliana]

Seq. No. 41162

Seq. ID LIB3139-025-P1-N1-D2

Method BLASTX
NCBI GI g124224
BLAST score 215
E value 2.0e-17
Match length 42
% identity 95

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi_100345_pir__S21060 translation initiation factor eIF-5A

- common tobacco >gi 19887 emb CAA45105 (X63543)

eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 41163

Seq. ID LIB3139-025-P1-N1-F5

Method BLASTX
NCBI GI g4454019
BLAST score 192
E value 5.0e-17
Match length 100
% identity 51

NCBI Description (AL035396) SRG1-like protein [Arabidopsis thaliana]

% identity

Seq. No.

NCBI Description

41169



```
Seq. No.
Seq. ID
                  LIB3139-025-P1-N1-F6
                  BLASTX
Method
                   g629561
NCBI GI
BLAST score
                   112
                   2.0e-10
E value
                   105
Match length
                   41
% identity
                   SRG1 protein - Arabidopsis thaliana
NCBI Description
                   >gi 479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis
                   thaliana]
                   41165
Seq. No.
                   LIB3139-025-P1-N1-F7
Seq. ID
                   BLASTX
Method
                   g2979547
NCBI GI
                   230
BLAST score
                   4.0e-19
E value
Match length
                   123
% identity
                   42
                   (AC003680) putative 7-ethoxycoumarin O-deethylase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   41166
                   LIB3139-025-P1-N1-H12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q255407
BLAST score
                   298
E value
                   1.0e-167
Match length
                   310
% identity
                   11
                   repetitive proline-rich protein {cDNA clone 1A10-2}
NCBI Description
                   [Glycine max=soybeans, axes germinated for 31 hours, mRNA,
                   943 nt]
                   41167
Seq. No.
Seq. ID
                   LIB3139-025-P1-N1-H9
                   BLASTX
Method
                   q4538939
NCBI GI
                   385
BLAST score
E value
                   2.0e-37
Match length
                   115
% identity
                   (AL049483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   41168
Seq. No.
Seq. ID
                   LIB3139-026-P1-N1-A6
Method
                   BLASTX
NCBI GI
                   g3426038
BLAST score
                   163
E value
                   2.0e-11
Match length
                   99
                   44
```

(AC005168) unknown protein [Arabidopsis thaliana]



```
LIB3139-026-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2997593
                  338
BLAST score
                  8.0e-32
E value
                  114
Match length
                  56
% identity
                  (AF020816) glucose-6-phosphate/phosphate-translocator
NCBI Description
                  precursor [Solanum tuberosum]
Seq. No.
                  41170
Seq. ID
                  LIB3139-026-P1-N1-G10
                  BLASTX
Method
                  g2244816
NCBI GI
                  205
BLAST score
                  3.0e-16
E value
                  58
Match length
                  78
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  41171
                  LIB3139-027-P1-N1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567282
                  198
BLAST score
                   4.0e-32
E value
Match length
                  103
                  70
% identity
NCBI Description (AC006841) putative DNAJ protein [Arabidopsis thaliana]
Seq. No.
                   41172
Seq. ID
                  LIB3139-027-P1-N1-C10
Method
                  BLASTX
NCBI GI
                   g2970051
BLAST score
                   338
E value
                   7.0e-32
Match length
                   88
                   77
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
                   41173
Seq. No.
                  LIB3139-027-P1-N1-D6
Seq. ID
Method
                  BLASTN
                   g210811
NCBI GI
BLAST score
                   122
E value
                   4.0e-62
Match length
                   303
% identity
                   87
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   41174
                  LIB3139-027-P1-N1-D8
Seq. ID
                   BLASTN
Method
```

.....

NCBI GI g3192930 BLAST score 221 E value 1.0e-121



Match length 225 % identity 100

NCBI Description Glycine max clone a2 malate dehydrogenase (Mdh-1) mRNA, nuclear gene encoding mitochondrial protein, partial cds

Seq. No. 41175

Seq. ID LIB3139-027-P1-N1-E12

Method BLASTN
NCBI GI g210811
BLAST score 63
E value 6.0e-27
Match length 193

E value 6.06-2 Match length 193 % identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41176

Seq. ID LIB3139-027-P1-N1-E4

Method BLASTX
NCBI GI g3021348
BLAST score 392
E value 4.0e-38
Match length 96
% identity 81

NCBI Description (AJ004961) ribosomal protein L18 [Cicer arietinum]

Seq. No. 41177

Seq. ID LIB3139-027-P1-N1-F4

Method BLASTX
NCBI GI 94469008
BLAST score 358
E value 3.0e-34
Match length 120
% identity 59

NCBI Description (AL035602) UDP rhamnose--anthocyanidin-3-glucoside

rhamnosyltransferase-like protein [Arabidopsis thaliana]

Seq. No. 41178

Seq. ID LIB3139-028-P1-N1-A4

Method BLASTX
NCBI GI g229707
BLAST score 309
E value 1.0e-28
Match length 74
% identity 82

NCBI Description Bean pod mottle virus

Seq. No. 41179

Seq. ID LIB3139-028-P1-N1-A8

Method BLASTN
NCBI GI g1778375
BLAST score 88
E value 7.0e-42
Match length 168
% identity 88

NCBI Description Pisum sativum PsRT17-1 mRNA, complete cds

Seq. ID Method



```
Seq. No.
Seq. ID
                  LIB3139-028-P1-N1-D4
                  BLASTN
Method
NCBI GI
                  g4097879
                  113
BLAST score
                  9.0e-57
E value
Match length
                  317
                  84
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
                  41181
Seq. No.
                  LIB3139-028-P1-N1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4567269
                  208
BLAST score
                  2.0e-18
E value
                  78
Match length
                   65
% identity
                 (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                  41182
Seq. No.
                  LIB3139-028-P1-N1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4544443
BLAST score
                   176
                   8.0e-13
E value
                   58
Match length
                   67
% identity
                   (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   41183
Seq. No.
                   LIB3139-028-P1-N1-G12
Seq. ID
                   BLASTN
Method
                   g2995694
NCBI GI
BLAST score
                   39
                   1.0e-12
E value
                   51
Match length
                   94
% identity
                   Glomerella cingulata pectate lyase B (PELB) gene, complete
NCBI Description
                   41184
Seq. No.
                   LIB3139-028-P1-N1-H10
Seq. ID
                   BLASTN
Method
NCBI GI
                   q456567
BLAST score
                   104
                   2.0e-51
E value
Match length
                   215
                   89
% identity
                   Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                   cds
                   41185
Seq. No.
```

LIB3139-028-P1-N1-H6

BLASTX



```
g4510376
NCBI GI
                    163
 BLAST score
                    3.0e-11
 E value
                    52
 Match length
                    63
  % identity
 NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                    41186
 Seq. No.
                    LIB3139-029-P1-N1-B5
 Seq. ID
 Method
                    BLASTN
                    q1177602
 NCBI GI
 BLAST score
                    81
                    1.0e-37
 E value
                    180
 Match length
  % identity
                    87
  NCBI Description P.sativum mRNA for pyruvate decarboxylase (PDC1)
                    41187
  Seq. No.
                    LIB3139-029-P1-N1-C10
  Seq. ID
                    BLASTX
  Method
                    q4580471
  NCBI GI
  BLAST score
                    201
  E value
                    3.0e-19
                    105
  Match length
                    53
  % identity
  NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
  Seq. No.
                    41188
                    LIB3139-029-P1-N1-D1
  Seq. ID
                    BLASTN
  Method
                    g2317899
  NCBI GI
                    33
  BLAST score
                    2.0e-09
  E value
                    85
  Match length
                    85
  % identity
  NCBI Description Glycine max Sali3-2 mRNA, complete cds
                    41189
  Seq. No.
                    LIB3139-029-P1-N1-D9
  Seq. ID
                    BLASTN
  Method
                    g210811
  NCBI GI
  BLAST score
                    75
                     3.0e-34
  E value
                     95
  Match length
                     95
  % identity
                    Bean pod mottle virus coat protein gene, complete cds,
  NCBI Description
                    complete middle component (M) RNA
                     41190
  Seq. No.
                    LIB3139-029-P1-N1-E12
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                     q138364
                     142
  BLAST score
                     3.0e-09
  E value
  Match length
                     52
                     60
  % identity
  NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
```

7, **



PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

 Seq. No.
 41191

 Seq. ID
 LIB3139-029-P1-N1-E6

 Method
 BLASTX

 NCBI GI
 g3402679

 BLAST score
 196

 E value
 1.0e-29

Match length 103 % identity 75

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 41192

Seq. ID LIB3139-029-P1-N1-F12

Method BLASTN
NCBI GI g2317899
BLAST score 309
E value 1.0e-173
Match length 331
% identity 99

NCBI Description Glycine max Sali3-2 mRNA, complete cds

Seq. No. 41193

Seq. ID LIB3139-029-P1-N1-H5

Method BLASTN
NCBI GI g210811
BLAST score 101
E value 1.0e-49
Match length 293
% identity 89

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41194

Seq. ID LIB3139-030-P1-N1-A12

Method BLASTN
NCBI GI g170089
BLAST score 141
E value 2.0e-73
Match length 209
% identity 96

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 41195

Seq. ID LIB3139-030-P1-N1-H11

Method BLASTX
NCBI GI 94097880
BLAST score 369
E value 2.0e-35
Match length 104
% identity 73

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 41196

Seq. ID LIB3139-030-P1-N1-H2

E value

Match length

1.0e-55

203



```
BLASTX
Method
NCBI GI
                  g229708
BLAST score
                   269
E value
                   8.0e-24
                   85
Match length
                   62
% identity
NCBI Description Bean pod mottle virus
                   41197
Seq. No.
Seq. ID
                  LIB3139-031-P1-N1-B1
                  BLASTN
Method
                  g1431628
NCBI GI
BLAST score
                   259
                   1.0e-144
E value
                   384
Match length
                   91
% identity
NCBI Description V.radiata mRNA for pectinacetylesterase
                   41198
Seq. No.
Seq. ID
                  LIB3139-031-P1-N1-C9
Method
                  {\tt BLASTN}
NCBI GI
                   g210811
                   176
BLAST score
                   2.0e-94
E value
                   316
Match length
                   89
% identity
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
                   41199
Seq. No.
Seq. ID
                   LIB3139-031-P1-N1-G12
Method
                   BLASTX
                   g2746086
NCBI GI
BLAST score
                   398
                   7.0e-39
E value
                   119
Match length
                   63
% identity
                   (AF025292) putative high-affinity potassium transporter
NCBI Description
                   [Hordeum vulgare]
Seq. No.
                   41200
                   LIB3139-031-P1-N1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4467095
BLAST score
                   257
                   3.0e-22
E value
Match length
                   91
                   56
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   41201
Seq. No.
Seq. ID
                   LIB3139-031-P1-N1-H6
                   BLASTN
Method
NCBI GI
                   q4097879
BLAST score
                   111
```



% identity 89

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41202

Seq. ID LIB3139-032-P1-N1-A7

Method BLASTN
NCBI GI g170091
BLAST score 149
E value 3.0e-78
Match length 293
% identity 88

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 41203

Seq. ID LIB3139-032-P1-N1-C8

Method BLASTX
NCBI GI g3914161
BLAST score 400
E value 4.0e-39
Match length 124
% identity 70

NCBI Description CYTOCHROME P450 55A2 (CYTOCHROME P450NOR1)

>gi 1107453 dbj BAA11408 (D78511) cytochrome P450nor1

[Cylindrocarpon lichenicola]

Seq. No. 41204

Seq. ID LIB3139-032-P1-N1-G11

Method BLASTN
NCBI GI g2677823
BLAST score 48
E value 5.0e-18
Match length 200
% identity 81

NCBI Description Prunus armeniaca abscisic stress ripening protein homolog

mRNA, complete cds

Seq. No. 41205

Seq. ID LIB3139-032-P1-N1-H10

Method BLASTX
NCBI GI g4097880
BLAST score 143
E value 2.0e-09
Match length 53
% identity 60

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

41206

Seq. ID LIB3139-033-P1-N1-C6

Method BLASTX
NCBI GI g4467126
BLAST score 400
E value 4.0e-39
Match length 119
% identity 66

NCBI Description (AL035538) guanine nucleotide-exchange protein-like



[Arabidopsis thaliana]

```
41207
Seq. No.
Seq. ID
                  LIB3139-033-P1-N1-E5
                  BLASTN
Method
                  q210811
NCBI GI
BLAST score
                  78
                  7.0e-36
E value
                  110
Match length
                  93
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                  41208
                  LIB3139-033-P1-N1-F4
Seq. ID
Method
                  BLASTN
                  g206371
NCBI GI
BLAST score
                  103
                  1.0e-50
E value
Match length
                  194
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene: exons IV, V and flanks
Seq. No.
                  41209
                  LIB3139-033-P1-N1-F7
Seq. ID
                  BLASTX
Method
                  q3885341
NCBI GI
                   385
BLAST score
E value
                   2.0e-37
                  82
Match length
% identity
                  (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41210
                  LIB3139-033-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g730452
BLAST score
                   442
E value
                   5.0e-44
Match length
                   111
% identity
                   77
                   60S RIBOSOMAL PROTEIN L13A (RP22) >gi_626321_pir__S48401
NCBI Description
                   ribosomal protein L16.e.A, cytosolic - yeast (Saccharomyces
                   cerevisiae) >gi_557790 emb CAA86145_ (Z38059) orf, len:
                   199, CAI: 0.62, predicted to be spliced, similar to A44367
                   A44367 P23=TUMOR-SPECIFIC TRANSPLANTATION ANTIGEN and
                   ribosomal proteins [Saccharomyces cerevisiae]
                   41211
Seq. No.
Seq. ID
                   LIB3139-033-P1-N1-H11
                   BLASTN
Method
                   g210811
NCBI GI
BLAST score
                   119
                   2.0e-60
E value
                   251
Match length
```

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

87

% identity



complete middle component (M) RNA

```
Seq. No.
                   41212
Seq. ID
                   LIB3139-033-P1-N1-H4
Method
                   BLASTX
NCBI GI
                   g3641838
BLAST score
                   287
E value
                   9.0e-26
Match length
                   79
% identity
                   68
NCBI Description
                   (AL023094) putative protein (fragment) [Arabidopsis
                   thaliana]
Seq. No.
                   41213
Seq. ID
                   LIB3139-034-P1-N1-A8
Method
                   BLASTN
NCBI GI
                   g4567090
BLAST score
                   80
E value
                   5.0e-37
Match length
                   240
% identity
                   92
NCBI Description
                   Glycine max SNF-1-like serine/threonine protein kinase
                   mRNA, complete cds
Seq. No.
                   41214
Seq. ID
                   LIB3139-034-P1-N1-B11
Method
                   BLASTX
NCBI GI
                   g4545262
BLAST score
                   195
E value
                   4.0e-15
Match length
                   57
% identity
                   65
NCBI Description
                   (AF118230) metallothionein-like protein [Gossypium
                   hirsutum]
Seq. No.
                   41215
Seq. ID
                   LIB3139-034-P1-N1-B4
Method
                   BLASTX
NCBI GI
                   g4235641
BLAST score
                   219
E value
                   7.0e-18
Match length
                   69
% identity
                   52
NCBI Description (AF119040) NLOD [Lycopersicon esculentum]
Seq. No.
                   41216
Seq. ID
                  LIB3139-034-P1-N1-D6
Method
                  BLASTX
NCBI GI
                  g3914359
BLAST score
                  429
E value
                  2.0e-42
Match length
                  98
% identity
                  86
NCBI Description
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
```

>gi_1928979 (U92656) phospholipase D [Vigna unguiculata]

NCBI GI

BLAST score



```
Seq. No.
                  LIB3139-034-P1-N1-E11
Seq. ID
                  BLASTX
Method
                  g2464890
NCBI GI
                  234
BLAST score
                  1.0e-19
E value
                  74
Match length
                  57
% identity
NCBI Description (Z99707) TINY-like protein [Arabidopsis thaliana]
                  41218
Seq. No.
                  LIB3139-034-P1-N1-F11
Seq. ID
                  BLASTX
Method
                  q3258571
NCBI GI
                  291
BLAST score
                  4.0e-30
E value
                  100
Match length
                  76
% identity
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]
                  41219
Seq. No.
                  LIB3139-034-P1-N1-F12
Seq. ID
Method
                  BLASTX
                  q3242785
NCBI GI
                  311
BLAST score
                  1.0e-28
E value
                  118
Match length
                   59
% identity
                   (AF055355) respiratory burst oxidase protein C [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   41220
                   LIB3139-034-P1-N1-G8
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   33
BLAST score
                   4.0e-09
E value
                   65
Match length
                   88
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   41221
                   LIB3139-035-P1-N1-D12
Seq. ID
                   BLASTX
Method
                   g229707
NCBI GI
                   142
BLAST score
                   6.0e-09
E value
                   85
Match length
                   52
% identity
NCBI Description Bean pod mottle virus
                   41222
Seq. No.
Seq. ID
                   LIB3139-035-P1-N1-H6
Method
                   BLASTX
```

6483

q2160175

146



E value 2.0e-09 Match length 77 % identity 44

NCBI Description (AC000132) Strong similarity to Dianthus cysteine proteinase (gb_U17135). [Arabidopsis thaliana]

Seq. No. 41223

Seq. ID LIB3139-036-P1-N1-A10

Method BLASTX
NCBI GI g4455210
BLAST score 150
E value 1.0e-09
Match length 112
% identity 41

NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis

thaliana]

Seq. No. 41224

Seq. ID LIB3139-036-P1-N1-C7

Method BLASTX
NCBI GI g229708
BLAST score 213
E value 1.0e-17
Match length 67
% identity 66

NCBI Description Bean pod mottle virus

Seq. No. 41225

Seq. ID LIB3139-036-P1-N1-D11

Method BLASTN
NCBI GI g3702736
BLAST score 36
E value 9.0e-11
Match length 80
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRI1, complete sequence [Arabidopsis thaliana]

Seq. No. 41226

Seq. ID LIB3139-036-P1-N1-F2

Method BLASTX
NCBI GI g3927825
BLAST score 352
E value 2.0e-33
Match length 146
% identity 52

NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase

[Arabidopsis thaliana]

Seq. No. 41227

Seq. ID LIB3139-036-P1-N1-G2

Method BLASTX
NCBI GI g131381
BLAST score 178
E value 3.0e-18
Match length 130
% identity 45



OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 99745 pir S11852

photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33

kDa oxygen-evolving protein [Arabidopsis thaliana]

41228 Seq. No.

Seq. ID LIB3139-036-P1-N1-H5

Method BLASTN NCBI GI q4097879 108 BLAST score 8.0e-54 E value 315 Match length

84 % identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

41229 Seq. No.

Seq. ID LIB3139-037-P1-N1-B3

Method BLASTX g1903359 NCBI GI 338 BLAST score 8.0e-32 E value 124 Match length 57 % identity

NCBI Description (AC000104) F19P19.21 [Arabidopsis thaliana]

41230 Seq. No.

LIB3139-037-P1-N1-C5 Seq. ID

BLASTX Method NCBI GI q2262170 BLAST score 222 E value 3.0e-18 Match length 122 58 % identity

(AC002329) predicted glycosyl hydrolase [Arabidopsis NCBI Description

thaliana]

41231 Seq. No.

Seq. ID LIB3139-037-P1-N1-D2

Method BLASTN NCBI GI g2618602 57 BLAST score 2.0e-23 E value 178 Match length % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MSJ1, complete sequence [Arabidopsis thaliana]

41232 Seq. No.

Seq. ID LIB3139-037-P1-N1-D6

BLASTN Method NCBI GI q2605886 BLAST score 43 E value 6.0e-15 Match length 151

% identity

NCBI Description

54

communis]



```
% identity
                  Pisum sativum dormancy-associated protein (DRM1) mRNA,
NCBI Description
                  complete cds
                  41233
Seq. No.
Seq. ID
                  LIB3139-037-P1-N1-D7
Method
                  BLASTN
NCBI GI
                  g1381677
BLAST score
                  195
                  1.0e-105
E value
                  315
Match length
                  97
% identity
NCBI Description Glycine max small GTP-binding protein (sra2) mRNA, complete
                  41234
Seq. No.
Seq. ID
                  LIB3139-037-P1-N1-E1
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  328
E value
                  7.0e-31
                  75
Match length
% identity
                  84
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  41235
Seq. ID
                  LIB3139-037-P1-N1-E5
                  BLASTX
Method
NCBI GI
                  g4538923
BLAST score
                  194
E value
                  6.0e-15
Match length
                  64
                  59
% identity
                  (AL049483) predicted protein destination factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  41236
                  LIB3139-037-P1-N1-H1
Seq. ID
                  BLASTX
Method
                  g4234955
NCBI GI
BLAST score
                  191
E value
                  1.0e-14
Match length
                  107
% identity
                  21
NCBI Description (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
Seq. No.
                   41237
Seq. ID
                  LIB3139-038-P1-N1-A10
                  BLASTX
Method
NCBI GI
                  g3243234
BLAST score
                   220
E value
                   4.0e-18
Match length
                   80
```

6486

(AF071477) isoflavone reductase related protein [Pyrus



```
Seq. No.
Seq. ID
                  LIB3139-038-P1-N1-C1
                  BLASTX
Method
NCBI GI
                  g3096931
BLAST score
                  221
                  5.0e-18
E value
Match length
                  81
                  70
% identity
                  (AL023094) putative ribosomal protein S16 [Arabidopsis
NCBI Description
                  thaliana]
                  41239
Seq. No.
Seq. ID
                  LIB3139-038-P1-N1-D1
                  BLASTX
Method
                  g3695019
NCBI GI
                  189
BLAST score
                  1.0e-14
E value
                  85
Match length
                  47
% identity
NCBI Description (AF055848) subtilisin-like protease [Arabidopsis thaliana]
                  41240
Seq. No.
                  LIB3139-038-P1-N1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832658
BLAST score
                  390
                  8.0e-38
E value
                  81
Match length
                  81
% identity
NCBI Description (AL021710) putative protein [Arabidopsis thaliana]
Seq. No.
                  41241
                  LIB3139-038-P1-N1-E3
Seq. ID
Method
                  BLASTX
                  q138364
NCBI GI
BLAST score
                   234
                   5.0e-20
E value
                   130
Match length
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41242
Seq. No.
Seq. ID
                  LIB3139-038-P1-N1-F12
Method
                   BLASTX
NCBI GI
                   g2130096
BLAST score
                   325
E value
                   3.0e-30
Match length
                   84
% identity
                   69
                  cytochrome P450tyr - sorghum >gi 984543 (U32624) cytochrome
NCBI Description
                   P-450 [Sorghum bicolor]
```

Seq. No. 41243

Seq. ID LIB3139-038-P1-N1-G1

E value

Match length

6.0e-18

117



```
BLASTX
Method
                                    ٤.
                  q2894378
NCBI GI
BLAST score
                  160
                  6.0e-11
E value
                  51
Match length
                  57
% identity
                  (Y14573) putative ribophorin I homologue [Hordeum vulgare]
NCBI Description
                  41244
Seq. No.
Seq. ID
                  LIB3139-038-P1-N1-G11
                  BLASTX
Method
NCBI GI
                  g4097880
BLAST score
                  143
                  1.0e-11
E value
Match length
                  139
                   41
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41245
Seq. No.
                  LIB3139-039-P1-N1-B11
Seq. ID
Method
                  BLASTN
                  g169036
NCBI GI
                  100
BLAST score
                   6.0e-49
E value
                  232
Match length
                   86
% identity
NCBI Description Pisum sativum L. aldolase gene, 3' end cds
                   41246
Seq. No.
                  LIB3139-039-P1-N1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2493318
BLAST score
                   203
                   5.0e-16
E value
                   86
Match length
                   45
% identity
                  BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
NCBI Description
                   (Z25471) blue copper protein [Pisum sativum]
                   >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]
                   41247
Seq. No.
                   LIB3139-039-P1-N1-D2
Seq. ID
                   BLASTX
Method
                   q2191130
NCBI GI
                   221
BLAST score
                   4.0e-18
E value
Match length
                   115
                   43
% identity
                   (AF007269) A IG002N01.7 gene product [Arabidopsis thaliana]
NCBI Description
                   41248
Seq. No.
Seq. ID
                   LIB3139-039-P1-N1-D9
                   BLASTX
Method
NCBI GI
                   q728882
BLAST score
                   220
```

6488



% identity 51

NCBI Description ADP-RIBOSYLATION FACTOR 3 > gi_541846_pir_S41938 ADP-ribosylation factor 3 - Arabidopsis thaliana

>gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3

[Arabidopsis thaliana]

Seq. No. 41249

Seq. ID LIB3139-039-P1-N1-G12

Method BLASTN
NCBI GI g1431628
BLAST score 197
E value 1.0e-107
Match length 273
% identity 93

NCBI Description V.radiata mRNA for pectinacetylesterase

Seq. No. 41250

Seq. ID LIB3139-039-P1-N1-G2

Method BLASTX
NCBI GI g3169178
BLAST score 175
E value 1.0e-12
Match length 62
% identity 47

NCBI Description (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No. 41251

Seq. ID LIB3139-039-P1-N1-G4

Method BLASTN
NCBI GI g4097879
BLAST score 157
E value 6.0e-83
Match length 353
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41252

Seq. ID LIB3139-039-P1-N1-H6

Method BLASTX
NCBI GI g2541876
BLAST score 229
E value 4.0e-19
Match length 99
% identity 45

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 41253

Seq. ID LIB3139-039-P1-N1-H7

Method BLASTX
NCBI GI g1170938
BLAST score 257
E value 1.0e-22
Match length 85
% identity 62

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE



ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 481566 pir_S38875 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429106_emb_CAA80866_ (Z24742) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 41254

Seq. ID LIB3139-040-P1-N1-C11

90

Method BLASTN
NCBI GI g210811
BLAST score 235
E value 1.0e-129
Match length 386

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41255

% identity

Seq. ID LIB3139-040-P1-N1-C12

Method BLASTX
NCBI GI g1172874
BLAST score 145
E value 4.0e-09
Match length 62
% identity 50

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi_479589_pir__S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 41256

Seq. ID LIB3139-040-P1-N1-D1

Method BLASTX
NCBI GI g1814424
BLAST score 526
E value 9.0e-54
Match length 132
% identity 76

NCBI Description (U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No. 41257

Seq. ID LIB3139-040-P1-N1-D5

Method BLASTN
NCBI GI g210811
BLAST score 110
E value 4.0e-55
Match length 221
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41258

Seq. ID LIB3139-040-P1-N1-E3

Method BLASTX NCBI GI g229708 BLAST score 193



```
2.0e-15
E value
Match length
                  64
% identity
                   67
                  Bean pod mottle virus
NCBI Description
Seq. No.
                  41259
                  LIB3139-040-P1-N1-F10
Seq. ID
                  BLASTN
Method
                  q210811
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
                  264
Match length
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41260
Seq. No.
Seq. ID
                  LIB3139-040-P1-N1-H3
Method
                   BLASTN
NCBI GI
                   q4097879
BLAST score
                   144
                   3.0e-75
E value
                   327
Match length
                   87
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41261
Seq. No.
                   LIB3139-040-P1-N1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1255951
BLAST score
                   356
                   7.0e - 34
E value
Match length
                   103
                   59
% identity
                  (X96932) PS60 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   41262
                   LIB3139-041-P1-N1-A3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   49
                   9.0e-19
E value
                   81
Match length
                   90
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   41263
                   LIB3139-041-P1-N1-A6
Seq. ID
Method
                   BLASTX
```

NCBI GI g2935416
BLAST score 327
E value 1.0e-30
Match length 113
% identity 62

NCBI Description (AF047896) isoflavone reductase homolog [Betula pendula]

E value

Match length

% identity

8.0e-12

45

76



41264 Seq. No. Seq. ID LIB3139-041-P1-N1-A8 Method BLASTX NCBI GI g138364 137 BLAST score 1.0e-18 E value 87 Match length 62 % identity GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus] 41265 Seq. No. LIB3139-041-P1-N1-B3 Seq. ID BLASTX Method g1019946 NCBI GI 266 BLAST score 2.0e-23 E value Match length 66 % identity 71 NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum] 41266 Seq. No. Seq. ID LIB3139-041-P1-N1-E1 BLASTX Method NCBI GI g3641837 BLAST score 341 4.0e-32 E value Match length 115 % identity 63 NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana] Seq. No. 41267 LIB3139-041-P1-N1-E12 Seq. ID Method BLASTX NCBI GI g113449 BLAST score 157 1.0e-10 E value Match length 78 49 % identity PROBABLE ATP-DEPENDENT PERMEASE PRECURSOR NCBI Description >gi 83202 pir S19421 ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae) >gi 1907154 emb CAA42328 (X59720) YCR011c, len:1049 [Saccharomyces cerevisiae] 41268 Seq. No. Seq. ID LIB3139-041-P1-N1-G1 Method BLASTX NCBI GI g2827143 BLAST score 168

6492



(AF027174) cellulose synthase catalytic subunit NCBI Description [Arabidopsis thaliana] 41269 Seq. No. LIB3139-041-P1-N1-G11 Seq. ID BLASTN Method g3785968 NCBI GI 33 BLAST score 5.0e-09 E value 145 Match length

% identity Arabidopsis thaliana chromosome II BAC F2I9 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

41270 Seq. No. LIB3139-041-P1-N1-G9 Seq. ID BLASTN Method

86

g2687725 NCBI GI 139 BLAST score 3.0e-72 E value 315 Match length % identity 86

Glycine max mRNA for putative 2-hydroxydihydrodaidzein NCBI Description

reductase

41271 Seq. No.

LIB3139-042-P1-N1-A3 Seq. ID

Method BLASTX g4234941 NCBI GI 251 BLAST score 1.0e-21 E value Match length 61 % identity

(AF097938) cytosolic phosphoglucomutase [Populus tremula x NCBI Description

Populus tremuloides]

41272 Seq. No.

Seq. ID LIB3139-042-P1-N1-B10

BLASTX Method g1899175 NCBI GI 281 BLAST score E value 4.0e-25 101 Match length 53 % identity

(U90262) calcium-dependent calmodulin-independent protein NCBI Description

kinase CDPK [Cucurbita pepo]

41273 Seq. No.

Seq. ID LIB3139-042-P1-N1-B4

Method BLASTN g1143321 NCBI GI BLAST score 48 6.0e-18 E value 68 Match length % identity

Glycine max alfa-carboxyltransferase (accA-2) precursor NCBI Description

mRNA, complete cds



```
41274
Seq. No.
                  LIB3139-042-P1-N1-C11
Seq. ID
                  BLASTX
Method
                  g2809247
NCBI GI
                  254
BLAST score
                  6.0e-22
E value
                  120
Match length
% identity
                 (AC002560) F21B7.16 [Arabidopsis thaliana]
NCBI Description
                  41275
Seq. No.
                  LIB3139-042-P1-N1-C8
Seq. ID
Method
                  BLASTX
                  g125606
NCBI GI
BLAST score
                  170
                  4.0e-12
E value
Match length
                  57
                  61
% identity
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463_pir S12248
NCBI Description
                  pyruvate kinase (EC 2.7.1.40) - potato
                  >gi 22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
                  tuberosum]
                  41276
Seq. No.
                  LIB3139-042-P1-N1-E4
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
BLAST score
                   148
                   2.0e-09
E value
                   68
Match length
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
                   41277
Seq. No.
                   LIB3139-042-P1-N1-F10
Seq. ID
                   BLASTX
Method
                   g3482933
NCBI GI
BLAST score
                   147
                   2.0e-09
E value
                   93
Match length
                   44
% identity
                   (AC003970) Similar to cdc2 protein kinases [Arabidopsis
NCBI Description
                   thaliana]
                   41278
Seq. No.
                   LIB3139-042-P1-N1-G2
Seq. ID
                   BLASTN
Method
                   g1209533
NCBI GI
                   33
BLAST score
                   5.0e-09
E value
                   33
Match length
 % identity
                   Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2
NCBI Description
                   chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low
```

molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds

NCBI GI

BLAST score

204



```
Seq. No.
                  LIB3139-042-P1-N1-H2
Seq. ID
                  BLASTN
Method
                  g607187
NCBI GI
                  82
BLAST score
                  3.0e-38
E value
                  310
Match length
                  83
% identity
NCBI Description S.hamata mRNA for low affinity sulphate transporter
                   41280
Seq. No.
                  LIB3139-042-P1-N1-H6
Seq. ID
                  BLASTN
Method
                  g217902
NCBI GI
BLAST score
                   55
                   4.0e-22
E value
Match length
                   174
% identity
                   84
NCBI Description Catharanthus roseus cyc07 mRNA, complete cds
                   41281
Seq. No.
Seq. ID
                   LIB3139-042-P1-N1-H8
Method
                   BLASTN
                   g347454
NCBI GI
BLAST score
                   98
                   8.0e-48
E value
                   217
Match length
                   38
% identity
                   Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'
NCBI Description
                   41282
Seq. No.
Seq. ID
                   LIB3139-043-P1-N1-G1
                   BLASTN
Method
NCBI GI
                   q210811
                   186
BLAST score
                   1.0e-100
E value
                   346
Match length
% identity
                   88
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41283
Seq. No.
                   LIB3139-043-P1-N1-G10
Seq. ID
                   BLASTX
Method
                   q4519671
NCBI GI
                   385
BLAST score
                   5.0e-43
E value
                   111
Match length
                   83
 % identity
                   (AB017693) transfactor [Nicotiana tabacum]
NCBI Description
                   41284
 Seq. No.
                   LIB3139-043-P1-N1-G3
Seq. ID
                   BLASTX
Method
                   g3617770
```



```
4.0e-16
E value
                  72
Match length
% identity
                  58
                  (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  41285
Seq. No.
                  LIB3139-043-P1-N1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g210811
                  118
BLAST score
                  1.0e-59
E value
Match length
                  281
% identity
                  85
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  41286
Seq. No.
                  LIB3139-044-P1-N1-A10
Seq. ID
Method
                  BLASTN
                  g169936
NCBI GI
                  288
BLAST score
                   1.0e-161
E value
Match length
                   349
% identity
                   99
NCBI Description Glycine max chalcone synthase (chs7) gene, complete cds
                   41287
Seq. No.
Seq. ID
                  LIB3139-044-P1-N1-A6
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   190
                   1.0e-102
E value
Match length
                   378
% identity
                   88
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41288
Seq. No.
                   LIB3139-044-P1-N1-B10
Seq. ID
                   BLASTX
Method
                   g2702269
NCBI GI
                   348
BLAST score
                   2.0e-40
E value
                   103
Match length
% identity
                   86
                   (AC003033) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41289
                   LIB3139-044-P1-N1-B9
Seq. ID
                   BLASTN
Method
```

Method BLASTN
NCBI GI g4097879
BLAST score 105
E value 5.0e-52
Match length 253
% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds



```
41290
Seq. No.
Seq. ID
                  LIB3139-044-P1-N1-F2
                  BLASTN
Method
                  g310560
NCBI GI
                  236
BLAST score
                  1.0e-130
E value
                  248
Match length
% identity
NCBI Description Soybean ascorbate peroxidase mRNA, complete cds
                  41291
Seq. No.
                  LIB3139-044-P1-N1-F5
Seq. ID
                  BLASTN
Method
                  g1208536
NCBI GI
                  359
BLAST score
                  0.0e+00
E value
                  383
Match length
% identity
                  Glycine max guanine nucleotide regulatory protein (rab2)
NCBI Description
                  mRNA, complete cds
                  41292
Seq. No.
                  LIB3139-044-P1-N1-G12
Seq. ID
                  BLASTN
Method
                  q4097879
NCBI GI
BLAST score
                  104
                  1.0e-51
E value
                  172
Match length
                  90
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
                  41293
Seq. No.
                  LIB3139-044-P1-N1-H2
Seq. ID
                  BLASTX
Method
                  g1172703
NCBI GI
BLAST score
                  276
                   2.0e-24
E value
                  127
Match length
                   40
% identity
                  PEPTIDE TRANSPORTER PTR2-A >gi 575427 (U01171) similar to
NCBI Description
                   S. cerevisiae PTR2 gene, GenBank Accession Number L11994
                   [Arabidopsis thaliana]
                   41294
Seq. No.
Seq. ID
                  LIB3139-044-P1-N1-H5
Method
                  BLASTX
```

Method BLASTX
NCBI GI 94210330
BLAST score 424
E value 6.0e-42
Match length 102
% identity 75

NCBI Description (AJ223802) 2-oxoglutarate dehydrogenase, El subunit

[Arabidopsis thaliana]

Seq. No. 41295



```
LIB3139-044-P1-N1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3243234
                  318
BLAST score
                  2.0e-29
E value
                  84
Match length
% identity
                  (AF071477) isoflavone reductase related protein [Pyrus
NCBI Description
                  communis]
                  41296
Seq. No.
                  LIB3139-045-P1-N1-B11
Seq. ID
                  BLASTX
Method
                  g807698
NCBI GI
BLAST score
                  431
                   9.0e-43
E value
                  116
Match length
                   66
% identity
NCBI Description (D32206) prepro-cucumisin [Cucumis melo]
                   41297
Seq. No.
                  LIB3139-045-P1-N1-B5
Seq. ID
                  BLASTX
Method
                   g2462760
NCBI GI
                   190
BLAST score
                   2.0e-14
E value
                   91
Match length
                   42
% identity
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
                   41298
Seq. No.
                   LIB3139-045-P1-N1-H1
Seq. ID
                   BLASTX
Method
                   q3695403
NCBI GI
                   480
BLAST score
                   2.0e-48
E value
Match length
                   107
                   84
% identity
                   (AF096373) contains similarity to the pfkB family of
NCBI Description
                   carbohydrate kinases (Pfam: PF00294, E=1.6e-75)
                   [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1
                   (AL049488) fructokinase-like protein [Arabidopsis thaliana]
                   41299
Seq. No.
                   LIB3139-045-P1-N1-H5
Seq. ID
                   BLASTX
Method
                   q2459420
NCBI GI
BLAST score
                   586
                   8.0e-61
E value
                   116
Match length
 % identity
                   (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                   thaliana]
                   41300
 Seq. No.
                   LIB3139-046-P1-N1-B10
 Seq. ID
```

BLASTX

Method



```
q3420054
NCBI GI
                  210
BLAST score
                  8.0e-17
E value
                  71
Match length
                  65
% identity
NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]
                  41301
Seq. No.
                  LIB3139-046-P1-N1-E7
Seq. ID
                  BLASTX
Method
                  g2583108
NCBI GI
                  185
BLAST score
                  7.0e-14
E value
                  90
Match length
                   48
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
                   41302
Seq. No.
                   LIB3139-046-P1-N1-E8
Seq. ID
                   BLASTX
Method
                   g2245074
NCBI GI
BLAST score
                   207
                   2.0e-16
E value
                   66
Match length
                   59
% identity
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                   41303
Seq. No.
                   LIB3139-046-P1-N1-H3
Seq. ID
                   BLASTN
Method
                   g4097879
NCBI GI
                   86
BLAST score
                   8.0e-41
E value
                   190
Match length
% identity
                   86
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                   gene, complete cds
                   41304
Seq. No.
                   LIB3139-047-P1-N1-A8
Seq. ID
                   BLASTN
Method
                   g4097879
NCBI GI
                   157
BLAST score
                   5.0e-83
 E value
                   317
Match length
                   87
 % identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                   gene, complete cds
                   41305
 Seq. No.
                   LIB3139-047-P1-N1-B6
 Seq. ID
                   BLASTX
 Method
                   g2132995
 NCBI GI
                   170
 BLAST score
                   8.0e-14
 E value
 Match length
                   61
```

% identity



```
probable membrane protein YPL189w - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi_1370395_emb_CAA97902_ (Z73545) ORF YPL189w
                   [Saccharomyces cerevisiae]
                   41306
Seq. No.
                  LIB3139-047-P1-N1-D11
Seq. ID
                  BLASTX
Method
                  q2598575
NCBI GI
                   370
BLAST score
                   1.0e-35
E value
                   125
Match length
                   60
% identity
                  (Y15293) MtN21 [Medicago truncatula]
NCBI Description
                   41307
Seq. No.
                   LIB3139-047-P1-N1-E2
Seq. ID
                   BLASTX
Method
                   q3450842
NCBI GI
                   241
BLAST score
                   2.0e-20
E value
                   69
Match length
                   67
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
                   41308
Seq. No.
                   LIB3139-048-P1-N1-A8
Seq. ID
                   BLASTX
Method
                   g3158476
NCBI GI
                   250
BLAST score
                   2.0e-23
E value
Match length
                   87
% identity
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
                   41309
Seq. No.
                   LIB3139-048-P1-N1-B10
Seq. ID
                   BLASTN
Method
                   q4097879
NCBI GI
                   51
BLAST score
                   9.0e-20
E value
                   83
Match length
 % identity
                   Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41310
 Seq. No.
```

Method BLASTX
NCBI GI 94263517
BLAST score 233
E value 3.0e-28
Match length 104
% identity 63

NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of

phenazine-1-carboxylic acid to

2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis

NCBI Description



```
41311
Seq. No.
                  LIB3139-048-P1-N1-C10
Seq. ID
                  BLASTX
Method
                  g2852449
NCBI GI
                  198
BLAST score
                  3.0e-15
E value
                  115
Match length
                  37
% identity
                  (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061
NCBI Description
                   (AC002521) putative protein kinase [Arabidopsis thaliana]
                   41312
Seq. No.
                  LIB3139-048-P1-N1-C7
Seq. ID
                  BLASTX
Method
                   g3928150
NCBI GI
                   148
BLAST score
                   2.0e-09
E value
                   83
Match length
                   36
% identity
                   (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                   41313
Seq. No.
                   LIB3139-048-P1-N1-D2
Seq. ID
                   BLASTN
Method
                   g3873174
NCBI GI
BLAST score
                   62
                   3.0e-26
E value
                   191
Match length
% identity
                   Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   41314
Seq. No.
Seq. ID
                   LIB3139-048-P1-N1-D4
                   BLASTX
Method
                   g3738298
NCBI GI
                   224
BLAST score
                   2.0e-18
E value
Match length
                   130
                   38
 % identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4249394 (AC006072) unknown protein [Arabidopsis
                   thaliana]
                   41315
Seq. No.
                   LIB3139-048-P1-N1-D8
 Seq. ID
                   BLASTN
Method
                   g210811
 NCBI GI
 BLAST score
                   74
                   2.0e-33
 E value
                   122
 Match length
                   90
 % identity
                   Bean pod mottle virus coat protein gene, complete cds,
```

complete middle component (M) RNA

```
41316
Seq. No.
                  LIB3139-048-P1-N1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4191791
BLAST score
                  237
                  7.0e-20
E value
Match length
                  66
                  68
% identity
NCBI Description (AC005917) putative sf21 {Helianthus annuus} protein
                  [Arabidopsis thaliana]
Seq. No.
                  41317
Seq. ID
                  LIB3139-048-P1-N1-F8
Method
                  BLASTX
NCBI GI
                  q4097880
BLAST score
                  147
E value
                  1.0e-09
Match length
                  47
% identity
                  74
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  41318
                  LIB3139-048-P1-N1-G4
Seq. ID
                  BLASTN
Method
                  g210811
NCBI GI
BLAST score
                  193
E value
                  1.0e-104
                  381
Match length
                  88
% identity
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  41319
Seq. ID
                  LIB3139-048-P1-N1-G7
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  231
E value
                  1.0e-127
Match length
                  437
% identity
                  88
NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                  complete middle component (M) RNA
Seq. No.
                  41320
                  LIB3139-048-P1-N1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g229708
BLAST score
                  247
```

E value 2.0e-21 Match length 79 65 % identity

NCBI Description Bean pod mottle virus

Seq. No. 41321

Seq. ID LIB3139-048-P1-N1-H1

Method BLASTN NCBI GI g210811

BLAST score 95 E value 6.0e-46 Match length 306 % identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41322

Seq. ID LIB3139-048-P1-N1-H12

Method BLASTN
NCBI GI g210811
BLAST score 223
E value 1.0e-122
Match length 439

% identity 88
NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41323

Seq. ID LIB3139-049-P1-N1-B12

Method BLASTN
NCBI GI g210811
BLAST score 80
E value 5.0e-37
Match length 206
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41324

Seq. ID LIB3139-049-P1-N1-C6

Method BLASTX
NCBI GI 94572458
BLAST score 512
E value 4.0e-52
Match length 120
% identity 82

NCBI Description (AF123482) NAD-dependent formate dehydrogenase

[Mycosphaerella graminicola]

Seq. No. 41325

Seq. ID LIB3139-049-P1-N1-D2

Method BLASTX
NCBI GI g586784
BLAST score 154
E value 4.0e-10
Match length 130
% identity 24

NCBI Description MITOCHONDRIAL CARRIER PROTEIN YMC2 PRECURSOR

>gi_1078116_pir__S48269 mitochondrial carrier protein YMC2

precursor - yeast (Saccharomyces cerevisiae)

>gi_476060_emb_CAA55607_ (X78993) YBR0833 [Saccharomyces cerevisiae] >gi_536390_emb_CAA85059_ (Z35973) ORF YBR104w

[Saccharomyces cerevisiae]

Seq. No. 41326

Seq. ID LIB3139-049-P1-N1-E1

```
Method
NCBI GI
                  q229708
BLAST score
                   276
                  1.0e-24
E value
                  79
Match length
                  71
% identity
NCBI Description Bean pod mottle virus
                   41327
Seq. No.
                  LIB3139-049-P1-N1-E9
Seq. ID
                   BLASTX
Method
                   g2316016
NCBI GI
                   554
BLAST score
                   4.0e-57
E value
                   120
Match length
                   42
% identity
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
                   41328
Seq. No.
                   LIB3139-049-P1-N1-F12
Seq. ID
                   BLASTX
Method
                   g2961346
NCBI GI
                   201
BLAST score
                   1.0e-15
E value
                   108
Match length
                   35
% identity
                   (AL022140) pectinesterase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   41329
Seq. No.
                   LIB3139-049-P1-N1-H3
Seq. ID
                   BLASTX
Method
                   g3135269
NCBI GI
                   254
BLAST score
                   7.0e-22
E value
                   123
Match length
                   47
 % identity
                   (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
                   41330
 Seq. No.
 Seq. ID
                   LIB3139-050-P1-N1-A9
                   BLASTN
Method
NCBI GI
                   q296444
                   96
BLAST score
                   1.0e-46
E value
                   220
Match length
                   86
 % identity
 NCBI Description G.max ADR6 mRNA
                   41331
 Seq. No.
 Seq. ID
                   LIB3139-050-P1-N1-C9
```

Seq. No. LIB3139-050-P1-N1-C9
Method BLASTN
NCBI GI g1667372
BLAST score 192
E value 1.0e-104

Match length 352 % identity 83

Seq. No.

Seq. ID

Method NCBI GI 41337

BLASTN

q4097879

LIB3139-051-P1-N1-A6



NCBI Description M.sativa MMK4 mRNA for protein kinase

41332 Seq. No. LIB3139-050-P1-N1-E9 Seq. ID BLASTX Method g2443755 NCBI GI BLAST score 153 4.0e-10 E value 82 Match length 41 % identity (AF020433) cyclophilin [Arabidopsis thaliana] NCBI Description 41333 Seq. No. LIB3139-050-P1-N1-F3 Seq. ID BLASTX Method g3386611 NCBI GI 280 BLAST score 4.0e-25 E value 77 Match length 61 % identity (AC004665) unknown protein [Arabidopsis thaliana] NCBI Description 41334 Seq. No. LIB3139-050-P1-N1-F7 Seq. ID BLASTX Method g229707 NCBI GI 531 BLAST score 2.0e-54 E value 134 Match length 75 % identity NCBI Description Bean pod mottle virus 41335 Seq. No. Seq. ID LIB3139-050-P1-N1-G3 BLASTN Method NCBI GI g3695062 125 BLAST score 4.0e-64 E value 197 Match length 91 % identity Lotus japonicus rac GTPase activating protein 3 mRNA, NCBI Description partial cds 41336 Seq. No. LIB3139-050-P1-N1-H8 Seq. ID BLASTX Method NCBI GI q2244867 BLAST score 519 1.0e-54 E value Match length 176 63 % identity (Z97337) hydroxynitrile lyase [Arabidopsis thaliana] NCBI Description

- 6505

```
BLAST score
                  8.0e-17
E value
                  66
Match length
                   92
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                   41338
Seq. No.
                  LIB3139-051-P1-N1-D4
Seq. ID
                  BLASTX
Method
                   q584794
NCBI GI
                   406
BLAST score
                   6.0e-40
E value
                   98
Match length
                   88
% identity
                   PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
NCBI Description
                   >gi_282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35)
                   - curled-leaved tobacco >gi_170289 (M80489) plasma membrane
                   H+ ATPase [Nicotiana plumbaginifolia]
                   41339
Seq. No.
                   LIB3139-051-P1-N1-D6
Seq. ID
                   BLASTN
Method
                   g4097879
NCBI GI
                   43
BLAST score
                   6.0e-15
E value
                   95
Match length
                   86
% identity
```

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein gene, complete cds

Seq. No. 41340

Seq. ID LIB3139-051-P1-N1-E4

Method BLASTN
NCBI GI g210811
BLAST score 158
E value 2.0e-83
Match length 370
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41341

Seq. ID LIB3139-051-P1-N1-G4

Method BLASTX
NCBI GI g1173209
BLAST score 287
E value 1.0e-25
Match length 95
% identity 59

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal

protein S16 protein - upland cotton

>gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit

[Gossypium hirsutum]

Seq. No. 41342

Seq. ID LIB3139-051-P1-N1-G9

```
Method
NCBI GI
                  q3639081
BLAST score
                  173
                  2.0e-12
E value
Match length
                  41
% identity
                  76
NCBI Description
                  (AF090194) non-selenium glutathione phospholipid
                  hydroperoxide peroxidase [Bos taurus] >gi 3703050
                  (AF080228) ciliary body glutathione peroxidase [Bos taurus]
Seq. No.
                  41343
Seq. ID
                  LIB3139-052-P1-N1-D4
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  56
                  9.0e-23
E value
Match length
                  126
                  90
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
Seq. No.
                  41344
                  LIB3139-052-P1-N1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3805962
BLAST score
                  483
                  8.0e-49
E value
Match length
                  102
% identity
NCBI Description
                 (Y13772) laccase [Populus balsamifera subsp. trichocarpa]
Seq. No.
                  41345
                  LIB3139-052-P1-N1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g886100
BLAST score
                  168
E value
                  6.0e-12
Match length
                  58
% identity
                  59
NCBI Description
                  (U27347) putative water channel protein; plasmalemma
                  intrinsic protein; similar to Arabidopsis Pip2a gene
                  product, PIR Accession Number S44084 [Glycine max]
Seq. No.
                  41346
Seq. ID
                  LIB3139-052-P1-N1-D8
Method
                  BLASTN
NCBI GI
                  g56539
BLAST score
                  68
                  7.0e-30
E value
```

Match length 254 90 % identity

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi 206360 gb J00764 RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 41347

LIB3139-053-P1-N1-A10 Seq. ID

Method BLASTX
NCBI GI g2760843
BLAST score 157
E value 1.0e-10
Match length 122
% identity 36

NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]

Seq. No. 41348

Seq. ID LIB3139-053-P1-N1-A6

Method BLASTN
NCBI GI g18735
BLAST score 249
E value 1.0e-138
Match length 373
% identity 92

NCBI Description Soybean RPB1-C gene for largest subunit of RNA polymerase

TT

Seq. No. 41349

Seq. ID LIB3139-053-P1-N1-E2

Method BLASTX
NCBI GI g3914361
BLAST score 172
E value 2.0e-12
Match length 99
% identity 37

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_2281951_emb_CAB06620_ (Z84822) phospholipase D

[Nicotiana tabacum]

Seq. No. 41350

Seq. ID LIB3139-053-P1-N1-G1

Method BLASTN
NCBI GI g210811
BLAST score 42
E value 2.0e-14
Match length 70
% identity 90

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41351

Seq. ID LIB3139-053-P1-N1-G11

Method BLASTN
NCBI GI 94097879
BLAST score 147
E value 5.0e-77
Match length 287
% identity 88

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41352

Seq. ID LIB3139-054-P1-N1-B7

Method BLASTX

```
g2618687
NCBI GI
                   260
BLAST score
                   1.0e-22
E value
                   124
Match length
                   47
% identity
                  (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   41353
Seq. No.
                   LIB3139-054-P1-N1-F12
Seq. ID
                   BLASTX
Method
                   g3559814
NCBI GI
                   186
BLAST score
                   5.0e-14
E value
                   88
Match length
                   49
% identity
                   (Y15781) transketolase 1 [Capsicum annuum]
NCBI Description
                   41354
Seq. No.
                   LIB3139-054-P1-N1-H3
Seq. ID
                   BLASTX
Method
                   g1730981
NCBI GI
BLAST score
                   189
                    2.0e-14
E value
                    113
Match length
                    38
% identity
                   HYPOTHETICAL 41.0 KD PROTEIN IN NUCB-AROD INTERGENIC REGION
NCBI Description
                   >gi_1303788_dbj_BAA12444_ (D84432) YqeH [Bacillus subtilis]
>gi_2635013_emb_CAB14509_ (Z99117) similar to hypothetical
                    proteins [Bacillus subtilis]
                    41355
Seq. No.
                    LIB3139-055-P1-N1-A12
Seq. ID
Method
                    BLASTX
                    q2129889
NCBI GI
                    120
BLAST score
                    2.0e-11
E value
                    85
Match length
                    55
% identity
NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
                    41356
Seq. No.
                    LIB3139-055-P1-N1-C8
Seq. ID
                    BLASTX
Method
                    g2827139
NCBI GI
BLAST score
                    207
                    5.0e-30
 E value
                    114
Match length
                    63
 % identity
                    (AF027172) cellulose synthase catalytic subunit
 NCBI Description
                    [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_
                    cellulose synthase catalytic subunit (RSW1) [Arabidopsis
```

Seq. No. 41357

Seq. ID LIB3139-055-P1-N1-D11

thaliana]

Method BLASTX NCBI GI g4468990

BLAST score 206
E value 3.0e-16
Match length 52
% identity 75

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 41358

Seq. ID LIB3139-055-P1-N1-D2

Method BLASTX
NCBI GI g3193320
BLAST score 446
E value 2.0e-44
Match length 134
% identity 65

NCBI Description (AF069299) contains similarity to the subtilase family of

serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin

(GB:D32206) [Arabidopsis thaliana]

Seq. No. 41359

Seq. ID LIB3139-055-P1-N1-F12

Method BLASTX
NCBI GI g4235093
BLAST score 160
E value 5.0e-11
Match length 81
% identity 47

NCBI Description (AF108944) beta-xylosidase [Aspergillus niger]

Seq. No. 41360

Seq. ID LIB3139-055-P1-N1-G3

Method BLASTX
NCBI GI g229708
BLAST score 315
E value 3.0e-29
Match length 84
% identity 71

NCBI Description Bean pod mottle virus

Seq. No. 41361

Seq. ID LIB3139-055-P1-N1-H8

Method BLASTN
NCBI GI g3183639
BLAST score 46
E value 4.0e-17
Match length 62
% identity 94

NCBI Description Cicer arietinum mRNA for putative transmembrane channel

protein, partial

Seq. No. 41362

Seq. ID LIB3139-056-P1-N1-A2

Method BLASTX
NCBI GI g3953467
BLAST score 230
E value 3.0e-19
Match length 55



% identity 46
NCBI Description (AC002328) F20N2.12 [Arabidopsis thaliana]

Seq. No. 41363

Seq. ID LIB3139-056-P1-N1-A8

Method BLASTN
NCBI GI g1663536
BLAST score 55
E value 4.0e-22

E value 4.0e-22 Match length 225 % identity 83

NCBI Description Glycine max clone RLG1 disease resistance protein homolog

gene, partial cds

Seq. No. 41364

Seq. ID LIB3139-056-P1-N1-C2

Method BLASTX
NCBI GI g3292829
BLAST score 290
E value 3.0e-26
Match length 82
% identity 70

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 41365

Seq. ID LIB3139-056-P1-N1-D8

Method BLASTN
NCBI GI g210811
BLAST score 56
E value 1.0e-22
Match length 100
% identity 89

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41366

Seq. ID LIB3139-056-P1-N1-F6

Method BLASTX
NCBI GI g1076685
BLAST score 199
E value 6.0e-16
Match length 55
% identity 37

NCBI Description SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_

(D30038) SPF1 protein [Ipomoea batatas]

Seq. No. 41367

Seq. ID LIB3139-057-P1-N1-B10

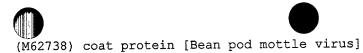
Method BLASTX
NCBI GI g138364
BLAST score 258
E value 2.0e-35
Match length 123
% identity 65

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi 75639_pir__GNWXG7 genome polyprotein M -

6511

bean pod mottle virus (strain Kentucky G7) >gi_210812

Seq. ID



```
Seq. No.
Seq. ID
                  LIB3139-057-P1-N1-B7
Method
                  BLASTN
NCBI GI
                  q210811
                  130
BLAST score
                   6.0e-67
E value
Match length
                  290
                  86
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   41369
Seq. No.
                  LIB3139-057-P1-N1-D4
Seq. ID
                  BLASTN
Method
                   g456567
NCBI GI
                   105
BLAST score
                   6.0e-52
E value
Match length
                   220
% identity
                   89
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                   cds
                   41370
Seq. No.
Seq. ID
                   LIB3139-057-P1-N1-D5
                   BLASTX
Method
                   g3152607
NCBI GI
                   191
BLAST score
                   1.0e-14
E value
Match length
                   119
                   32
% identity
                  (AC004482) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41371
                   LIB3139-057-P1-N1-F3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3860333
BLAST score
                   346
                   9.0e-33
E value
Match length
                   91
                   70
% identity
                   (AJ012693) basic blue copper protein [Cicer arietinum]
NCBI Description
Seq. No.
                   41372
                   LIB3139-057-P1-N1-G4
Seq. ID
Method
                   BLASTX
                   g1841355
NCBI GI
BLAST score
                   145
                   3.0e-09
E value
Match length
                   39
% identity
                   67
                   (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
NCBI Description
                   sativa]
                   41373
Seq. No.
```

LIB3139-057-P1-N1-G6

```
Method
                  g3650379
NCBI GI
                  475
BLAST score
                  7.0e-48
E value
                  121
Match length
                  76
% identity
                  (AL031740) 60s ribosomal protein 110a. [Schizosaccharomyces
NCBI Description
                  pombe]
                   41374
Seq. No.
                  LIB3139-059-P1-N1-D5
Seq. ID
                  BLASTN
Method
                   q166419
NCBI GI
                   137
BLAST score
                   5.0e-71
E value
```

% identity 88
NCBI Description Medicago sativa S-adenosyl-L-methionine: caffeic acid

3-0-methyltransferase mRNA, complete cds

Seq. No. 41375

Match length

Seq. ID LIB3139-059-P1-N1-G1

277

Method BLASTN
NCBI GI g1518539
BLAST score 119
E value 2.0e-60
Match length 219
% identity 89

NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No. 41376

Seq. ID LIB3139-059-P1-N1-G2

Method BLASTX
NCBI GI g728905
BLAST score 380
E value 1.0e-36
Match length 113
% identity 65

NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC

RETICULUM CA2+-ATPASE) >gi_1078206_pir__S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae)

>gi_171114 (L01795) ATPase [Saccharomyces cerevisiae]

>gi_595560 (U12980) Drs2p: Membrane spanning

Ca-ATPase(P-type), member of the cation transport(E1-E2)

ATPase [Saccharomyces cerevisiae]

Seq. No. 41377

Seq. ID LIB3139-059-P1-N1-H10

Method BLASTX
NCBI GI g3292826
BLAST score 201
E value 7.0e-16
Match length 60
% identity 62

NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No. 41378

```
LIB3139-059-P1-N1-H12
Seq. ID
                  BLASTN
Method
                  g210811
NCBI GI
                  230
BLAST score
                  1.0e-126
E value
                  397
Match length
                  89
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   41379
Seq. No.
                   LIB3139-060-P1-N1-B5
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   192
BLAST score
                   1.0e-104
E value
                   368
Match length
% identity
                   88
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41380
Seq. No.
                   LIB3139-060-P1-N1-D8
Seq. ID
                   BLASTX
Method
                   g462013
NCBI GI
                   266
BLAST score
                   3.0e-23
E value
Match length
                   119
                   51
% identity
                   ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
NCBI Description
                   >gi_542022_pir__S39558 HSP90 homolog - Madagascar
                   periwinkle >gi_348696 (L14594) heat shock protein 90
                   [Catharanthus roseus]
Seq. No.
                   41381
                   LIB3139-060-P1-N1-F3
Seq. ID
                   BLASTX
Method
                   g2146731
NCBI GI
```

Method BLASTX
NCBI GI g2146731
BLAST score 490
E value 1.0e-49
Match length 112
% identity 31

NCBI Description FK506-binding protein - Arabidopsis thaliana >gi_1354207

(U49453) rof1 [Arabidopsis thaliana]

Seq. No. 41382

Seq. ID LIB3139-060-P1-N1-G7

Method BLASTX
NCBI GI g2435522
BLAST score 297
E value 7.0e-27
Match length 143
% identity 47

NCBI Description (AF024504) contains similarity to other AMP-binding enzymes

[Arabidopsis thaliana]

Seq. No. 41383

```
LIB3139-060-P1-N1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1943751
                  320
BLAST score
E value
                  7.0e-30
Match length
                  79
% identity
                  77
                  (U93845) Arabidopsis thaliana ER-type calcium pump
NCBI Description
                  protein, complete sequence >gi_2078292 (U96455) ER-type
                  Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
                  41384
Seq. No.
                  LIB3139-061-P1-N1-B1
Seq. ID
Method
                  BLASTN
                  g170087
NCBI GI
BLAST score
                  166
                  2.0e-88
E value
Match length
                  234
% identity
                  94
                  G.max vegetative storage protein mRNA (VSP25 gene)
NCBI Description
                  41385
Seq. No.
                  LIB3139-061-P1-N1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935187
                   440
BLAST score
                   8.0e-44
E value
                  111
Match length
                   71
% identity
                  (AC004557) F17L21.30 [Arabidopsis thaliana]
NCBI Description
                   41386
Seq. No.
Seq. ID
                   LIB3139-061-P1-N1-C5
                   BLASTX
Method
NCBI GI
                   q3297819
BLAST score
                   443
                   5.0e-44
E value
Match length
                   97
                   87
% identity
NCBI Description
                   (AL031032) protein kinase - like protein [Arabidopsis
                   thaliana]
Seq. No.
                   41387
                   LIB3139-062-P1-N1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3451074
BLAST score
                   557
                   2.0e-57
E value
Match length
                   155
% identity
                   65
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   41388
Seq. No.
                   LIB3139-062-P1-N1-F5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q169974
```

87

BLAST score

```
E value
Match length
                   151
% identity
                   89
NCBI Description
Seq. No.
                   41389
Seq. ID
                   BLASTX
Method
```

Glycine max vspA gene, complete cds

LIB3139-062-P1-N1-F9

NCBI GI q1663648 BLAST score 266 3.0e-23 E value 79 Match length 66 % identity

(U75321) chromaffin granule ATPase II homolog [Mus NCBI Description

musculus]

41390 Seq. No.

Seq. ID LIB3139-062-P1-N1-H9

BLASTX Method NCBI GI q1350594 597 BLAST score 4.0e-62 E value 136 Match length % identity 83

RHO1 PROTEIN >qi 1076922 pir JC4044 Rho1 protein - fission NCBI Description

yeast (Schizosaccharomyces pombe) >gi 2130296 pir S62576

hypothetical protein SPAC1F7.04 - fission yeast

(Schizosaccharomyces pombe) >gi_1064856_dbj_BAA07377

(D38180) Rho1 [Schizosaccharomyces pombe] >gi 1067206 emb CAA91951 (Z67998) unknown

[Schizosaccharomyces pombe]

Seq. No. 41391

LIB3139-063-P1-N1-B2 Seq. ID

Method BLASTX NCBI GI g4097880 BLAST score 303 9.0e-28 E value Match length 115 77 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No. 41392

LIB3139-063-P1-N1-C10 Seq. ID

Method BLASTN NCBI GI g1675195 BLAST score 100 5.0e-49E value Match length 186 89 % identity

Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, NCBI Description

complete cds

41393 Seq. No.

LIB3139-063-P1-N1-C9 Seq. ID

Method BLASTX NCBI GI q4097880

```
BLAST score
                  5.0e-42
E value
                  102
Match length
% identity
                  81
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41394
Seq. No.
                  LIB3139-063-P1-N1-F5
Seq. ID
                  BLASTX
Method
                   g138364
NCBI GI
                   254
BLAST score
```

NCBI GI g138364
BLAST score 254
E value 2.0e-22
Match length 71
% identity 73

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

, · · :

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 41395

Seq. ID LIB3139-063-P1-N1-F6

Method BLASTX
NCBI GI g2414609
BLAST score 433
E value 5.0e-43
Match length 119
% identity 68

NCBI Description (Z99295) citrate lyase [Schizosaccharomyces pombe]

Seq. No. 41396

Seq. ID LIB3139-063-P1-N1-H7

Method BLASTN
NCBI GI g210811
BLAST score 34
E value 1.0e-09
Match length 42
% identity 95

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41397

Seq. ID LIB3139-064-P1-N1-A2

Method BLASTN
NCBI GI g4097879
BLAST score 112
E value 4.0e-56
Match length 295
% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41398

Seq. ID LIB3139-064-P1-N1-A9

Method BLASTX
NCBI GI g3033381
BLAST score 172
E value 3.0e-27

BLAST score

% identity

NCBI Description

E value Match length 293 1.0e-26

116

57



```
Match length
                   74
% identity
                   (AC004238) putative UDP-galactose-4-epimerase [Arabidopsis
NCBI Description
                  thaliana]
                  41399
Seq. No.
                  LIB3139-064-P1-N1-C3
Seq. ID
                  BLASTX
Method
                  g1752734
NCBI GI
BLAST score
                  159
E value
                  7.0e-11
                  59
Match length
                  54
% identity
                  (D78510) beta-glucan-elicitor receptor [Glycine max]
NCBI Description
                   41400
Seq. No.
                  LIB3139-064-P1-N1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4521246
                   181
BLAST score
E value
                   3.0e-97
                   292
Match length
                   93
% identity
                  Aspergillus oryzae tef gene for translation elongation
NCBI Description
                   factor 1 alpha, complete cds
                   41401
Seq. No.
Seq. ID
                   LIB3139-064-P1-N1-G12
                   BLASTX
Method
NCBI GI
                   g4097880
BLAST score
                   187
                   7.0e-22
E value
                   104
Match length
                   56
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   41402
Seq. ID
                   LIB3139-064-P1-N1-H12
                   BLASTN
Method
                   q4097879
NCBI GI
BLAST score
                   100
                   5.0e-49
E value
Match length
                   292
                   84
% identity
                   Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41403
Seq. No.
Seq. ID
                   LIB3139-064-P1-N1-H3
                   BLASTX
Method
NCBI GI
                   g4097880
```

6518

(U70866) polyprotein [Bean pod mottle virus]

```
Seq. No.
                  LIB3139-064-P1-N1-H4
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
                  117
BLAST score
                  2.0e-09
E value
                  65
Match length
                  50
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  41405
Seq. No.
                  LIB3139-065-P1-N1-A2
Seq. ID
                  BLASTN
Method
                  q210811
NCBI GI
                  79
BLAST score
                  1.0e-36
E value
Match length
                  119
% identity
                  92
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                   41406
                  LIB3139-065-P1-N1-B1
Seq. ID
                  BLASTN
Method
                   q210811
NCBI GI
                   195
BLAST score
                   1.0e-105
E value
                   307
Match length
                   91
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   41407
                   LIB3139-065-P1-N1-B4
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
BLAST score
                   83
                   8.0e-39
E value
                   190
Match length
                   86
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41408
Seq. No.
                   LIB3139-065-P1-N1-C8
Seq. ID
                   BLASTN
Method
NCBI GI
                   q609556
                   138
```

Method BLASTN
NCBI GI g609556
BLAST score 138
E value 9.0e-72
Match length 274
% identity 88

NCBI Description Pisum sativum S-adenosylmethionine synthase mRNA, 3' end

Seq. No. 41409

Seq. ID LIB3139-065-P1-N1-D11

Method BLASTN NCBI GI g4097879



```
BLAST score
                   7.0e-64
E value
                   308
Match length
                   85
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41410
Seq. No.
                   LIB3139-065-P1-N1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2264373
BLAST score
                   395
E value
                   2.0e-38
                   86
Match length
                   78
% identity
                   (AC002354) putative NAM/no apical meristem protein
NCBI Description
                   [Arabidopsis thaliana]
                   41411
Seq. No.
                   LIB3139-065-P1-N1-E8
Seq. ID
                   BLASTN
Method
                   q210811
NCBI GI
BLAST score
                   57
E value
                   1.0e-23
Match length
                   125
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41412
Seq. No.
                   LIB3139-065-P1-N1-F8
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1335861
                   189
BLAST score
E value
                   1.0e-102
                   225
Match length
 % identity
                   96
NCBI Description Glycine max clathrin heavy chain mRNA, complete cds
                   41413
 Seq. No.
                   LIB3139-065-P1-N1-G6
 Seq. ID
                   BLASTN
 Method
                   g1518539
 NCBI GI
                   106
 BLAST score
                   1.0e-52
 E value
                   170
 Match length
 % identity
                    91
 NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
 Seq. No.
                    41414
                   LIB3139-065-P1-N1-H10
 Seq. ID
                   BLASTX
 Method
```

g4097880

9.0e-46

302

128

81

NCBI GI

E value

BLAST score

Match length

% identity





```
(U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  41415
Seq. No.
                  LIB3139-065-P1-N1-H7
Seq. ID
                  BLASTX
Method
                  q4097880
NCBI GI
BLAST score
                  126
                  1.0e-24
E value
Match length
                  112
                   60
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  41416
Seq. No.
Seq. ID
                  LIB3139-066-P1-N1-A5
Method
                  BLASTN
                   g210811
NCBI GI
                   102
BLAST score
                   3.0e-50
E value
                   246
Match length
                   85
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   41417
Seq. No.
                  LIB3139-066-P1-N1-C12
Seq. ID
                   BLASTX
Method
                   g1174613
NCBI GI
BLAST score
                   336
                   9.0e-32
E value
                   102
Match length
                   67
% identity
                   26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                   PROTEIN HOMOLOG 1) (TBP-1) >qi 556560 dbj BAA04614
                   (D17788) rice homologue of Tat binding protein [Oryza
                   sativa]
                   41418
Seq. No.
Seq. ID
                   LIB3139-066-P1-N1-C5
                   BLASTN
Method
                   q4038029
NCBI GI
BLAST score
                   52
                   2.0e-20
E value
Match length
                   76
% identity
                   92
                   Arabidopsis thaliana chromosome II BAC F504 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   41419
Seq. No.
                   LIB3139-066-P1-N1-E3
Seq. ID
```

Method BLASTX
NCBI GI g3023751
BLAST score 138
E value 7.0e-09
Match length 39
% identity 74

NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi 1076772 pir S55383

```
peptidylprolyl isomerase (EC 5.2.1.8) - wheat
>qi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase
[Triticum aestivum]
41420
LIB3139-066-P1-N1-F5
BLASTX
a4490297
183
1.0e-13
124
26
```

% identity (AL035678) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. Seq. ID LIB3139-066-P1-N1-G10 BLASTX Method NCBI GI g4325344 BLAST score 484 E value 5.0e-49 Match length 107

41421

85 % identity (AF128393) similar to beta-transducins (Pfam: PF00400, NCBI Description Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]

Seq. No. 41422

Seq. No.

Seq. ID

NCBI GI BLAST score

E value Match length

Method

Seq. ID LIB3139-067-P1-N1-A4

Method BLASTN NCBI GI g210811 BLAST score 200 E value 1.0e-108 415 Match length % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

41423 Seq. No.

LIB3139-067-P1-N1-C11 Seq. ID

BLASTX Method q3176690 NCBI GI BLAST score 353 2.0e-33 E value Match length 72 % identity 92

(AC003671) Similar to ubiquitin ligase gb_D63905 from S. NCBI Description

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 41424

Seq. ID LIB3139-067-P1-N1-D11

Method BLASTX NCBI GI g3776559 BLAST score 203 E value 6.0e-16 Match length 62 % identity 69

(ACO05388) Strong similarity to gene F14J9.26 gi_3482933 NCBI Description

```
cdc2 protein kinase homolog from A. thaliana BAC gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this gene. [Arabidopsis thaliana]
```

```
41425
Seq. No.
                  LIB3139-067-P1-N1-D4
Seq. ID
                  BLASTX
Method
                  g2961377
NCBI GI
                  321
BLAST score
                  1.0e-29
E value
                  109
Match length
% identity
                  63
                  (AL022141) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  41426
Seq. No.
                  LIB3139-067-P1-N1-D8
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
                  342
BLAST score
                  2.0e-32
E value
Match length
                  107
% identity
                   66
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41427
Seq. No.
                  LIB3139-067-P1-N1-E12
Seq. ID
Method
                  BLASTN
                   g210811
NCBI GI
                   191
BLAST score
                   1.0e-103
E value
                   403
Match length
% identity
                   87
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41428
Seq. No.
Seq. ID
                   LIB3139-067-P1-N1-F4
                   BLASTN
Method
                   g18685
NCBI GI
                   50
BLAST score
                   3.0e-19
E value
                   50
Match length
                   100
% identity
NCBI Description Soybean Ngm-16 gene coding for nodulin
                   41429
Seq. No.
                   LIB3139-067-P1-N1-H3
Seq. ID
                   BLASTX
Method
                   q3759184
NCBI GI
BLAST score
                   104
E value
                   3.0e-10
                   99
Match length
                   46
% identity
```

Seq. No. 41430

NCBI Description

(AB018441) phi-1 [Nicotiana tabacum]

```
LIB3139-068-P1-N1-D10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2454182
 BLAST score
                    275
 E value
                    2.0e-24
 Match length
                    80
 % identity
                    66
                    (U80185) pyruvate dehydrogenase E1 alpha subunit
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                   41431
 Seq. ID
                   LIB3139-068-P1-N1-E10
 Method
                   BLASTN
 NCBI GI
                   g210811
 BLAST score
                   153
 E value
                   1.0e-80
Match length
                   377
 % identity
                   85
NCBI Description
                   Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
Seq. No.
                   41432
Seq. ID
                   LIB3139-068-P1-N1-F2
Method
                   BLASTX
NCBI GI
                   g2213601
BLAST score
                   484
E value
                   6.0e-49
Match length
                   126
% identity
                   69
NCBI Description
                   (AC000348) T7N9.21 [Arabidopsis thaliana]
Seq. No.
                   41433
Seq. ID
                   LIB3139-068-P1-N1-H5
Method
                   BLASTX
NCBI GI
                   q3036807
BLAST score
                   232
E value
                   2.0e-19
Match length
                   91
% identity
                   53
NCBI Description
                  (AL022373) putative protein [Arabidopsis thaliana]
Seq. No.
                   41434
Seq. ID
                   LIB3139-069-P1-N1-A1
Method
                   BLASTX
NCBI GI
                   g2149955
BLAST score
                   185
E value
                   6.0e-16
Match length
                   98
% identity
                   57
NCBI Description
                  (U97023) putative aquaporin-1 [Phaseolus vulgaris]
Seq. No.
                   41435
Seq. ID
                  LIB3139-069-P1-N1-A11
Method
                  BLASTX
NCBI GI
                  q2493086
BLAST score
                  374
E value
                  5.0e-36
```

Match length 121 % identity 57

NCBI Description ATP SYNTHASE D CHAIN, MITOCHONDRIAL

>gi 1490232_emb_CAA67981_ (X99667) mitochondrial ATP

synthase [Drosophila melanogaster]

Seq. No. 41436

Seq. ID LIB3139-069-P1-N1-C11

Method BLASTN
NCBI GI g210811
BLAST score 190
E value 1.0e-102
Match length 358
% identity 88

% identity 88
NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41437

Seq. ID LIB3139-069-P1-N1-C3

Method BLASTN
NCBI GI g210811
BLAST score 35
E value 1.0e-10
Match length 43
% identity 95

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41438

Seq. ID LIB3139-069-P1-N1-D5

Method BLASTX
NCBI GI g3341693
BLAST score 163
E value 1.0e-11
Match length 37
% identity 76

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 41439

Seq. ID LIB3139-069-P1-N1-D9

Method BLASTX
NCBI GI g138364
BLAST score 328
E value 8.0e-31
Match length 98
% identity 65

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -bean pod mottle virus (strain Kentucky G7) >gi_210812

bean pod mottre virus (Berain Renedery 6,7 - 91_

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 41440

Seq. ID LIB3139-069-P1-N1-F1

Method BLASTN
NCBI GI g4097879
BLAST score 142
E value 5.0e-74



Match length 362 % identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41441

Seq. ID LIB3139-069-P1-N1-F2

Method BLASTN
NCBI GI g4097879
BLAST score 66
E value 9.0e-29
Match length 162

% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41442

Seq. ID LIB3139-069-P1-N1-F3

Method BLASTX
NCBI GI g4008010
BLAST score 498
E value 1.0e-50
Match length 122
% identity 77

NCBI Description (AF084036) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 41443

Seq. ID LIB3139-069-P1-N1-G6

Method BLASTN
NCBI GI g210811
BLAST score 43
E value 5.0e-15
Match length 161
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41444

Seq. ID LIB3139-069-P1-N1-G9

Method BLASTX
NCBI GI g4105772
BLAST score 250
E value 2.0e-21
Match length 64
% identity 47

NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 41445

Seq. ID LIB3139-069-P1-N1-H5

Method BLASTX
NCBI GI g3643085
BLAST score 465
E value 1.0e-46
Match length 113
% identity 77

NCBI Description (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum



41446 Seq. No. LIB3139-070-P1-N1-A3 Seq. ID Method BLASTX NCBI GI g138364 BLAST score 163 1.0e-11 E value Match length 83 47 % identity GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus] 41447 Seq. No. LIB3139-070-P1-N1-D3 Seq. ID Method BLASTX q2960364 NCBI GI BLAST score 255 5.0e-22 E value 76 Match length 62 % identity (AJ224986) cinnamoyl CoA reductase [Populus balsamifera NCBI Description subsp. trichocarpa] 41448 Seq. No. LIB3139-070-P1-N1-D5 Seq. ID BLASTX Method NCBI GI q4263722 BLAST score 300 1.0e-34 E value 116 Match length 62 % identity (AC006223) putative glucan synthase [Arabidopsis thaliana] NCBI Description 41449 Seq. No. LIB3139-070-P1-N1-E6 Seq. ID Method BLASTX NCBI GI g3335337 BLAST score 206 2.0e-16 E value Match length 90 53 % identity (AC004512) Similar to acyl carrier protein, mitochondrial NCBI Description precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330 come from this gene Seq. No. 41450 LIB3139-070-P1-N1-F8 Seq. ID Method BLASTN

Method BLASTN
NCBI GI g1675195
BLAST score 120
E value 6.0e-61
Match length 262



% identity 87

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

Seq. No.

41451

Seq. ID LIB3139-070-P1-N1-H5

Method BLASTX
NCBI GI g3914996
BLAST score 537
E value 5.0e-55
Match length 126
% identity 81

NCBI Description

PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)

>gi_1665831_dbj_BAA13640_ (D88541) phosphoserine

aminotransferase [Arabidopsis thaliana]

>gi 2804260_dbj_BAA24441_ (AB010408) phosphoserine

aminotransferase [Arabidopsis thaliana]

>gi_3367581_emb_CAA20033_ (AL031135) phosphoserine

aminotransferase [Arabidopsis thaliana]

Seq. No. 41452

Seq. ID LIB3139-071-P1-N1-A3

Method BLASTX
NCBI GI g2493390
BLAST score 248
E value 4.0e-21
Match length 125
% identity 45

NCBI Description PROBABLE STERIGMATOCYSTIN BIOSYNTHESIS P450 MONOOXYGENASE

STCL (CYTOCHROME P450 60B) >gi_1235628 (U34740) putative

p450 monooxygenase [Emericella nidulans]

Seq. No. 41453

Seq. ID LIB3139-071-P1-N1-B2

Method BLASTX
NCBI GI g2129668
BLAST score 419
E value 3.0e-41
Match length 93
% identity 88

NCBI Description phosphoglycerate kinase - Arabidopsis thaliana (fragment)

>gi_1022803 (U37700) phosphoglycerate kinase [Arabidopsis

thaliana]

Seq. No. 41454

Seq. ID LIB3139-071-P1-N1-C11

Method BLASTX
NCBI GI g2673908
BLAST score 232
E value 2.0e-19
Match length 108
% identity 50

NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 41455

Seq. ID LIB3139-071-P1-N1-C5

Method BLASTN

```
g210811
NCBI GI
                  91
BLAST score
                  1.0e-43
E value
                  207
Match length
                  86
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  41456
Seq. No.
                  LIB3139-071-P1-N1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3176659
                  284
BLAST score
                  2.0e-25
E value
                  122
Match length
                  49
% identity
                   (AC004393) Strong similarity to receptor kinase gb M80238
NCBI Description
                  from A. thaliana. [Arabidopsis thaliana]
                  41457
Seq. No.
                  LIB3139-072-P1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q138364
                  183
BLAST score
                  1.0e-13
E value
                   63
Match length
                   65
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41458
Seq. No.
                   LIB3139-072-P1-N1-A5
Seq. ID
                   BLASTX
Method
                   q138364
NCBI GI
BLAST score
                   586
                   7.0e-61
E value
                   130
Match length
                   88
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi 75639 pir_GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41459
Seq. No.
```

Seq. ID LIB3139-072-P1-N1-D1

Method BLASTX
NCBI GI g3953466
BLAST score 499
E value 1.0e-50
Match length 129
% identity 71

NCBI Description (AC002328) F20N2.11 [Arabidopsis thaliana]

Seq. No. 41460

Seq. ID LIB3139-072-P1-N1-D11



BLASTX Method g3482929 NCBI GI 455 BLAST score 2.0e-45 E value 98 Match length 80 % identity

(AC003970) Putative transcription factor [Arabidopsis NCBI Description

thaliana]

41461 Seq. No.

LIB3139-072-P1-N1-E3 Seq. ID

BLASTX Method g1346396 NCBI GI 301 BLAST score 2.0e-27 E value 112 Match length

54 % identity

PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR NCBI Description

>gi_100913_pir__S10930 probable receptor protein kinase (EC 2.7.1.-) precursor - maize >gi_22432_emb_CAA36611_ (X52384)

precursor protein (AA -26 to 791) [Zea mays]

>gi_22436_emb_CAA47962_ (X67733) receptor-like protein

kinase [Zea mays] >gi_226927_prf__1611404A receptor protein

kinase [Zea mays]

41462 Seq. No.

LIB3139-072-P1-N1-G7 Seq. ID

BLASTXMethod g3123308 NCBI GI 192 BLAST score 1.0e-14 E value 95 Match length % identity 45

HYPOTHETICAL OXIDOREDUCTASE IN COMK-SIPV INTERGENIC REGION NCBI Description

(ORFY) >gi_2226172_emb_CAA74462_ (Y14081) hypothetical protein [Bacillus subtilis] >gi_2633379_emb_CAB12883_ (Z99109) similar to ribitol dehydrogenase [Bacillus

subtilis]

41463 Seq. No.

Seq. ID LIB3139-072-P1-N1-G9

BLASTN Method q4097879 NCBI GI BLAST score 153 1.0e-80 E value 365 Match length % identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

41464 Seq. No.

Seq. ID LIB3139-072-P1-N1-H3

BLASTX Method g2582381 NCBI GI BLAST score 235 E value 9.0e-20 Match length 89

```
% identity
                  (AF021220) cation-chloride co-transporter [Nicotiana
NCBI Description
                  tabacum]
                  41465
Seq. No.
                  LIB3139-072-P1-N1-H9
Seq. ID
Method
                  BLASTX
                  g4097880
NCBI GI
                  149
BLAST score
E value
                  1.0e-09
Match length
                  101
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41466
Seq. No.
                  LIB3139-073-P1-N1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4097880
                   245
BLAST score
                   6.0e-23
E value
                   88
Match length
                   67
% identity
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41467
Seq. No.
                   LIB3139-073-P1-N1-E6
Seq. ID
                   BLASTN
Method
                   q4324966
NCBI GI
BLAST score
                   171
                   2.0e-91
E value
                   219
Match length
                   95
% identity
NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds
Seq. No.
                   41468
                   LIB3139-073-P1-N1-F5
Seq. ID
                   BLASTN
Method
                   q4099920
NCBI GI
BLAST score
                   64
                   2.0e-27
E value
                   136
Match length
                   87
% identity
NCBI Description Stylosanthes hamata EREBP-3 homolog mRNA, complete cds
                   41469
Seq. No.
                   LIB3139-073-P1-N1-G5
Seq. ID
                   BLASTX
Method
                   g4006886
NCBI GI
```

NCBI GI g4006888
BLAST score 318
E value 2.0e-29
Match length 66
% identity 85

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3139-073-P1-N1-G9

41470

Method BLASTN

```
q1498327
NCBI GI
                  60
BLAST score
                  3.0e-25
E value
                  92
Match length
                  92
% identity
NCBI Description Glycine max actin (Soy70) gene, partial cds
                  41471
Seq. No.
                  LIB3139-073-P1-N1-H8
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
                  430
BLAST score
                  1.0e-42
E value
                  116
Match length
                  72
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41472
Seq. No.
                  LIB3139-074-P1-N1-C10
Seq. ID
                  BLASTX
Method
                  g138364
NCBI GI
BLAST score
                   160
E value
                   4.0e-17
                   118
Match length
                   47
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41473
Seq. No.
                   LIB3139-074-P1-N1-C2
Seq. ID
                   BLASTX
Method
                   q4210806
NCBI GI
                   127
BLAST score
                   8.0e-15
E value
                   102
Match length
                   52
% identity
                  (Y17906) polygalacturonase [Phaedon cochleariae]
NCBI Description
                   41474
Seq. No.
Seq. ID
                   LIB3139-074-P1-N1-C3
                   BLASTN
Method
                   q4097879
NCBI GI
                   93
BLAST score
```

7.0e-45 E value Match length 261 84 % identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

Seq. No. 41475

LIB3139-074-P1-N1-H1 Seq. ID

BLASTN Method NCBI GI q169922 131 BLAST score 2.0e-67 E value



```
Match length
                   95
% identity
```

Soybean beta-1,3-endoglucanase mRNA, complete cds NCBI Description

Seq. No. Seq. ID

41476

LIB3139-075-P1-N1-B2

BLASTN Method g210811 NCBI GI 151 BLAST score 2.0e-79 E value 325 Match length

% identity 86 Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

Seq. No.

41477

LIB3139-075-P1-N1-B4 Seq. ID BLASTX Method

g4539292 NCBI GI 390 BLAST score 6.0e-38 E value Match length 88 % identity 82

(AL049480) putative ribosomal protein S10 [Arabidopsis NCBI Description

thaliana]

41478 Seq. No.

LIB3139-075-P1-N1-C1 Seq. ID

BLASTN Method g3176097 NCBI GI 78 BLAST score E value 6.0e-36 186 Match length 85 % identity

Medicago truncatula mRNA for annexin NCBI Description

Seq. No.

41479

Seq. ID LIB3139-075-P1-N1-D4

BLASTN Method g3021374 NCBI GI BLAST score 107 3.0e-53 E value 211 Match length 88 % identity

Glycine max mRNA for profilin, PRO1 NCBI Description

Seq. No.

41480

Seq. ID LIB3139-075-P1-N1-F3

BLASTN Method g210811 NCBI GI BLAST score 86 E value 1.0e-40 240 Match length 85 % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

```
Seq. No.
                  LIB3139-075-P1-N1-G11
Seq. ID
                  BLASTN
Method
                  g3204105
NCBI GI
                  36
BLAST score
                  6.0e-11
E value
                  40
Match length
                  97
% identity
                  Cicer arietinum mRNA for putative beta-amilase, partial
NCBI Description
                  41482
Seq. No.
                  LIB3139-075-P1-N1-G7
Seq. ID
                  BLASTX
Method
                   q2706450
NCBI GI
                   193
BLAST score
                   5.0e-15
E value
                   70
Match length
                   60
% identity
                   (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                   pyrophosphatase [Solanum tuberosum]
Seq. No.
                   41483
                   LIB3139-075-P1-N1-H2
Seq. ID
                   BLASTX
Method
                   q138364
NCBI GI
                   146
BLAST score
                   6.0e-16
E value
                   96
Match length
                   56
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41484
Seq. No.
Seq. ID
                   LIB3139-076-P1-N1-C11
                   BLASTN
Method
                   q210811
NCBI GI
                   45
BLAST score
                   4.0e-16
E value
                   77
Match length
                   90
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41485
Seq. No.
Seq. ID
                   LIB3139-076-P1-N1-D1
                   BLASTN
Method
```

Method BLASTN
NCBI GI 94097879
BLAST score 173
E value 1.0e-92
Match length 369
% identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41486

```
LIB3139-076-P1-N1-F2
Seq. ID
                  BLASTN
Method
                  g1431621
NCBI GI
                  45
BLAST score
                  2.0e-16
E value
Match length
                  105
                  87
% identity
NCBI Description T.repens mRNA for protein kinase
Seq. No.
                  41487
                  LIB3139-076-P1-N1-H12
Seq. ID
Method
                  BLASTX
                  q3643085
NCBI GI
BLAST score
                  303
                  1.0e-27
E value
Match length
                  94
                   60
% identity
                  (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  41488
Seq. ID
                  LIB3139-077-P1-N1-A7
Method
                  BLASTX
NCBI GI
                  g4097880
                  297
BLAST score
                   6.0e-27
E value
Match length
                   132
                   54
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
                   41489
Seq. No.
                   LIB3139-077-P1-N1-A8
Seq. ID
Method
                   BLASTN
                   q18685
NCBI GI
                   284
BLAST score
                   1.0e-159
E value
                   406
Match length
                   100
% identity
NCBI Description Soybean Ngm-16 gene coding for nodulin
                   41490
Seq. No.
                   LIB3139-077-P1-N1-A9
Seq. ID
                   BLASTN
Method
                   g2317899
NCBI GI
                   153
BLAST score
                   1.0e-80
E value
                   297
Match length
                   87
% identity
NCBI Description Glycine max Sali3-2 mRNA, complete cds
```

41491 Seq. No.

Seq. ID LIB3139-077-P1-N1-B1

Method BLASTX g1932938 NCBI GI BLAST score 192 1.0e-14 E value Match length 84

```
% identity
                  (U80191) TFIID subunit TAFII100 [Homo sapiens]
NCBI Description
                  41492
Seq. No.
Seq. ID
                  LIB3139-077-P1-N1-B12
                  BLASTX
Method
                  q3641838
NCBI GI
                  134
BLAST score
                   5.0e-09
E value
                   80
Match length
                   55
% identity
                   (AL023094) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                   41493
Seq. No.
Seq. ID
                  LIB3139-077-P1-N1-B9
                   BLASTX
Method
NCBI GI
                   g2642450
BLAST score
                   287
                   9.0e-26
E value
                   71
Match length
                   82
% identity
                   (AC002391) putative metal ion transporter (Nramp)
NCBI Description
                   [Arabidopsis thaliana] >gi 3169188 (AC004401) putative
                   metal ion transporter (Nramp) [Arabidopsis thaliana]
                   41494
Seq. No.
                   LIB3139-077-P1-N1-C6
Seq. ID
                   BLASTX
Method
                   g3157927
NCBI GI
BLAST score
                   262
E value
                   7.0e-23
                   102
Match length
% identity
                   56
                   (AC002131) Contains similarity to GDP-dissociation
NCBI Description
                   inhibitor gb_L07918 from Mus musculus. [Arabidopsis
                   thaliana]
                   41495
Seq. No.
                   LIB3139-077-P1-N1-D5
Seq. ID
Method
                   BLASTX
                   q3643608
NCBI GI
BLAST score
                   184
                   1.0e-13
E value
                   105
Match length
                   41
% identity
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 41496

Seq. ID LIB3139-077-P1-N1-D9

Method BLASTN
NCBI GI g4097879
BLAST score 136
E value 2.0e-70
Match length 355
% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein



gene, complete cds

```
41497
Seq. No.
                  LIB3139-077-P1-N1-E5
Seq. ID
                  BLASTX
Method
                  q2398679
NCBI GI
                  383
BLAST score
                  7.0e-38
E value
                  122
Match length
                  70
% identity
                  (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
NCBI Description
                  synthase [Morinda citrifolia]
                  41498
Seq. No.
Seq. ID
                  LIB3139-077-P1-N1-E8
                  BLASTX
Method
                  g2497790
NCBI GI
                  167
BLAST score
                   6.0e-12
E value
Match length
                   92
                   33
% identity
                  LYSOSOMAL ALPHA-GLUCOSIDASE PRECURSOR (ACID MALTASE)
NCBI Description
                   >gi 1515359 (U49351) lysosomal alpha-glucosidase [Mus
                  musculus]
                   41499
Seq. No.
                  LIB3139-077-P1-N1-F6
Seq. ID
                   BLASTX
Method
                   g138364
NCBI GI
                   162
BLAST score
                   3.0e-11
E value
Match length
                   107
                   38
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41500
Seq. No.
Seq. ID
                   LIB3139-077-P1-N1-H3
                   BLASTN
Method
                   q296444
NCBI GI
BLAST score
                   72
                   3.0e - 32
E value
                   262
Match length
                   83
% identity
NCBI Description G.max ADR6 mRNA
Seq. No.
                   41501
                   LIB3139-077-P1-N1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4097880
BLAST score
                   280
```

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

4.0e-29

105

69

E value Match length

% identity



```
41502
Seq. No.
                  LIB3139-078-P1-N1-A6
Seq. ID
                  BLASTN
Method
                  g4097879
NCBI GI
                  142
BLAST score
                  5.0e-74
E value
                  282
Match length
                  88
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  41503
Seq. No.
                  LIB3139-078-P1-N1-B6
Seq. ID
                  BLASTN
Method
                  g1632800
NCBI GI
BLAST score
                  82
                  1.0e-38
E value
                  114
Match length
                   93
% identity
NCBI Description G.intraradices 5' large ribosomal subunit
Seq. No.
                   41504
                   LIB3139-078-P1-N1-C4
Seq. ID
Method
                   BLASTN
                   q170050
NCBI GI
                   225
BLAST score
E value
                   1.0e-123
                   361
Match length
                   93
% identity
NCBI Description Soybean pyruvate kinase mRNA, complete cds
Seq. No.
                   41505
                   LIB3139-078-P1-N1-C9
Seq. ID
                   BLASTX
Method
                   g4559366
NCBI GI
BLAST score
                   267
                   2.0e-23
E value
                   113
Match length
                   49
% identity
                   (AC006585) putative tyrosine transaminase [Arabidopsis
NCBI Description
                   thaliana]
                   41506
Seq. No.
                   LIB3139-078-P1-N1-D6
Seq. ID
                   BLASTX
Method
                   g3522943
NCBI GI
BLAST score
                   268
                   9.0e-24
E value
                   90
Match length
                   29
% identity
                  (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
NCBI Description
                   41507
Seq. No.
Seq. ID
                   LIB3139-078-P1-N1-F10
```

BLASTX

q133320

Method

NCBI GI

```
BLAST score
                  1.0e-48
E value
Match length
                  122
                  75
% identity
                  DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (A135)
NCBI Description
                  (RNA POLYMERASE I SUBUNIT 2) >gi 101446_pir__A39607
                  DNA-directed RNA polymerase (EC 2.7.7.6) I 135K chain -
                  yeast (Saccharomyces cerevisiae) >gi_172464 (M62804) RNA
                  polymerase I (second largest subunit) [Saccharomyces
                  cerevisiae] >gi 887587 emb_CAA90154_ (Z49919) Rpa2p
                  [Saccharomyces cerevisiae] >gi_939744 (U31900) Rpa135p
                  [Saccharomyces cerevisiae] >gi 1314085 emb CAA95050
                  (Z71255) Rpa2p [Saccharomyces cerevisiae]
                  41508
Seq. No.
Seq. ID
                  LIB3139-079-P1-N1-B8
                  BLASTN
                  g4097879
```

Seq. ID LIB3139-079-P1-N1-B8
Method BLASTN
NCBI GI g4097879
BLAST score 71
E value 7.0e-32
Match length 131
% identity 89

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

 Seq. No.
 41509

 Seq. ID
 LIB3139-079-P1-N1-C8

 Method
 BLASTX

 NCBI GI
 g3421123

BLAST score 218
E value 8.0e-18
Match length 57
% identity 70

NCBI Description (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis

thaliana]

Seq. No. 41510

Seq. ID LIB3139-079-P1-N1-D10

Method BLASTX
NCBI GI g4559381
BLAST score 283
E value 2.0e-25
Match length 92
% identity 57

NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No. 41511

Seq. ID LIB3139-079-P1-N1-D3

Method BLASTN
NCBI GI g4138678
BLAST score 102
E value 4.0e-50
Match length 214
% identity 87

NCBI Description V.faba mRNA for amino acid transporter

Seq. No. 41512

```
LIB3139-079-P1-N1-D9
Seq. ID
                  BLASTX
Method
                  g2346976
NCBI GI
                  181
BLAST score
                  2.0e-13
E value
                  99
Match length
                  43
% identity
NCBI Description (AB006600) ZPT2-13 [Petunia x hybrida]
                  41513
Seq. No.
                  LIB3139-079-P1-N1-E12
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
                  323
BLAST score
                  3.0e - 32
E value
                  101
Match length
% identity
                   68
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41514
Seq. No.
                  LIB3139-079-P1-N1-E8
Seq. ID
Method
                  BLASTN
                  g210811
NCBI GI
                   47
BLAST score
                   1.0e-17
E value
                   123
Match length
                   85
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41515
Seq. No.
                   LIB3139-079-P1-N1-E9
Seq. ID
                   BLASTN
Method
                   q210811
NCBI GI
                   49
BLAST score
                   9.0e-19
E value
Match length
                   171
                   84
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41516
Seq. No.
Seq. ID
                   LIB3139-079-P1-N1-F12
                   BLASTN
Method
NCBI GI
                   q2815245
                   57
BLAST score
                   3.0e-23
```

E value 101 Match length % identity 89

C.arietinum mRNA for class I type 2 metallothionein (clone: NCBI Description

CanMT-2)

41517 Seq. No.

LIB3139-079-P1-N1-G4 Seq. ID

Method BLASTX NCBI GI g2511693 BLAST score 226

NCBI Description



```
1.0e-18
E value
                  82
Match length
                  57
% identity
                  (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
NCBI Description
                  41518
Seq. No.
                  LIB3139-079-P1-N1-H3
Seq. ID
                  BLASTX
Method
                  g229707
NCBI GI
                  307
BLAST score
                  3.0e-28
E value
                  102
Match length
                   65
% identity
NCBI Description Bean pod mottle virus
                   41519
Seq. No.
                  LIB3139-080-P1-N1-A3
Seq. ID
                  BLASTN
Method
                   g210811
NCBI GI
                   178
BLAST score
                   2.0e-95
E value
Match length
                   306
% identity
                   90
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41520
Seq. No.
                   LIB3139-080-P1-N1-A7
Seq. ID
                   {\tt BLASTX}
Method
                   g2654321
NCBI GI
BLAST score
                   248
                   9.0e-22
E value
                   59
Match length
                   83
% identity
                  (Y09664) translation elongation factor 2 [Candida albicans]
NCBI Description
                   41521
Seq. No.
                   LIB3139-080-P1-N1-B3
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   175
BLAST score
                   1.0e-93
E value
                   377
Match length
                   87
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   41522
Seq. ID
                   LIB3139-080-P1-N1-C1
                   BLASTX
Method
                   g2465923
NCBI GI
BLAST score
                   216
                   1.0e-17
E value
                   105
Match length
% identity
```

[Arabidopsis thaliana]

(AF024648) receptor-like serine/threonine kinase



Seq. No. Seq. ID

41523

LIB3139-080-P1-N1-E12

```
BLASTX
Method
                  g2827714
NCBI GI
                  243
BLAST score
                  1.0e-20
E value
                  110
Match length
                  47
% identity
                  (AL021684) receptor protein kinase - like protein
NCBI Description
                  [Arabidopsis thaliana]
                  41524
Seq. No.
                  LIB3139-080-P1-N1-E3
Seq. ID
                  BLASTX
Method
                  g3043656
NCBI GI
                  406
BLAST score
                  9.0e-40
E value
                  121
Match length
                  60
% identity
NCBI Description (AB011138) KIAA0566 protein [Homo sapiens]
                  41525
Seq. No.
                  LIB3139-080-P1-N1-E6
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
BLAST score
                  388
                  5.0e-39
E value
                  110
Match length
                  77
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
                   41526
Seq. No.
                  LIB3139-080-P1-N1-G9
Seq. ID
                  BLASTX
Method
                   g1351014
NCBI GI
BLAST score
                   402
                   3.0e-39
E value
                   106
Match length
                   76
% identity
                   40S RIBOSOMAL PROTEIN S8 >gi 968902_dbj_BAA07207_ (D38010)
NCBI Description
                   ribosomal protein S8 [Oryza sativa]
Seq. No.
                   41527
                   LIB3139-080-P1-N1-H4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g127277
BLAST score
                   243
                   1.0e-20
E value
                   72
Match length
% identity
                   MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN (PHOSPHATE
NCBI Description
                   TRANSPORT PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR) (P32)
                   >gi_83332_pir__S12318 phosphate transport protein,
                   mitochondrial - yeast (Saccharomyces cerevisiae) >gi_171957
                   (M54879) mitochondrial phosphate transport protein
                   [Saccharomyces cerevisiae] >gi_296863_emb_CAA40716_
```

Match length

104

```
>gi 1015764 emb CAA89605 (Z49577) ORF YJR077c
                  [Saccharomyces cerevisiae] >gi_1019698 (L47993)
                  Saccharomyces cerevisiae ORF genes, complete cds's
                  [Saccharomyces cerevisiae] >gi 227212 prf 1616363A
                  mitochondrial import receptor [Saccharomyces cerevisiae]
                  41528
Seq. No.
Seq. ID
                  LIB3139-081-P1-N1-A8
Method
                  BLASTX
                  q138364
NCBI GI
                  147
BLAST score
                  6.0e-10
E value
                  47
Match length
                  62
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                  (M62738) coat protein [Bean pod mottle virus]
                  41529
Seq. No.
                  LIB3139-081-P1-N1-D12
Seq. ID
                  BLASTN
Method
                  g3860307
NCBI GI
                  32
BLAST score
                  1.0e-08
E value
                  52
Match length
                  90
% identity
NCBI Description Cicer arietinum mRNA for hypothetical protein, clone Can137
                  41530
Seq. No.
Seq. ID
                  LIB3139-081-P1-N1-E10
                  BLASTX
Method
                  g4263522
NCBI GI
                  344
BLAST score
                  2.0e-32
E value
Match length
                  120
% identity
                  48
                  (AC004044) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  41531
Seq. No.
                  LIB3139-081-P1-N1-H10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g456713
BLAST score
                  295
E value
                  1.0e-165
Match length
                  303
                  25
% identity
                  Glycine max gene for ubiquitin, complete cds
NCBI Description
Seq. No.
                   41532
Seq. ID
                  LIB3139-082-P1-N1-A6
                  BLASTX
Method
                  q3482967
NCBI GI
BLAST score
                   401
E value
                   4.0e-39
```

(X57478) MIR1 [Saccharomyces cerevisiae]



% identity NCBI Description

(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >qi 4559345 qb AAD23006.1 AC006585 1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.

41533

Seq. ID

LIB3139-082-P1-N1-B7

Method NCBI GI BLASTX q1710840

BLAST score E value

4.0e-13 68

176

Match length % identity

54

NCBI Description

ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57) >gi 441217 dbj BAA03709 (D16138) S-adenosyl-L-homocystein hydrolase [Nicotiana sylvestris] >gi_1857024_dbj_BAA08142_ (D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana

tabacum] >gi 2588781 dbj BAA23164 (D49804)

S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]

Seq. No.

41534

LIB3139-082-P1-N1-C3 Seq. ID

BLASTX Method q3426048 NCBI GI BLAST score 226 1.0e-18 E value 55 Match length % identity

NCBI Description

(AC005168) putative hydroxymethylglutaryl-CoA lyase

precursor [Arabidopsis thaliana]

Seq. No.

41535

Seq. ID

LIB3139-082-P1-N1-C5

Method BLASTN q4097879 NCBI GI 70 BLAST score 5.0e-31 E value 237 Match length 84 % identity

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No.

41536

Seq. ID

LIB3139-082-P1-N1-G11

BLASTX Method NCBI GI q138364 BLAST score 333 2.0e-33 E value Match length 125 70 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No.



```
LIB3139-082-P1-N1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2828147
                  193
BLAST score
E value
                   9.0e-15
Match length
                   56
% identity
                  (AF042384) BC-2 protein [Homo sapiens]
NCBI Description
                   41538
Seq. No.
Seq. ID
                  LIB3139-082-P1-N1-H4
Method
                  BLASTX
                  g4097880
NCBI GI
BLAST score
                   321
                   4.0e-42
E value
                   114
Match length
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   41539
Seq. ID
                   LIB3139-082-P1-N1-H6
Method
                   BLASTX
                   q4468813
NCBI GI
                   219
BLAST score
                   8.0e-18
E value
                   80
Match length
                   49
% identity
                   (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                   41540
Seq. No.
Seq. ID
                   LIB3139-083-P1-N1-C11
                   BLASTX
Method
                   q1825645
NCBI GI
                   176
BLAST score
                   9.0e-13
E value
Match length
                   72
                   51
% identity
                   (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                   ubiquitin-like protein 8 [Caenorhabditis elegans]
Seq. No.
                   41541
Seq. ID
                   LIB3139-083-P1-N1-C6
Method
                   BLASTX
NCBI GI
                   q421810
BLAST score
                   233
                   1.0e-19
E value
Match length
                   74
                   68
% identity
                   acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor -
NCBI Description
                   cucumber
                   41542
Seq. No.
                   LIB3139-083-P1-N1-F1
Seq. ID
Method
                   BLASTX
                   q3901012
NCBI GI
```

406

1.0e-39

BLAST score

E value

```
Match length
                   85
% identity
```

(AJ130885) xyloglucan endotransglycosylase 1 [Fagus NCBI Description

sylvatica]

41543

Seq. No.

LIB3139-083-P1-N1-G12 Seq. ID

BLASTX Method g1078614 NCBI GI 164 BLAST score 2.0e-11 E value 80 Match length

40 % identity

stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces NCBI Description

capsulata >gi_757862_emb_CAA59938 (X85962) delta-9 fatty

acid desaturase [Ajellomyces capsulatus]

41544 Seq. No.

LIB3139-083-P1-N1-H1 Seq. ID

BLASTN Method g296444 NCBI GI BLAST score 205 E value 1.0e-111 397 Match length 88 % identity

NCBI Description G.max ADR6 mRNA

Seq. No. 41545

LIB3139-083-P1-N1-H6 Seq. ID

BLASTX Method g445126 NCBI GI BLAST score 510 6.0e-52 E value 111 Match length 97

% identity

NCBI Description heat shock protein HSP81-1 [Arabidopsis thaliana]

41546 Seq. No.

LIB3139-084-P1-N1-B7 Seq. ID

BLASTN Method g2145472 NCBI GI BLAST score 42 2.0e-14 E value Match length 106 85 % identity

NCBI Description S.tuberosum mRNA for aconitase/aconitate hydratase

41547 Seq. No.

LIB3139-084-P1-N1-B8 Seq. ID

BLASTX Method g3080434 NCBI GI BLAST score 144 3.0e-09 E value 66 Match length % identity

(AL022605) putative gamma-glutamyltransferase [Arabidopsis NCBI Description

thaliana]



```
Seq. No.
                  41548
                  LIB3139-084-P1-N1-D12
Seq. ID
                  BLASTX
Method
                  g2494176
NCBI GI
BLAST score
                  147
                  2.0e-09
E value
Match length
                  82
% identity
                  PUTATIVE GLUTAMATE DECARBOXYLASE (GAD)
NCBI Description
                   >gi_1078596_pir__S53072 probable membrane protein YMR250w -
                   yeast (Saccharomyces cerevisiae) >gi_732928 emb CAA88577
                   (Z48639) unknown [Saccharomyces cerevisiae]
Seq. No.
                   LIB3139-084-P1-N1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4097879
BLAST score
                   101
E value
                   1.0e-49
                   309
Match length
                   83
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41550
Seq. No.
                   LIB3139-084-P1-N1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2181186
BLAST score
                   174
                   1.0e-25
E value
Match length
                   101
% identity
                   63
                   (X97323) outward rectifying potassium channel KCO1
NCBI Description
                   [Arabidopsis thaliana] >gi 2230761 emb CAA69158 (Y07825)
                   kcol [Arabidopsis thaliana]
                   41551
Seq. No.
                   LIB3139-084-P1-N1-G8
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   64
BLAST score
                   2.0e-27
E value
                   184
Match length
                   84
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41552
Seq. No.
Seq. ID
                   LIB3139-084-P1-N1-H7
                   BLASTX
Method
                   g4190952
NCBI GI
BLAST score
                   488
                   2.0e-49
E value
                   131
Match length
                   69
% identity
```

NCBI Description (AB022689) similar to hsr203J [Lycopersicon esculentum]



```
41553
Seq. No.
                  LIB3139-085-P1-N1-C11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g210811
                  57
BLAST score
                  3.0e-23
E value
                  97
Match length
                  90
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   41554
Seq. No.
                  LIB3139-085-P1-N1-E1
Seq. ID
                  BLASTX
Method
                  g322670
NCBI GI
BLAST score
                   437
                   1.0e-43
E value
                   99
Match length
                   82
% identity
                  hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) -
NCBI Description
                   radish >gi_21104_emb_CAA48611 (X68652)
                   hydroxymethylglutaryl-CoA reductase (NADPH) [Raphanus
                   sativus]
                   41555
Seq. No.
                   LIB3139-085-P1-N1-E5
Seq. ID
Method
                   BLASTN
                   g210811
NCBI GI
                   49
BLAST score
                   1.0e-18
E value
                   77
Match length
% identity
                   92
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41556
Seq. No.
Seq. ID
                   LIB3139-085-P1-N1-G3
                   BLASTX
Method
                   g169900
NCBI GI
BLAST score
                   169
                   2.0e-12
E value
Match length
                   65
                   57
% identity
                   (M37529) 31 kDa protein [Glycine max]
NCBI Description
                   41557
Seq. No.
Seq. ID
                   LIB3139-085-P1-N1-H6
                   BLASTX
Method
                   g3702332
NCBI GI
BLAST score
                   286
                   1.0e-25
E value
Match length
                   118
                   52
% identity
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
```

41558

Seq. No.



```
LIB3139-085-P4-N4-A5
Seq. ID
                  BLASTX
Method
                  q3510251
NCBI GI
                   401
BLAST score
                   3.0e-39
E value
Match length
                  115
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                   41559
Seq. No.
                  LIB3139-085-P4-N4-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                   q18727
                   33
BLAST score
                   3.0e-09
E value
                   57
Match length
                   89
% identity
                   Soybean mRNA for reductase involved in deoxychalcone
NCBI Description
                   synthesis (NAD(P)H dependent 6'-deoxychalcone synthase)
                   41560
Seq. No.
                   LIB3139-086-P1-N1-A10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q609224
                   168
BLAST score
                   2.0e-89
E value
                   307
Match length
                   89
% identity
                   P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB
NCBI Description
                   Pisum sativum S-adenosylmethionine synthase mRNA, complete
                   41561
Seq. No.
                   LIB3139-086-P1-N1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1143717
BLAST score
                   211
                   7.0e-17
E value
Match length
                   79
% identity
                   51
                   (U17603) rS-Rex-s [Rattus norvegicus]
NCBI Description
                   41562
Seq. No.
                   LIB3139-086-P1-N1-A7
Seq. ID
                   BLASTX
Method
                   g2827555
NCBI GI
                   204
BLAST score
                   5.0e-16
E value
                   68
Match length
 % identity
                   65
                   (AL021635) Translation factor EF-1 alpha - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   41563
 Seq. No.
                   LIB3139-086-P1-N1-B7
 Seq. ID
```

6549

BLASTX

q1680686

Method NCBI GI



BLAST score 390 E value 8.0e-38 Match length 110 % identity 71

NCBI Description (U51330) rust resistance kinase Lr10 [Triticum aestivum]

Seq. No. 41564

Seq. ID LIB3139-086-P1-N1-C3

Method BLASTN
NCBI GI g343022
BLAST score 37
E value 2.0e-11
Match length 85
% identity 86

NCBI Description Pea chloroplast photosystem II gene encoding the D2 and

44kd chlorophyll a-binding proteins, complete cds

Seq. No. 41565

Seq. ID LIB3139-086-P1-N1-D10

Method BLASTN
NCBI GI 9408791
BLAST score 101
E value 1.0e-49
Match length 168
% identity 93

NCBI Description Glycine soja chloroplast omega-3 fatty acid desaturase

(Fadd) mRNA, complete cds

Seq. No. 41566

Seq. ID LIB3139-086-P1-N1-D3

Method BLASTN
NCBI GI g1184986
BLAST score 147
E value 6.0e-77
Match length 263
% identity 89

NCBI Description Nicotiana tabacum GTP-binding protein NTGB1 mRNA, partial

cds

Seq. No. 41567

Seq. ID LIB3139-086-P1-N1-D8

Method BLASTN
NCBI GI g4097879
BLAST score 140
E value 8.0e-73
Match length 384
% identity 84

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41568

Seq. ID LIB3139-086-P1-N1-H11

Method BLASTN
NCBI GI g4097879
BLAST score 76
E value 5.0e-35
Match length 120



% identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

41569 Seq. No.

Seq. ID LIB3139-086-P1-N1-H12

BLASTX Method NCBI GI g138364 BLAST score 151 8.0e-10 E value 49 Match length

% identity 61

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

41570 Seq. No.

LIB3139-087-P1-N1-A7 Seq. ID

BLASTX Method g833835 NCBI GI BLAST score 105 1.0e-10 E value 85 Match length 52 % identity

(U26025) amygdalin hydrolase isoform AH I precursor [Prunus NCBI Description

serotina]

41571 Seq. No.

LIB3139-087-P1-N1-E7 Seq. ID

BLASTN Method g255407 NCBI GI BLAST score 148 8.0e-78 E value 252 Match length 90 % identity

repetitive proline-rich protein {cDNA clone 1A10-2} NCBI Description

[Glycine max=soybeans, axes germinated for 31 hours, mRNA,

943 nt]

41572 Seq. No.

Seq. ID LIB3139-087-P1-N1-G3

BLASTX Method NCBI GI g4263712 BLAST score 163 E value 1.0e-11 48 Match length 67 % identity

(AC006223) putative ribosomal protein S12 [Arabidopsis NCBI Description

thaliana]

Seq. No. 41573

LIB3139-087-P1-N1-H10 Seq. ID

BLASTN Method NCBI GI q3818415 BLAST score 54 E value 1.0e-21



Match length 280 % identity 30

NCBI Description Medicago sativa proline-rich cell wall protein gene,

complete cds

Seq. No. 41574

Seq. ID LIB3139-088-P1-N1-E1

Method BLASTX
NCBI GI g2244915
BLAST score 159
E value 1.0e-10
Match length 78
% identity 38

NCBI Description (Z97339) strong homology to reverse transcriptase

[Arabidopsis thaliana]

Seq. No. 41575

Seq. ID LIB3139-088-P1-N1-F8

Method BLASTX
NCBI GI g4105633'
BLAST score 363
E value 1.0e-34
Match length 114
% identity 61

NCBI Description (AF048982) putative ethylene receptor [Arabidopsis

thaliana]

Seq. No. 41576

Seq. ID LIB3139-088-P1-N1-G6

Method BLASTN
NCBI GI g210811
BLAST score 120
E value 8.0e-61
Match length 276
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41577

Seq. ID LIB3139-089-P1-N1-B12

Method BLASTX
NCBI GI g4206210
BLAST score 245
E value 6.0e-21
Match length 111
% identity 47

NCBI Description (AF071527) putative calcium channel [Arabidopsis thaliana]

>qi 4263043 gb AAD15312 (AC005142) putative calcium

channel [Arabidopsis thaliana]

Seq. No. 41578

Seq. ID LIB3139-089-P1-N1-C6

Method BLASTN
NCBI GI g4097879
BLAST score 77
E value 2.0e-35
Match length 249



% identity 83
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
gene, complete cds

Seq. No. 41579

Seq. ID LIB3139-089-P1-N1-E5

Method BLASTX
NCBI GI g818849
BLAST score 175
E value 4.0e-13
Match length 65

% identity 56
NCBI Description (U25430) nucleotide pyrophosphatase precursor [Oryza

sativa]

Seq. No. 41580

Seq. ID LIB3139-089-P1-N1-G8

Method BLASTN
NCBI GI g4097879
BLAST score 166
E value 2.0e-88
Match length 362
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41581

Seq. ID LIB3139-089-P1-N1-H4

Method BLASTX
NCBI GI g3913008
BLAST score 113
E value 9.0e-11
Match length 68
% identity 62

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_3021338_emb_CAA06308_ (AJ005041) cytosolic

fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No. 41582

Seq. ID LIB3139-090-P1-N1-A1

Method BLASTN
NCBI GI g210811
BLAST score 42
E value 2.0e-14
Match length 70
% identity 90

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41583

Seq. ID LIB3139-090-P1-N1-B10

Method BLASTN
NCBI GI g558142
BLAST score 98
E value 9.0e-48
Match length 220
% identity 90



NCBI Description Vicia faba NADH ubiquinone oxidoreductase subunit 5 (nad5) gene, mitochondrial gene encoding mitochondrial protein,

exons c

41584

Seq. No.

Seq. ID LIB3139-090-P1-N1-C11

Method BLASTN
NCBI GI g2921337
BLAST score 34

E value 2.0e-09 Match length 62 % identity 89

NCBI Description Gossypium hirsutum MYB-like DNA-binding domain protein

(Cmy-N) mRNA, complete cds

Seq. No. 41585

Seq. ID LIB3139-090-P1-N1-E5

Method BLASTN
NCBI GI 94097879
BLAST score 182
E value 8.0e-98
Match length 428
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41586

Seq. ID LIB3139-090-P1-N1-E8

Method BLASTN
NCBI GI g210811
BLAST score 147
E value 6.0e-77
Match length 331
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41587

Seq. ID LIB3139-091-P1-N1-A1

Method BLASTN
NCBI GI g210811
BLAST score 115
E value 5.0e-58
Match length 242
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41588

Seq. ID LIB3139-091-P1-N1-A3

Method BLASTX
NCBI GI g1709970
BLAST score 306
E value 5.0e-28
Match length 109
% identity 61

NCBI Description 60S RIBOSOMAL PROTEIN L10A



```
Seq. No.
                  41589
                  LIB3139-091-P1-N1-A6
Seq. ID
                  BLASTX
Method
                  g2982431
NCBI GI
BLAST score
                  495
                  4.0e-50
E value
                  132
Match length
                  71
% identity
                  (AL022224) leucine rich repeat-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  41590
                  LIB3139-091-P1-N1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500004
BLAST score
                  431
E value
                  1.0e-42
                  124
Match length
                   67
% identity
                  PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (GARS) (GLYCINAMIDE
NCBI Description
                  RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE
                  SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINAMIDINE
                   CYCLO-LIGASE (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE
                   SYNTHETASE)... >gi 1117927 (U40565) Adelp [Yarrowia
                   lipolytica]
                   41591
Seq. No.
                   LIB3139-091-P1-N1-E7
Seq. ID
Method
                  BLASTX
                   g2827082
NCBI GI
BLAST score
                   339
E value
                   4.0e-32
                   97
Match length
                   68
% identity
NCBI Description (AF020272) malate dehydrogenase [Medicago sativa]
                   41592
Seq. No.
                   LIB3139-092-P1-N1-A6
Seq. ID
                   BLASTX
Method
                   g3914893
NCBI GI
                   152
BLAST score
                   6.0e-10
E value
                   70
Match length
                   47
% identity
                   30S RIBOSOMAL PROTEIN S17 >gi 2982774 (AE000669) ribosomal
NCBI Description
                   protein S17 [Aquifex aeolicus]
                   41593
Seq. No.
                   LIB3139-092-P1-N1-B4
Seq. ID
                   BLASTX
Method
                   g3834322
NCBI GI
BLAST score
                   206
                   3.0e-16
E value
                   52
Match length
                   81
% identity
NCBI Description (AC005679) EST gb R30300 comes from this gene. [Arabidopsis
```



thaliana]

```
41594
Seq. No.
                  LIB3139-092-P1-N1-B5
Seq. ID
                  BLASTX
Method
                  g3834322
NCBI GI
BLAST score
                  161
                  7.0e-11
E value
                  52
Match length
                  69
% identity
                  (AC005679) EST gb R30300 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  41595
Seq. No.
                  LIB3139-092-P1-N1-D11
Seq. ID
                  BLASTX
Method
                  g2529663
NCBI GI
                  265
BLAST score
                  4.0e-23
E value
                   97
Match length
                   52
% identity
                   (AC002535) putative lysophospholipase [Arabidopsis
NCBI Description
                   thaliana] >gi_3738277 (AC005309) putative lysophospholipase
                   [Arabidopsis Thaliana]
                   41596
Seq. No.
                  LIB3139-092-P1-N1-F12
Seq. ID
                  BLASTX
Method
                  g2244993
NCBI GI
                   154
BLAST score
                   4.0e-10
E value
Match length
                   45
                   64
% identity
                   (Z97341) similarity to AMP-activated protein kinase beta
NCBI Description
                   [Arabidopsis thaliana]
                   41597
Seq. No.
Seq. ID
                   LIB3139-092-P1-N1-F6
                   BLASTX
Method
                   q138364
NCBI GI
BLAST score
                   139
                   8.0e-09
E value
Match length
                   77
                   48
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                   bean pod mottle vīrus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41598
Seq. No.
                   LIB3139-092-P1-N1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510339
BLAST score
                   208
```

1.0e-16

80

58

E value Match length

% identity

```
(AC006921) putative ABC transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  41599
Seq. No.
Seq. ID
                  LIB3139-092-P1-N1-H12
                  BLASTN
Method
                  g210811
NCBI GI
                  52
BLAST score
                  3.0e-20
E value
                  280
Match length
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                  41600
Seq. No.
                  LIB3139-092-P1-N1-H4
Seq. ID
                  BLASTX
Method
                  g549811
NCBI GI
                  230
BLAST score
                  2.0e-19
E value
Match length
                  89
                   51
% identity
                  GTP-BINDING PROTEIN YPTV4 (RAB2 HOMOLOG)
NCBI Description
                  >gi 486946_pir__S36367 GTP-binding protein yptV4 - Volvox
                   carteri >gi 409166 (L08130) GTP-binding protein [Volvox
                   carteri]
                   41601
Seq. No.
                   LIB3139-092-P1-N1-H5
Seq. ID
                   BLASTX
Method
                   g3202028
NCBI GI
BLAST score
                   631
                   5.0e-66
E value
                   140
Match length
% identity
                   (AF069317) cystathionine gamma-synthase [Mesembryanthemum
NCBI Description
                   crystallinum]
                   41602
Seq. No.
                   LIB3139-093-P1-N1-E10
Seq. ID
                   BLASTX
Method
                   q3023637
NCBI GI
BLAST score
                   154
                   3.0e-10
E value
                   78
Match length
                   42
% identity
                   PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN
NCBI Description
                   8) >gi_1362899_pir__A56236 probable RNA helicase 1 - human
                   >gi 807817_dbj_BAA09078_ (D50487) RNA helicase (HRH1) [Homo
                   sapiens]
Seq. No.
                   41603
                   LIB3139-093-P1-N1-G10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4468979
                   174
BLAST score
                   2.0e-12
E value
```

% identity

NCBI Description

55



```
Match length
% identity
                   (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
                   41604
Seq. No.
Seq. ID
                  LIB3139-093-P1-N1-G12
                  BLASTX
Method
NCBI GI
                  q1169528
BLAST score
                   248
                   2.0e-21
E value
Match length
                   86
                   63
% identity
                  ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973)
                   enolase [Zea mays]
                   41605
Seq. No.
Seq. ID
                   LIB3139-093-P1-N1-H1
Method
                   BLASTX
NCBI GI
                   q3098603
                   553
BLAST score
E value
                   6.0e-57
                   126
Match length
                   82
% identity
                  (AF052191) katanin p60 subunit [Strongylocentrotus
NCBI Description
                   purpuratus]
                   41606
Seq. No.
Seq. ID
                   LIB3139-093-P1-N1-H2
                   BLASTX
Method
NCBI GI
                   q3243234
                   279
BLAST score
                   1.0e-45
E value
Match length
                   111
% identity
                   (AF071477) isoflavone reductase related protein [Pyrus
NCBI Description
                   communis]
                   41607
Seq. No.
                   LIB3139-093-P1-N1-H8
Seq. ID
Method
                   BLASTX
                   q1619300
NCBI GI
BLAST score
                   269
                   1.0e-23
E value
                   101
Match length
                   53
% identity
                   (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   41608
Seq. No.
                   LIB3139-094-P1-N1-A7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1785621
BLAST score
                   379
                   1.0e-36
E value
Match length
                   132
```

6558

(Z84202) AtPK2324 [Arabidopsis thaliana] >gi_2465927

(AF024650) receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi_4249408 (AC006072) putative serine/threonine protein kinase [Arabidopsis thaliana]

```
41609
Seq. No.
                  LIB3139-094-P1-N1-B12
Seq. ID
                  BLASTX
Method
                  q417444
NCBI GI
                  190
BLAST score
                  2.0e-14
E value
                  100
Match length
% identity
                  44
                  PHENYLALANINE AMMONIA-LYASE 2 >gi 217984 dbj_BAA00887_
NCBI Description
                  (D10003) phenylalanine ammonia-lyase [Pisum sativum]
                  41610
Seq. No.
                  LIB3139-094-P1-N1-C12
Seq. ID
Method
                  BLASTX
                  q3941498
NCBI GI
                  183
BLAST score
                  2.0e-13
E value
Match length
                   42
                  76
% identity
                   (AF062903) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                   41611
Seq. No.
                  LIB3139-094-P1-N1-E2
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
                   239
BLAST score
                   5.0e-20
E value
Match length
                   67
                   72
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41612
Seq. No.
                   LIB3139-094-P1-N1-E3
Seq. ID
                   BLASTX
Method
                   g684942
NCBI GI
BLAST score
                   342
                   4.0e-32
E value
                   91
Match length
                   71
% identity
                   (U20736) S-adenosyl-L-methionine:trans-caffeoyl-CoA
NCBI Description
                   3-O-methyltransferase [Medicago sativa subsp. sativa]
                   41613
Seq. No.
                   LIB3139-094-P1-N1-G1
Seq. ID
Method
                   BLASTX
                   g2914703
NCBI GI
BLAST score
                   208
                   1.0e-16
E value
Match length
                   57
```

(AC003974) unknown protein [Arabidopsis thaliana]

65

% identity

NCBI Description

Seq. ID

Method



```
Seq. No.
                  LIB3139-094-P1-N1-G2
Seq. ID
                  BLASTX
Method
                  g3023361
NCBI GI
                  356
BLAST score
                  8.0e-34
E value
                  146
Match length
% identity
                  46
                  BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL
NCBI Description
                  PRECURSOR (BCAT) >gi_2231619 (U88029) branched-chain amino
                  acids aminotransferase [Schizosaccharomyces pombe]
                  41615
Seq. No.
                  LIB3139-094-P1-N1-H9
Seq. ID
                  {\tt BLASTX}
Method
                  g1841475
NCBI GI
                  219
BLAST score
                  7.0e-18
E value
                   43
Match length
                  86
% identity
                  (Y11105) Myb26 [Pisum sativum]
NCBI Description
Seq. No.
                   41616
                  LIB3139-095-P1-N1-A11
Seq. ID
Method
                   BLASTX
                   q4097880
NCBI GI
                   272
BLAST score
E value
                   3.0e-38
                   123
Match length
                   76
% identity
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   41617
                   LIB3139-095-P1-N1-C1
Seq. ID
                   BLASTX
Method
                   g4063751
NCBI GI
                   459
BLAST score
                   6.0e-46
E value
                   132
Match length
                   62
% identity
                   (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4510409_gb_AAD21495.1_ (AC006929) putative white
                   protein [Arabidopsis thaliana]
                   41618
Seq. No.
                   LIB3139-095-P1-N1-C9
Seq. ID
                   BLASTX
Method
                   g3243136
NCBI GI
                   179
BLAST score
                   4.0e-13
E value
                   81
Match length
                   43
% identity
                   (AF047702) fragile histidine triad protein [Mus musculus]
NCBI Description
                   41619
Seq. No.
```

LIB3139-095-P1-N1-E1

BLASTX

```
NCBI GI
                     q3341686
BLAST score
                     565
                    2.0e-58
  E value
  Match length
                     133
  % identity
                     (AC003672) putative glycosyl transferase [Arabidopsis
  NCBI Description
                    thaliana]
```

41620 Seq. No. Seq. ID LIB3139-096-P1-N1-A11

Method BLASTX NCBI GI g3287695 BLAST score 518 E value 9.0e-53 148 Match length 67 % identity

(AC003979) Similar to hypothetical protein C34B7.2 NCBI Description

gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis

thaliana]

Seq. No.

41621

Seq. ID LIB3139-096-P1-N1-B2

Method BLASTX NCBI GI g138364 BLAST score 260 6.0e-23 E value 85 Match length 62 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

41622 Seq. No.

LIB3139-096-P1-N1-C1 Seq. ID

BLASTX Method g2829870 NCBI GI BLAST score 310 1.0e-28 E value 114 Match length 52 % identity

(AC002396) Hypothetical protein [Arabidopsis thaliana] NCBI Description

41623 Seq. No.

Seq. ID LIB3139-096-P1-N1-C3

BLASTX Method g267136 NCBI GI 350 BLAST score 4.0e-33 E value 88 Match length 78 % identity

PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED NCBI Description

TONOPLAST INTRINSIC PROTEIN) (WSI-TIP)

>gi_217869_dbj_BAA02520 (D13254) transmembrane channel protein [Arabidopsis thaliana] >gi 4371283_gb_AAD18141_ (AC006260) putative plasma membrane intrinsic protein 2C

[Arabidopsis thaliana] >gi_384324_prf__1905411A





transmembrane channel [Arabidopsis thaliana]

```
41624
Seq. No.
                  LIB3139-096-P1-N1-E6
Seq. ID
                  BLASTX
Method
                  g2853039
NCBI GI
                  265
BLAST score
                   4.0e-23
E value
                  138
Match length
                   41
% identity
                   (X94289) phosphoinositide-specific phospholipase C [Solanum
NCBI Description
                   tuberosum]
                   41625
Seq. No.
                   LIB3139-096-P1-N1-F12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   112
                   3.0e-56
E value
                   336
Match length
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   41626
                   LIB3139-096-P1-N1-G1
Seq. ID
                   BLASTX
Method
                   q3668091
NCBI GI
BLAST score
                   202
                   9.0e-16
E value
                   138
Match length
% identity
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41627
                   LIB3139-096-P1-N1-G4
Seq. ID
                   BLASTX
Method
                   q4567312
NCBI GI
BLAST score
                   450
                   8.0e-45
E value
                   122
Match length
                   71
% identity
                   (AC005956) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   41628
Seq. No.
                   LIB3139-096-P1-N1-G7
Seq. ID
                   BLASTX
Method
                   q1705486
NCBI GI
                   390
BLAST score
                   8.0e-38
E value
                   141
Match length
                   55
 % identity
                   BLOOM'S SYNDROME PROTEIN >gi_2134831_pir__A57570 Bloom's
 NCBI Description
                   syndrome related protein BLM - human >gi_1072122 (U39817)
```

>gi_4557365_ref_NP_000048.1_pBLM_ Bloom syndrome protein

Bloom's syndrome protein [Homo sapiens]

```
41629
LIB3139-0
```

Seq. No. Seq. ID LIB3139-097-P1-N1-B11 BLASTX Method q138364 NCBI GI 233 BLAST score 7.0e-20 E value 66 Match length 74 % identity NCBI Description

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (Strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 41630 Seq. ID LIB313

Seq. ID LIB3139-097-P1-N1-C3

Method BLASTX
NCBI GI g3212877
BLAST score 534
E value 1.0e-54
Match length 127
% identity 78

NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No. 41631

Seq. ID LIB3139-097-P1-N1-C6

Method BLASTN
NCBI GI g210811
BLAST score 152
E value 6.0e-80
Match length 412
% identity 84

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41632

Seq. ID LIB3139-097-P1-N1-D3

Method BLASTX
NCBI GI 94097880
BLAST score 336
E value 2.0e-31
Match length 123
% identity 61

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 41633

Seq. ID LIB3139-097-P1-N1-D6

Method BLASTX
NCBI GI g2827623
BLAST score 501
E value 1.0e-57
Match length 137
% identity 85

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 41634

Seq. ID LIB3139-097-P1-N1-D7

Method BLASTX

% identity



```
NCBI GI
                  q2827623
BLAST score
                  233
                  7.0e-24
E value
Match length
                  83
                  72
% identity
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                  41635
Seq. No.
                  LIB3139-097-P1-N1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                   101
E value
                   1.0e-49
                   217
Match length
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41636
Seq. No.
                   LIB3139-097-P1-N1-F10
Seq. ID
Method
                   BLASTX
                   q3608137
NCBI GI
BLAST score
                   200
E value
                   1.0e-15
                   92
Match length
                   47
% identity
                  (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41637
                   LIB3139-097-P1-N1-F12
Seq. ID
                   BLASTX
Method
                   g3170230
NCBI GI
BLAST score
                   327
                   2.0e-30
E value
Match length
                   106
                   62
% identity
                   (AF041848) fructose-6-phosphate 2-kinase
NCBI Description
                   /fructose-2,6-bisphosphatase [Spinacia oleracea]
                   41638
Seq. No.
                   LIB3139-097-P1-N1-F3
Seq. ID
                   BLASTN
Method
                   g170087
NCBI GI
                   132
BLAST score
                   5.0e-68
E value
                   236
Match length
                   90
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
                   41639
Seq. No.
                   LIB3139-097-P1-N1-F6
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4097879
                   97
BLAST score
                   4.0e-47
E value
                   257
Match length
```

```
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
                  41640
Seq. No.
                  LIB3139-097-P1-N1-F7
Seq. ID
```

Method BLASTX g4097880 NCBI GI BLAST score 371 1.0e-35 E value Match length 129

% identity NCBI Description (U70866) polyprotein [Bean pod mottle virus]

41641 Seq. No. LIB3139-098-P1-N1-A8 Seq. ID Method BLASTX NCBI GI g2344891

BLAST score 169 6.0e-12 E value 98 Match length 37 % identity

(AC002388) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 41642

LIB3139-098-P1-N1-B3 Seq. ID

Method BLASTX q4490300 NCBI GI 378 BLAST score E value 2.0e-36 106 Match length 74 % identity

(AL035678) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 41643

LIB3139-098-P1-N1-C6 Seq. ID

BLASTN Method g210811 NCBI GI 95 BLAST score 3.0e-46 E value 235 Match length 86 % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

41644 Seq. No.

LIB3139-098-P1-N1-D9 Seq. ID

BLASTX Method g2980793 NCBI GI 148 BLAST score 1.0e-13 E value 92 Match length 46 % identity

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No.

41645 Seq. ID LIB3139-098-P1-N1-E12

Method BLASTN

Match length



```
NCBI GI
                   g4204764
BLAST score
                   85
E value
                   4.0e-40
Match length
                   233
% identity
                   86
NCBI Description
                   Glycine max peroxidase (sEPb2) mRNA, partial cds
Seq. No.
                   41646
                   LIB3139-098-P1-N1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4263818
BLAST score
                   199
E value
                   2.0e-15
Match length
                   80
% identity
                   44
NCBI Description
                  (AC006067) unknown protein [Arabidopsis thaliana]
Seq. No.
                   41647
Seq. ID
                   LIB3139-099-P1-N1-A12
Method
                   BLASTX
NCBI GI
                   g1402918
BLAST score
                   369
E value
                   2.0e-35
Match length
                   87
% identity
                   83
NCBI Description
                   (X98320) peroxidase [Arabidopsis thaliana]
                   >gi_1429215 emb CAA67310 (X98774) peroxidase ATP6a
                   [Arabidopsis thaliana]
Seq. No.
                   41648
Seq. ID
                   LIB3139-099-P1-N1-A3
Method
                   BLASTN
NCBI GI
                   q169936
BLAST score
                   344
E value
                   0.0e + 00
Match length
                   372
% identity
                   99
NCBI Description Glycine max chalcone synthase (chs7) gene, complete cds
Seq. No.
                  41649
Seq. ID
                  LIB3139-099-P1-N1-G8
Method
                  BLASTN
NCBI GI
                  g12147
BLAST score
                  211
E value
                  1.0e-115
Match length
                  299
% identity
                  93
NCBI Description
                  Pea chloroplast genes for ATP synthetase subunits beta and
                  epsilon (atpB and atpE)
Seq. No.
                  41650
Seq. ID
                  LIB3139-100-P1-N1-B2
Method
                  BLASTX
NCBI GI
                  g2239083
BLAST score
                  159
E value
                  7.0e-11
```



% identity (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase NCBI Description [Dianthus caryophyllus] >gi 2239087_emb_CAB06429 (Z84385) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] 41651 Seq. No. LIB3139-100-P1-N1-B3 Seq. ID BLASTX Method g322772 NCBI GI 615 BLAST score 5.0e-64 E value 142 Match length 77 % identity 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) -NCBI Description garden petunia >gi_20508_emb_CAA79478_ (Z18953) 1-aminocyclopropane-1-carboxylate synthase [Petunia x hybrida] >gi 1513090 (U64804) 1-aminocyclopropane-1-carboxylate synthase [Petunia hybrida] Seq. No. 41652 LIB3139-100-P1-N1-B8 Seq. ID BLASTX Method q3193316 NCBI GI 237 BLAST score 1.0e-19 E value Match length 143 43 % identity (AF069299) contains similarity to nucleotide sugar NCBI Description epimerases [Arabidopsis thaliana] Seq. No. 41653 LIB3139-100-P1-N1-C5 Seq. ID BLASTX Method g2618686 NCBI GI 217 BLAST score 3.0e-17 E value 101 Match length 39 % identity (AC002510) hypothetical protein [Arabidopsis thaliana] NCBI Description 41654 Seq. No. Seq. ID LIB3139-100-P1-N1-G11 Method BLASTX g4218001 NCBI GI BLAST score 199 1.0e-25 E value 175 Match length 40 % identity

(AC006135) putative Ac transposase [Arabidopsis thaliana] NCBI Description

41655 Seq. No.

Seq. ID LIB3139-100-P1-N1-H10 BLASTX Method

NCBI GI q1255448 BLAST score 311

```
2.0e-28
E value
                  82
Match length
                   72
% identity
                   (D50468) mitogen-activated protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   41656
Seq. No.
                   LIB3139-101-P1-N1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g229708
BLAST score
                   270
E value
                   8.0e-24
                   122
Match length
                   51
% identity
NCBI Description Bean pod mottle virus
                   41657
Seq. No.
                   LIB3139-101-P1-N1-G7
Seq. ID
Method
                   BLASTX
                   g3080374
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
Match length
                   123
% identity
NCBI Description (AL022580) putative protein [Arabidopsis thaliana]
Seq. No.
                   LIB3139-102-P1-N1-A11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g210811
BLAST score
                   79
                   2.0e-36
E value
Match length
                   203
% identity
                   86
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41659
Seq. No.
                   LIB3139-102-P1-N1-A2
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   214
BLAST score
                   1.0e-117
E value
                   358
Match length
                   90
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
```

Seq. No.

41660

LIB3139-102-P1-N1-C3 Seq. ID

BLASTX Method g951116 NCBI GI 212 BLAST score 6.0e-17 E value 100 Match length 51 % identity

NCBI Description (U22472) mannose/glucose-binding lectin [Arachis hypogaea]

% identity

Seq. No.

Seq. ID

NCBI Description

41666

LIB3139-102-P1-N1-F10



```
41661
Seq. No.
Seq. ID
                  LIB3139-102-P1-N1-C9
Method
                  BLASTX
                  g3913952
NCBI GI
                  222
BLAST score
                  4.0e-18
E value
                  55
Match length
                  71
% identity
                  ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) >gi_2351578
NCBI Description
                  (U82330) adenylate kinase homolog [Prunus armeniaca]
                  41662
Seq. No.
Seq. ID
                  LIB3139-102-P1-N1-D10
                  BLASTX
Method
                  g2852447
NCBI GI
BLAST score
                  285
                  1.0e-35
E value
                  128
Match length
                  60
% identity
NCBI Description (D88206) protein kinase [Arabidopsis thaliana]
                  41663
Seq. No.
                  LIB3139-102-P1-N1-D9
Seq. ID
                  BLASTX
Method
                  q138364
NCBI GI
BLAST score
                   362
                  1.0e-34
E value
                   124
Match length
                   60
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41664
Seq. No.
                   LIB3139-102-P1-N1-E10
Seq. ID
                   BLASTX
Method
                   g1256771
NCBI GI
                   215
BLAST score
                   2.0e-17
E value
Match length
                   105
                   46
% identity
                  (U51270) COP9 [Spinacia oleracea]
NCBI Description
                   41665
Seq. No.
Seq. ID
                   LIB3139-102-P1-N1-E7
                   BLASTN
Method
                   q18651
NCBI GI
BLAST score
                   61
                   9.0e-26
E value
Match length
                   145
```

6569

Soybean gene for heat shock protein Gmhsp17.9-D (class VI)

```
BLASTN
Method
                  g170065
NCBI GI
BLAST score
                  239
                  1.0e-132
E value
Match length
                  394
                  11
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP2)
NCBI Description
                  gene, complete cds
                  41667
Seq. No.
                  LIB3139-102-P1-N1-F11
Seq. ID
                  BLASTX
Method
                  g138364
NCBI GI
BLAST score
                  422
                  1.0e-41
E value
                   133
Match length
                   63
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41668
Seq. No.
                   LIB3139-102-P1-N1-F12
Seq. ID
                   BLASTX
Method
                   g229707
NCBI GI
                   533
BLAST score
                   1.0e-54
E value
                   134
Match length
                   75
% identity
NCBI Description Bean pod mottle virus
                   41669
Seq. No.
                   LIB3139-102-P1-N1-F7
Seq. ID
                   BLASTX
Method
                   q4097880
NCBI GI
                   225
BLAST score
                   9.0e-19
E value
                   92
Match length
                   52
 % identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41670
 Seq. No.
                   LIB3139-102-P1-N1-G4
Seq. ID
                   BLASTX
Method
                   g2224663
NCBI GI
BLAST score
                   403
                   3.0e-39
E value
                   155
Match length
                   52
 % identity
                  (AB002359) KIAA0361 [Homo sapiens]
 NCBI Description
                   41671
```

Seq. No.

Seq. ID LIB3139-102-P1-N1-G7

Method BLASTX NCBI GI q138364 183 BLAST score



```
E value
                  91
Match length
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  41672
                  LIB3139-102-P1-N1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g229707
                  173
BLAST score
                  7.0e-13
E value
                  69
Match length
                  52
% identity
NCBI Description Bean pod mottle virus
                  41673
Seq. No.
                  LIB3139-102-P1-N1-H8
Seq. ID
Method
                  BLASTX
                  g229707
NCBI GI
BLAST score
                  512
E value
                   4.0e-52
                  120
Match length
                  79
% identity
NCBI Description Bean pod mottle virus
Seq. No.
                   41674
                  LIB3139-103-P1-N1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q549077
BLAST score
                   216
                   1.0e-17
E value
Match length
                   92
                   48
% identity
                   3-KETOACYL-COA THIOLASE PEROXISOMAL PRECURSOR
NCBI Description
                   (BETA-KETOTHIOLASE) (ACETYL-COA ACYLTRANSFERASE)
                   (PEROXISOMAL 3-OXOACYL-COA THIOLASE) >gi_480423 pir__S36838
                   acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal -
                   yeast (Yarrowia lipolytica) >gi 5532 emb CAA49605 (X69988)
                   acetyl-CoA acyltransferase [Yarrowia lipolytica]
                   41675
Seq. No.
                   LIB3139-103-P1-N1-E8
Seq. ID
                   BLASTX
Method
                   g400988
NCBI GI
                   202
BLAST score
                   7.0e-16
```

E value 66

Match length 56 % identity

60S RIBOSOMAL PROTEIN L21E A >gi_322959_pir__S28921 NCBI Description

ribosomal protein L21.e.A, cytosolic - yeast (Saccharomyces

cerevisiae) >gi 173155 (M86408) ribosomal protein [Saccharomyces cerevisiae] >gi 536555 emb CAA85153

(Z36059) ORF YBR191w [Saccharomyces cerevisiae] >gi_575917

(U02073) homolog of rat ribosomal protein L21



[Saccharomyces cerevisiae]

```
Seq. No.
                  41676
                  LIB3139-103-P1-N1-G1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q210811
                  187
BLAST score
                  1.0e-101
E value
Match length
                  299
                  91
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                  41677
                  LIB3139-103-P1-N1-G9
Seq. ID
                  BLASTX
Method
                  g3548809
NCBI GI
BLAST score
                  168
                   2.0e-12
E value
Match length
                   60
% identity
                   (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   41678
Seq. No.
Seq. ID
                   LIB3139-103-P1-N1-H6
                   BLASTX
Method
                   g138364
NCBI GI
                   173
BLAST score
                   6.0e-13
E value
                   42
Match length
                   79
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41679
Seq. No.
                   LIB3139-104-P1-N1-A2
Seq. ID
                   BLASTX
Method
                   g1644402
NCBI GI
BLAST score
                   153
                   5.0e-10
E value
Match length
                   65
                   49
% identity
                   (U73524) putative ATP/GTP-binding protein [Homo sapiens]
NCBI Description
Seq. No.
                   41680
Seq. ID
                   LIB3139-104-P1-N1-A5
                   BLASTX
Method
                   g4314366
NCBI GI
BLAST score
                   446
                   2.0e-44
E value
Match length
                   128
 % identity
                   62
                   (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

41681

Seq. No.

```
LIB3139-104-P1-N1-A9
Seq. ID
                  BLASTN
Method
                  g210811
NCBI GI
                  175
BLAST score
                  1.0e-93
E value
Match length
                   364
                   90
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
```

 Seq. No.
 41682

 Seq. ID
 LIB3139-104-P1-N1-B8

 Method
 BLASTX

 NCBI GI
 g3342552

 BLAST score
 199

 E value
 2.0e-15

Match length 68 % identity 56

NCBI Description (AF076979) putative strictosidine synthase [Arabidopsis

33

thaliana]

Seq. No. 41683

Seq. ID LIB3139-104-P1-N1-F7

Method BLASTX
NCBI GI g2864625
BLAST score 534
E value 1.0e-54
Match length 135
% identity 76

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 41684

Seq. ID LIB3139-104-P1-N1-G7

Method BLASTN
NCBI GI g531828
BLAST score 50
E value 4.0e-19
Match length 102
% identity 87

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 41685

Seq. ID LIB3139-105-P1-N1-B3

Method BLASTN
NCBI GI g210811
BLAST score 218
E value 1.0e-119
Match length 366
% identity 90

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41686

Seq. ID LIB3139-105-P1-N1-B8

Method BLASTX NCBI GI g4335731 BLAST score 324

```
E value
                  106
Match length
                   58
% identity
                  (AC006248) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                   41687
Seq. No.
                  LIB3139-105-P1-N1-D6
Seq. ID
                   {\tt BLASTX}
Method
                   g2464914
NCBI GI
                   277
BLAST score
                   1.0e-24
E value
Match length
                   88
% identity
                   69
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41688
                   LIB3139-105-P1-N1-E2
Seq. ID
                   BLASTX
Method
                   g685035
NCBI GI
                   292
BLAST score
                   4.0e-29
E value
Match length
                   78
% identity
                   92
                   histone H2A homolog [Phaseolus vulgaris, Great Northern,
NCBI Description
                   immature embryos, Peptide Partial, 146 aa]
                   41689
```

Seq. No. LIB3139-105-P1-N1-F12 Seq. ID BLASTX Method g4097880 NCBI GI 308 BLAST score 8.0e-29 E value Match length 73 81 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

41690 Seq. No. LIB3139-106-P1-N1-C7 Seq. ID BLASTX Method

q2842493 NCBI GI BLAST score 508 1.0e-51 E value 107 Match length 84 % identity

(AL021749) predicted protein [Arabidopsis thaliana] NCBI Description

41691 Seq. No.

LIB3139-106-P1-N1-D11 Seq. ID

BLASTX Method g1899058 NCBI GI BLAST score 265 3.0e-23 E value Match length 88 62 % identity

(U77378) transcriptional activator CBF1 [Arabidopsis NCBI Description thaliana] >gi_4091982_gb_AAC99369 (AF076155) CRT/CRE

binding factor 1 [Arabidopsis thaliana]



```
41692
Seq. No.
                  LIB3139-106-P1-N1-D12
Seq. ID
                  BLASTN
Method
                  g170075
NCBI GI
                  73
BLAST score
                  8.0e-33
E value
                  81
Match length
                  98
% identity
NCBI Description Soybean calmodulin (SCaM-4) mRNA, complete cds
                   41693
Seq. No.
                  LIB3139-106-P1-N1-D9
Seq. ID
                  BLASTX
Method
                  g2634023
NCBI GI
                   195
BLAST score
                   1.0e-22
E value
                   119
Match length
                   53
% identity
NCBI Description (Z99112) uridylate kinase [Bacillus subtilis]
                   41694
Seq. No.
                   LIB3139-106-P1-N1-E9
Seq. ID
                   BLASTN
Method
                   g210811
NCBI GI
                   135
BLAST score
                   8.0e-70
E value
Match length
                   331
                   85
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No. Seq. ID
                   41695
                   LIB3139-106-P1-N1-F12
                   BLASTN
Method
                   g262045
NCBI GI
                   79
BLAST score
                   2.0e-36
E value
                   172
Match length
                   91
% identity
                   Ncypt1=putative small GTP-binding protein [Neurospora
NCBI Description
                   crassa, Genomic/mRNA, 3157 nt]
                   41696
Seq. No.
                   LIB3139-106-P1-N1-G12
Seq. ID
                   BLASTX
Method
                   q4097880
NCBI GI
                   295
BLAST score
                   6.0e-27
E value
                   89
Match length
                   71
 % identity
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41697
 Seq. No.
 Seq. ID
                   LIB3139-106-P1-N1-H3
```

6575

BLASTN

q1217993

Method

NCBI GI



BLAST score 237 E value 1.0e-131 Match length 288 % identity 95

NCBI Description Glycine max dynamin-like protein SDL12A mRNA, complete cds

Seq. No. 41698

Seq. ID LIB3139-107-P1-N1-A12

Method BLASTN
NCBI GI 94097879
BLAST score 136
E value 2.0e-70
Match length 335
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41699

Seq. ID LIB3139-107-P1-N1-A6

Method BLASTN
NCBI GI g4097879
BLAST score 47
E value 2.0e-17
Match length 97
% identity 85

% identity 85 NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41700

Seq. ID LIB3139-107-P1-N1-B6

Method BLASTN
NCBI GI g3449329
BLAST score 35
E value 4.0e-10
Match length 75
% identity 93

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDH9, complete sequence [Arabidopsis thaliana]

Seq. No. 41701

Seq. ID LIB3139-107-P1-N1-B7

Method BLASTX
NCBI GI g3687250
BLAST score 157
E value 3.0e-13
Match length 93
% identity 44

NCBI Description (AC005169) putative arginine n-methyltransferase

[Arabidopsis thaliana]

Seq. No. 41702

Seq. ID LIB3139-107-P1-N1-C11

Method BLASTN
NCBI GI g1418126
BLAST score 45
E value 4.0e-16
Match length 85

% identity 88

NCBI Description Brassica napus mRNA for CTP:phosphocholine cytidylyltransferase, complete cds

Seq. No. 41703

Seq. ID LIB3139-107-P1-N1-C5

Method BLASTN
NCBI GI g210811
BLAST score 173
E value 2.0e-92
Match length 365
% identity 87

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41704

Seq. ID LIB3139-107-P1-N1-D11

Method BLASTN
NCBI GI g2072155
BLAST score 157
E value 6.0e-83
Match length 246
% identity 90

NCBI Description Neurospora crassa actin gene, complete cds

Seq. No. 41705

Seq. ID LIB3139-107-P1-N1-E3

Method BLASTX
NCBI GI g731284
BLAST score 226
E value 1.0e-18
Match length 115
% identity 43

NCBI Description HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION

>gi_1077482_pir__S51971 probable membrane protein YAL048c -

yeast (Saccharomyces cerevisiae) >gi_595536 (U12980)

Yal048cp [Saccharomyces cerevisiae]

Seq. No. 41706

Seq. ID LIB3139-107-P1-N1-F6

Method BLASTX
NCBI GI 94097880
BLAST score 441
E value 8.0e-51
Match length 131
% identity 82

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

41707

Seq. ID LIB3139-107-P1-N1-G11

Method BLASTN
NCBI GI 9758249
BLAST score 87
E value 3.0e-41
Match length 199
% identity 86

NCBI Description P.vulgaris mRNA for plasma membrane H+ ATPase



41708 Seq. No. LIB3139-107-P1-N1-G5 Seq. ID BLASTX Method g2341045 NCBI GI BLAST score 187 5.0e-14 E value Match length 114 % identity 35 NCBI Description (AC000104) F19P19.16 [Arabidopsis thaliana] Seq. No. 41709 LIB3139-109-P1-N1-B12 Seq. ID BLASTX Method g229707 NCBI GI 521 BLAST score 3.0e-53 E value Match length 118 % identity 83 NCBI Description Bean pod mottle virus Seq. No. 41710 LIB3139-109-P1-N1-C4 Seq. ID BLASTX Method q4097880 NCBI GI 412 BLAST score 1.0e-45 E value Match length 118 % identity 74 (U70866) polyprotein [Bean pod mottle virus] NCBI Description 41711 Seq. No. LIB3139-109-P1-N1-F6 Seq. ID BLASTX Method g2507455 NCBI GI 217 BLAST score 1.0e-17 E value 75 Match length 64 % identity FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE NCBI Description SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi 170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea] 41712 Seq. No. Seq. ID LIB3139-109-P1-N1-G11 BLASTX Method NCBI GI q138364 BLAST score 300 E value 3.0e-27 130 Match length % identity GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

(M62738) coat protein [Bean pod mottle virus]

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi 210812

NCBI GI



```
41713
Seq. No.
                  LIB3139-109-P1-N1-G12
Seq. ID
                  BLASTN
Method
                  g210811
NCBI GI
BLAST score
                  195
                  1.0e-105
E value
Match length
                  395
                  87
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                  41714
Seq. ID
                  LIB3139-109-P1-N1-H3
Method
                  BLASTN
                  q210811
NCBI GI
BLAST score
                   157
E value
                   4.0e-83
                   241
Match length
                   91
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
Seq. No.
                   41715
                   LIB3139-110-P1-N1-A6
Seq. ID
                   BLASTN
Method
                   g1403674
NCBI GI
                   103
BLAST score
E value
                   1.0e-50
                   298
Match length
% identity
NCBI Description Glycine max beta-1,3-glucanase (SGN1) gene, complete cds
Seq. No.
                   41716
                   LIB3139-110-P1-N1-A7
Seq. ID
Method
                   BLASTN
                   g475601
NCBI GI
BLAST score
                   33
                   3.0e-09
E value
Match length
                   64
                   97
% identity
NCBI Description Glycine max Century 84 BiP isoform A mRNA, complete cds
Seq. No.
                   41717
                   LIB3139-110-P1-N1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4097880
BLAST score
                   321
                   9.0e-30
E value
Match length
                   105
% identity
                   62
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41718
Seq. No.
Seq. ID
                   LIB3139-110-P1-N1-B3
                   BLASTX
Method
```

g4455364



BLAST score 157 E value 2.0e-17 Match length 98 % identity 54

NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis

thaliana]

Seq. No. 41719

Seq. ID LIB3139-110-P1-N1-C9

Method BLASTN
NCBI GI g2444419
BLAST score 80
E value 6.0e-37
Match length 204
% identity 85

NCBI Description Glycine max ribosome-associated protein p40 mRNA, complete

cds

Seq. No. 41720

Seq. ID LIB3139-110-P1-N1-D12

Method BLASTN
NCBI GI g210811
BLAST score 56
E value 1.0e-22
Match length 256
% identity 81

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41721

Seq. ID LIB3139-110-P1-N1-F9

Method BLASTN
NCBI GI 94097879
BLAST score 154
E value 4.0e-81
Match length 333
% identity 87

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41722

Seq. ID LIB3139-110-P1-N1-G7

Method BLASTN
NCBI GI g4097879
BLAST score 172
E value 7.0e-92
Match length 440
% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41723

Seq. ID LIB3139-110-P1-N1-H11

Method BLASTX
NCBI GI g138364
BLAST score 315
E value 2.0e-29

```
64
```

Match length % identity NCBI Description

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi 75639 pir__GNWXG7 genome polyprotein M bean pod mottle vīrus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

41724 Seq. No.

LIB3139-111-P1-N1-D3 Seq. ID

BLASTN Method q4097879 NCBI GI 213 BLAST score 1.0e-116 E value 421 Match length 88 % identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

41725 Seq. No.

LIB3139-111-P1-N1-D7 Seq. ID

BLASTN Method NCBI GI g210811 BLAST score 145 1.0e-75 E value 428 Match length 84 % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

41726 Seq. No.

LIB3139-111-P1-N1-E11 Seq. ID

BLASTX Method g544276 NCBI GI 438 BLAST score 2.0e-43 E value 109 Match length 76 % identity

GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH) NCBI Description

(FALDH) >gi_323017_pir_ JN0447 FDH1 protein - yeast

(Candida maltosa) >gi 170871 (M58332) encoding formaldehyde

resistance [Candida maltosa]

41727 Seq. No.

Seq. ID LIB3139-111-P1-N1-F7

BLASTX Method g2129709 NCBI GI 154 BLAST score E value 5.0e-10 101 Match length 33 % identity

reverse transcriptase - Arabidopsis thaliana NCBI Description

retrotransposon Tall-1 >gi 976278 (L47193) reverse

transcriptase [Arabidopsis thaliana]

41728 Seq. No.

Seq. ID LIB3139-111-P1-N1-G12

BLASTN Method

BLAST score

Match length

E value

178

281

1.0e-95



```
NCBI GI
                  g2317899
BLAST score
                  97
                  3.0e-47
E value
Match length
                  316
% identity
                  84
NCBI Description
                  Glycine max Sali3-2 mRNA, complete cds
Seq. No.
                  41729
Seq. ID
                  LIB3139-111-P1-N1-H9
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  45
E value
                  2.0e-16
Match length
                  138
% identity
                  86
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                  41730
Seq. ID
                  LIB3139-112-P1-N1-B3
Method
                  BLASTX
                  q229707
NCBI GI
BLAST score
                  170
E value
                  3.0e-12
Match length
                  41
                  78
% identity
NCBI Description Bean pod mottle virus
Seq. No.
                  41731
Seq. ID
                  LIB3139-112-P1-N1-D11
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  169
                  5.0e-90
E value
Match length
                  480
% identity
                  85
NCBI Description
                  Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
Seq. No.
                  41732
Seq. ID
                  LIB3139-112-P1-N1-D7
Method
                  BLASTN
NCBI GI
                  g210811
BLAST score
                  174
E value
                  5.0e-93
Match length
                  414
                  86
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
Seq. No.
                  41733
Seq. ID
                  LIB3139-112-P1-N1-E5
Method
                  BLASTN
NCBI GI
                  g170065
```



% identity

Soybean (G.max) proline-rich cell wall protein (SbPRP2) NCBI Description

gene, complete cds

Seq. No.

% identity

LIB3139-112-P1-N1-G11 Seq. ID

41734

BLASTN Method NCBI GI g4204758 BLAST score 460 0.0e+00E value 472 Match length 100

Glycine max peroxidase precursor (sEPa1) mRNA, partial cds NCBI Description

41735 Seq. No.

LIB3139-112-P1-N1-G6 Seq. ID

BLASTX Method NCBI GI g2226427 BLAST score 337 E value 2.0e-31 Match length 157 % identity 47

(Z97204) hypothetical protein [Schizosaccharomyces pombe] NCBI Description

41736 Seq. No.

Seq. ID LIB3139-112-P1-N1-H5

Method BLASTX g3258575 NCBI GI BLAST score 263 E value 8.0e-23 Match length 169 % identity 45

(U89959) Hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 41737

Seq. ID LIB3139-113-P1-N1-B9

Method BLASTX NCBI GI g229708 BLAST score 185 E value 5.0e-14 Match length 92 46 % identity

NCBI Description Bean pod mottle virus

41738 Seq. No.

Seq. ID LIB3139-113-P1-N1-D11

Method BLASTN NCBI GI g210811 BLAST score 205 E value 1.0e-111 Match length 361 % identity 89

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41739

Seq. ID LIB3139-113-P1-N1-D8



Method g138364 NCBI GI 169 BLAST score 4.0e-12 E value 84 Match length 45 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi 75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

41740 Seq. No.

LIB3139-113-P1-N1-E2 Seq. ID

BLASTN Method NCBI GI g4097879 81 BLAST score 1.0e-37 E value

276 Match length 83 % identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

41741 Seq. No.

LIB3139-113-P1-N1-G1 Seq. ID

BLASTN Method NCBI GI g4097879 153 BLAST score 1.0e-80 E value 399 Match length 85 % identity

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

41742 Seq. No.

LIB3139-113-P1-N1-G12 Seq. ID

Method BLASTN g210811 NCBI GI 90 BLAST score 5.0e-43 E value 310 Match length % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

Seq. No. 41743

Seq. ID LIB3139-114-P1-N1-A10

Method BLASTN g609224 NCBI GI BLAST score 187 1.0e-101 E value Match length 327 % identity 89

P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB NCBI Description

Pisum sativum S-adenosylmethionine synthase mRNA, complete

cds

Seq. No. 41744

```
LIB3139-114-P1-N1-B4
Seq. ID
                  BLASTX
Method
                  g2501578
NCBI GI
                  167
BLAST score
                  3.0e-12
E value
                  42
Match length
                  79
% identity
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047
NCBI Description
                  ethylene-responsive protein 1 - Para rubber tree
                  >qi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  41745
Seq. No.
                  LIB3139-114-P1-N1-B5
Seq. ID
                  BLASTX
Method
                  q138364
NCBI GI
BLAST score
                  142
                  6.0e-09
E value
                  90
Match length
                  26
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41746
Seq. No.
Seq. ID
                  LIB3139-114-P1-N1-B9
Method
                  BLASTX
                   g1781330
NCBI GI
                   183
BLAST score
                   5.0e-14
E value
                   76
Match length
% identity
                   49
                  (Y10466) peroxidase [Spinacia oleracea]
NCBI Description
                   41747
Seq. No.
Seq. ID
                   LIB3139-114-P1-N1-D9
                   BLASTX
Method
                   g138364
NCBI GI
                   240
BLAST score
                   1.0e-20
E value
                   81
Match length
                   63
% identity
                   GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   41748
Seq. No.
Seq. ID
                   LIB3139-114-P1-N1-F1
                   BLASTX
Method
NCBI GI
                   q2244872
                   147
BLAST score
                   1.0e-09
E value
Match length
                   41
                   73
% identity
NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]
```

6585

٠, ٣



```
41749
Seq. No.
Seq. ID
                  LIB3139-114-P1-N1-H10
                  BLASTX
Method
NCBI GI
                  g4160280
                  707
BLAST score
                  6.0e-75
E value
                  152
Match length
                  80
% identity
                  (AJ006224) purple acid phosphatase [Ipomoea batatas]
NCBI Description
                  41750
Seq. No.
                  LIB3139-114-P1-N1-H5
Seq. ID
                  BLASTX
Method
                  g2642154
NCBI GI
                  204
BLAST score
                  6.0e-16
E value
                  142
Match length
                  42
% identity
                  (AC003000) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3790595 (AF079186) RING-H2 finger protein RHC2a
                   [Arabidopsis thaliana]
                  41751
Seq. No.
                  LIB3139-114-P1-N1-H8
Seq. ID
Method
                  BLASTX
                  q282963
NCBI GI
BLAST score
                  494
                  5.0e-50
E value
                  108
Match length
                  81
% identity
                  transforming protein (myb) homolog (clone myb.Ph2) - garden
NCBI Description
                  petunia >gi 20561 emb CAA78387 (Z13997) protein 2 [Petunia
                  x hybrida]
                  41752
Seq. No.
Seq. ID
                  LIB3139-115-P1-N1-A12
Method
                  BLASTN
NCBI GI
                  g210811
                  153
BLAST score
                  1.0e-80
E value
Match length
                   341
                   87
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   41753
Seq. No.
Seq. ID
                  LIB3139-115-P1-N1-A5
                   BLASTX
Method
NCBI GI
                   g4512617
                   171
BLAST score
                   4.0e-12
E value
                   71
Match length
                   54
% identity
NCBI Description
                  (AC004793) F28K20.16 [Arabidopsis thaliana]
```

6586

41754

Seq. No.



Seq. ID LIB3139-115-P1-N1-A6

Method BLASTN
NCBI GI g4097879
BLAST score 81
E value 1.0e-37
Match length 181
% identity 86

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 41755

Seq. ID LIB3139-115-P1-N1-B4

Method BLASTX
NCBI GI g138364
BLAST score 325
E value 2.0e-30
Match length 97
% identity 69

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -*

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 41756

Seq. ID LIB3139-115-P1-N1-C4

Method BLASTX
NCBI GI g4097880
BLAST score 433
E value 5.0e-43
Match length 101
% identity 82

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 41757

Seq. ID LIB3139-115-P1-N1-D4

Method BLASTX
NCBI GI g138364
BLAST score 372
E value 7.0e-45
Match length 138
% identity 73

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 41758

Seq. ID LIB3139-115-P1-N1-D5

Method BLASTN
NCBI GI g4138678
BLAST score 136
E value 2.0e-70
Match length 304
% identity 86

NCBI Description V.faba mRNA for amino acid transporter

Seq. No. 41759



```
LIB3139-115-P1-N1-F5
Seq. ID
                  BLASTN
Method
                  g210811
NCBI GI
                  173
BLAST score
                  2.0e-92
E value
Match length
                   317
% identity
                   89
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41760
Seq. No.
                  LIB3139-115-P1-N1-G6
Seq. ID
                  BLASTX
Method
                   q4097880
NCBI GI
                   175
BLAST score
                   7.0e-13
E value
Match length
                   56
% identity
                   64
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41761
Seq. No.
Seq. ID
                   LIB3139-115-P1-N1-G9
Method
                   BLASTX
NCBI GI
                   g542157
BLAST score
                   532
                   2.0e-54
E value
                   121
Match length
                   83
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
                   41762
Seq. No.
Seq. ID
                   LIB3139-115-P1-N1-H10
Method
                   BLASTX
NCBI GI
                   g1345933
                   369
BLAST score
                   2.0e-35
E value
                   115
Match length
                   64
% identity
                   CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS)
NCBI Description
                   >gi_1084323_pir__S53007 citrate synthase - cucurbit
                   >gi 975633 dbj BAA07328 (D38132) glyoxysomal citrate
                   synthase [Cucurbita sp.]
                   41763
Seq. No.
                   LIB3139-116-P1-N1-A1
Seq. ID
                   BLASTN
Method
                   g4097879
NCBI GI
                   116
BLAST score
                   2.0e-58
E value
                   224
Match length
                   88
% identity
```

Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description

gene, complete cds

41764 Seq. No.

Seq. ID LIB3139-116-P1-N1-B1

Method BLASTX



```
q3204106
NCBI GI
                  243
BLAST score
                  1.0e-20
E value
                  54
Match length
                  81
% identity
                  (AJ006763) putative beta-amilase [Cicer arietinum]
NCBI Description
                  41765
Seq. No.
                  LIB3139-116-P1-N1-B12
Seq. ID
                  BLASTN
Method
                  q210811
NCBI GI
                  162
BLAST score
                  7.0e-86
E value
                  382
Match length
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   41766
Seq. No.
                  LIB3139-116-P1-N1-B2
Seq. ID
                   BLASTX
Method
                   q719291
NCBI GI
BLAST score
                   358
                   4.0e-34
E value
                   104
Match length
% identity
                   (U19134) unknown [Arabidopsis thaliana]
NCBI Description
                   >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]
                   41767
Seq. No.
                   LIB3139-116-P1-N1-C12
Seq. ID
                   BLASTN
Method
                   g3334660
NCBI GI
                   387
BLAST score
                   0.0e + 00
E value
                   416
Match length
                   99
% identity
                   G.max mRNA for putative cytochrome P450, clone CP3
NCBI Description
                   41768
 Seq. No.
                   LIB3139-116-P1-N1-C2
 Seq. ID
                   BLASTX
Method
                   g1076389
NCBI GI
                   302
 BLAST score
                   9.0e-30
 E value
                   87
 Match length
 % identity
                   44
                   protein phosphatase 2A pDF1 - Arabidopsis thaliana
 NCBI Description
                   >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
                   kDa regulatory subunit [Arabidopsis thaliana]
                   41769
 Seq. No.
                   LIB3139-116-P1-N1-C7
 Seq. ID
                   BLASTX
 Method
                   g266945
 NCBI GI
                    165
 BLAST score
```

1.0e-11

E value

```
Match length
                  42
% identity
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                  >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                  >qi 20727 emb CAA46273 (X65155) GA [Pisum sativum]
                  >gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                  [Pisum sativum]
                  41770
Seq. No.
                  LIB3139-116-P1-N1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3947735
                  192
BLAST score
                  1.0e-14
E value
                   138
Match length
                   33
% identity
                  (AJ009720) NL27 [Solanum tuberosum]
NCBI Description
                   41771
Seq. No.
                   LIB3139-116-P1-N1-E12
Seq. ID
                   BLASTN
Method
                   q4097879
NCBI GI
BLAST score
                   84
E value
                   1.0e-39
                   128
Match length
                   91
% identity
                   Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
Seq. No.
                   41772
                   LIB3139-116-P1-N1-E7
Seq. ID
                   BLASTN
Method
                   g20061
NCBI GI
BLAST score
                   134
                   3.0e-69
E value
Match length
                   278
% identity
                   87
                   Oenothera elata subsp. hookeri mRNA for protein kinase C
NCBI Description
                   inhibitor homologue
                   41773
Seq. No.
                   LIB3139-116-P1-N1-E9
Seq. ID
                   BLASTN
Method
                   g1706955
NCBI GI
                   35
BLAST score
                   4.0e-10
E value
Match length
                   121
                   88
 % identity
                   Gossypium hirsutum cellulose synthase (celA1) mRNA,
 NCBI Description
                   complete cds
                   41774
 Seq. No.
                   LIB3139-116-P1-N1-F3
 Seq. ID
                   BLASTX
 Method
                   g3914019
 NCBI GI
```

6590

374

5.0e-36

BLAST score

E value



Match length % identity 81 NCBI Description

S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_2305014

(AF004317) S-adenosyl-L-methionine synthetase homolog [Musa

acuminata]

Seq. No.

41775

Seq. ID

LIB3139-116-P1-N1-F4

BLASTN Method NCBI GI q210811 BLAST score 173 E value 2.0e-92 316

Match length % identity

Bean pod mottle virus coat protein gene, complete cds, NCBI Description

complete middle component (M) RNA

Seq. No.

41776

Seq. ID

LIB3139-116-P1-N1-G11

BLASTX Method g2149127 NCBI GI BLAST score 188 E value 3.0e-14102 Match length 39

% identity NCBI Description

(U81293) UDP-glucose:indole-3-acetate

beta-D-glucosyltransferase [Arabidopsis thaliana]

Seq. No.

Seq. ID

LIB3139-116-P1-N1-G4

BLASTX Method g138364 NCBI GI BLAST score 556 3.0e-57 E value Match length 132 % identity 85

NCBI Description

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

41778 Seq. No.

LIB3139-116-P1-N1-G7 Seq. ID

BLASTN Method q3264758 NCBI GI BLAST score 46 5.0e-17 E value 65 Match length 92

% identity Prunus armeniaca 40S ribosomal protein S8 (RPS8) mRNA, NCBI Description

complete cds

41779 Seq. No.

LIB3139-117-P1-N1-A11 Seq. ID

BLASTN Method g4097879 NCBI GI

BLAST score

E value Match length 5.0e-49

186



```
BLAST score
E value
                  3.0e-50
Match length
                  214
                  87
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
               • · · 41780
Seq. No.
                  LIB3139-117-P1-N1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q532700
BLAST score
                  35
E value
                  1.0e-10
                   44
Match length
                   93
% identity
                  Glycine max clone GMFP1 isoprenylated protein mRNA, partial
NCBI Description
                   41781
Seq. No.
                   LIB3139-117-P1-N1-A3
Seq. ID
Method
                   BLASTN
                   q210811
NCBI GI
BLAST score
                   150
E value
                   7.0e-79
Match length
                   261
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   41782
Seq. No.
                   LIB3139-117-P1-N1-B4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4097879
BLAST score
                   117
E value
                   3.0e-59
Match length
                   305
% identity
                   85
                   Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   41783
Seq. No.
                   LIB3139-117-P1-N1-B8
Seq. ID
                   BLASTX
Method
                   g1922242
NCBI GI
                   200
BLAST score
                   9.0e-16
E value
                   58
Match length
% identity
                   64
NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]
                   41784
Seq. No.
Seq. ID
                   LIB3139-117-P1-N1-C6
                   BLASTN
Method
                   g1675195
NCBI GI
                   100
```



% identity 89

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

Seq. No. 41785

Seq. ID LIB3139-117-P1-N1-D11

Method BLASTX
NCBI GI g4127660
BLAST score 190
E value 7.0e-15
Match length 46
% identity 67

NCBI Description (Y11124) invertase [Cichorium intybus]

Seq. No. 41786

Seq. ID LIB3139-117-P1-N1-D4

Method BLASTN
NCBI GI g1944341
BLAST score 82
E value 2.0e-38
Match length 137
% identity 91

NCBI Description Glycine max DNA for cysteine proteinase inhibitor, complete

cds

Seq. No. 41787

Seq. ID LIB3139-117-P1-N1-D7

Method BLASTX
NCBI GI g3024764
BLAST score 204
E value 4.0e-16
Match length 116
% identity 45

NCBI Description UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (UBIQUITIN

THIOLESTERASE T) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T) (DEUBIQUITINATING ENZYME T) (ISOPEPTIDASE T) >gi_3287373

(AC002397) ISOT [Mus musculus]

Seq. No. 41788

Seq. ID LIB3139-117-P1-N1-E10

Method BLASTX
NCBI GI g2500347
BLAST score 136
E value 1.0e-08
Match length 58
% identity 55

NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG

>gi_3878691_emb_CAA90127_ (Z49911) similar to ribosomal
protein (L7AE family); cDNA EST EMBL:D73957 comes from this
gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST
EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393

comes from this gene; cD

Seq. No. 41789

Seq. ID LIB3139-117-P1-N1-E3

Method BLASTX NCBI GI g1495804

```
BLAST score
E value
                   4.0e-34
Match length
                   96
% identity
                   67
NCBI Description
                  (X96406) 13-lipoxygenase [Solanum tuberosum]
Seq. No.
                   41790
```

Seq. ID LIB3139-117-P1-N1-F4 Method BLASTX NCBI GI g3355486 BLAST score 295 E value 9.0e-27 Match length 97

% identity 57

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 41791 Seq. ID LIB3139-117-P1-N1-F8 Method BLASTN NCBI GI g4115338

BLAST score 175 E value 9.0e-94 Match length 309 % identity 20

NCBI Description Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds

Seq. No. 41792

Seq. ID LIB3139-117-P1-N1-G2

Method BLASTN NCBI GI g148682 BLAST score 136 E value 2.0e-70 Match length 196 % identity 92

NCBI Description Frankia sp. 5S, 16S, and 23S ribosomal RNA genes, complete

sequences

Seq. No. 41793

Seq. ID LIB3139-117-P1-N1-H5

Method BLASTX NCBI GI g4097880 BLAST score 281 E value 4.0e-25 Match length 104 % identity 59

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 41794

Seq. ID LIB3139-118-P1-N1-A8

Method BLASTN NCBI GI g643454 BLAST score 101 E value 1.0e-49 Match length 241 % identity 93

NCBI Description Aureobasidium pullulans translation elongation factor

1-alpha (tef1) gene, complete cds



Seq. No. 41795

Seq. ID LIB3139-118-P1-N1-C12

Method BLASTN
NCBI GI g210811
BLAST score 86
E value 9.0e-41
Match length 162
% identity 89

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41796

Seq. ID LIB3139-118-P1-N1-C2

Method BLASTN
NCBI GI g210811
BLAST score 169
E value 4.0e-90
Match length 325
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41797

Seq. ID LIB3139-118-P1-N1-D1

Method BLASTX
NCBI GI g1170936
BLAST score 278
E value 7.0e-25
Match length 72
% identity 76

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_1084406_pir__S46538 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi_429104_emb_CAA80865_ (Z24741) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 41798

Seq. ID LIB3139-118-P1-N1-D6

Method BLASTX
NCBI GI g3249084
BLAST score 216
E value 1.0e-17
Match length 62
% identity 60

NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene

gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No. 41799

Seq. ID LIB3139-118-P1-N1-E10

Method BLASTX
NCBI GI g2981202
BLAST score 345
E value 1.0e-32
Match length 96



% identity 72

NCBI Description (AF050672) ribosomal protein L13E [Candida albicans]

>gi_3859691_emb_CAA21966_ (AL033497) ribosomal protein L13e
[Candida albicans] >gi_4098854 (U80854) ribosomal protein

٠, ٠

L13 [Candida albicans]

Seq. No. 41800

Seq. ID LIB3139-118-P1-N1-F4

Method BLASTN
NCBI GI g210811
BLAST score 184
E value 4.0e-99
Match length 351
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41801

Seq. ID LIB3139-118-P1-N1-H7

Method BLASTN
NCBI GI g1518539
BLAST score 340
E value 0.0e+00
Match length 379
% identity 97

NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No. 41802

Seq. ID LIB3139-119-P1-N1-A12

Method BLASTN
NCBI GI g662929
BLAST score 39
E value 1.0e-12
Match length 99
% identity 85

NCBI Description G.max mRNA for heat shock transcription factor

Seq. No. 41803

Seq. ID LIB3139-119-P1-N1-D8

Method BLASTX
NCBI GI g3193296
BLAST score 274
E value 2.0e-24
Match length 109
% identity 56

NCBI Description (AF069298) similar to pectinesterase [Arabidopsis thaliana]

Seq. No. 41804

Seq. ID LIB3139-119-P1-N1-F11

Method BLASTX
NCBI GI g2583132
BLAST score 324
E value 4.0e-30
Match length 112
% identity 55

NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  LIB3139-119-P1-N1-G6
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
                  233
BLAST score
                  3.0e-22
E value
                  73
Match length
                  81
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  41806
Seq. No.
                  LIB3139-120-P1-N1-A5
Seq. ID
                  BLASTN
Method
                   q1680711
NCBI GI
                   176
BLAST score
                   2.0e-94
E value
                   212
Match length
                   96
% identity
NCBI Description Glycine max gamma glutamyl hydrolase mRNA, complete cds
                   41807
Seq. No.
                   LIB3139-120-P1-N1-B4
Seq. ID
Method
                   BLASTX
                   g464734
NCBI GI
                   147
BLAST score
                   1.0e-09
E value
                   60
Match length
                   57
% identity
                   ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379
                   adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle
                   >gi 407412 emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine
                   hydrolase [Catharanthus roseus]
                   41808
Seq. No.
Seq. ID
                   LIB3139-120-P1-N1-C10
                   BLASTX
Method
                   g4097880
NCBI GI
                   202
BLAST score
                   6.0e-16
E value
                   93
Match length
                   40
% identity
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   41809
Seq. No.
                   LIB3139-120-P1-N1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1172995
BLAST score
                   280
                   6.0e-25
E value
                   107
Match length
                   56
% identity
                   60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
NCBI Description
                   protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
```

6597

norvegicus]

ribosomal protein L22 [Rattus norvegicus]

>gi_1093952_prf__2105193A ribosomal protein L22 [Rattus



Seq. No.

41810

```
LIB3139-120-P1-N1-C12
Seq. ID
                  BLASTN
Method
                  g4097879
NCBI GI
                  32
BLAST score
                  1.0e-08
E value
                  60
Match length
                  88
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  41811
Seq. No.
                  LIB3139-120-P1-N1-C8
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
                   282
BLAST score
                  9.0e-26
E value
                   61
Match length
% identity
                   90
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   41812
                  LIB3139-120-P1-N1-D6
Seq. ID
                   BLASTN
Method
                   q4097879
NCBI GI
                   63
BLAST score
E value
                   6.0e-27
                   143
Match length
                   86
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
Seq. No.
                   41813
                   LIB3139-120-P1-N1-D7
Seq. ID
                   BLASTX
Method
                   g1742955
NCBI GI
                   389
BLAST score
                   7.0e-38
E value
                   91
Match length
% identity
                   (Z71446) CLC-b chloride channel protein [Arabidopsis
NCBI Description
                   thaliana]
                   41814
Seq. No.
                   LIB3139-120-P1-N1-E5
Seq. ID
                   BLASTX
Method
                   q2832661
NCBI GI
                   229
BLAST score
                   5.0e-19
E value
                   82
Match length
                   56
% identity
                   (AL021710) pherophorin - like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   41815
                   LIB3139-120-P1-N1-G12
Seq. ID
```



```
BLASTN
Method
                  g210811
NCBI GI
BLAST score
                  99
                  2.0e-48
E value
                  255
Match length
                  85
% identity
                  Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                  complete middle component (M) RNA
                   41816
Seq. No.
```

LIB3139-120-P1-N1-H5 Seq. ID BLASTX Method q138364 NCBI GI 255 BLAST score 2.0e-22 E value

76 Match length 71 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

41817 Seq. No.

LIB3139-121-P1-N1-C11 Seq. ID

BLASTX Method g3860272 NCBI GI 249 BLAST score 2.0e-21 E value 109 Match length 61 % identity

(AC005824) putative suppressor protein [Arabidopsis NCBI Description

thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1

protein [Arabidopsis thaliana]

41818 Seq. No.

LIB3139-121-P1-N1-D4 Seq. ID

BLASTX Method q1709798 NCBI GI 567 BLAST score 1.0e-58 E value 111 Match length 99 % identity

26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi 1155334 NCBI Description

(U43398) POTATP1 [Solanum tuberosum]

41819 Seq. No.

LIB3139-121-P1-N1-D9 Seq. ID

BLASTN Method g1208536 NCBI GI 49 BLAST score 1.0e-18 E value 77 Match length % identity

Glycine max guanine nucleotide regulatory protein (rab2) NCBI Description

mRNA, complete cds

41820 Seq. No.

```
LIB3139-121-P1-N1-H8
Seq. ID
Method
                  BLASTN
                  q1778375
NCBI GI
                  37
BLAST score
                  2.0e-11
E value
                  85
Match length
% identity
NCBI Description Pisum sativum PsRT17-1 mRNA, complete cds
                  41821
Seq. No.
                  LIB3139-122-P1-N1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g456713
                  281
BLAST score
                  1.0e-157
E value
                  333
Match length
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
                  41822
Seq. No.
                  LIB3139-122-P1-N1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406820
BLAST score
                  212
                  1.0e-17
E value
                   56
Match length
% identity
                  (AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                   thaliana]
                   41823
Seq. No.
                   LIB3139-122-P1-N1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4006873
BLAST score
                   368
E value
                   3.0e-35
Match length
                   132
                   45
% identity
                  (Z99707) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   41824
Seq. No.
                   LIB3139-122-P1-N1-C11
Seq. ID
                   BLASTX
Method
                   g3249084
NCBI GI
                   166
BLAST score
                   9.0e-12
E value
Match length
                   68
% identity
                   18
                   (AC004473) Similar to red-1 (related to thioredoxin) gene
NCBI Description
                   gb X92750 from Mus musculus. ESTs gb_AA712687 and
                   gb Z37223 come from this gene [Arabidopsis thaliana]
                   41825
Seq. No.
                   LIB3139-122-P1-N1-C3
Seq. ID
                   BLASTX
Method
```

6600

g2501494

150

NCBI GI BLAST score



E value 1.0e-09
Match length 115
% identity 30

NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID

3-O-GLUCOSYLTRANSFERASE 5) >gi 542015 pir S41951

UTP-glucose glucosyltransferase - cassava >gi_453249_emb_CAA54612_ (X77462) UTP-glucose

glucosyltransferase [Manihot esculenta]

Seq. No. 41826

Seq. ID LIB3139-122-P1-N1-C5

Method BLASTN
NCBI GI g210811
BLAST score 191
E value 1.0e-103
Match length 363
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41827

Seq. ID LIB3139-122-P1-N1-E2

Method BLASTN
NCBI GI g210811
BLAST score 117
E value 4.0e-59
Match length 303
% identity 85

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41828

Seq. ID LIB3139-122-P1-N1-E4

Method BLASTX
NCBI GI g4335771
BLAST score 184
E value 4.0e-14
Match length 83
% identity 53

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 41829

Seq. ID LIB3139-122-P1-N1-F6

Method BLASTN
NCBI GI g210811
BLAST score 121
E value 2.0e-61
Match length 241
% identity 88

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 41830

Seq. ID LIB3139-122-P1-N1-F9

Method BLASTX NCBI GI g138364 BLAST score 582



E value 2.0e-60 Match length 137 % identity 86

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 41831

Seq. ID LIB3139-122-P1-N1-G6

Method BLASTN
NCBI GI g3982595
BLAST score 268
E value 1.0e-149
Match length 348
% identity 94

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 41832

Seq. ID LIB3167-002-Q1-K1-B5

Method BLASTX
NCBI GI g2244885
BLAST score 232
E value 2.0e-19
Match length 124
% identity 40

NCBI Description (Z97338) strong similarity to UTP-glucose

glucosyltransferase [Arabidopsis thaliana]

Seq. No. 41833

Seq. ID LIB3167-002-Q1-K1-C3

Method BLASTN
NCBI GI g310575
BLAST score 89
E value 2.0e-42
Match length 255
% identity 87

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 41834

Seq. ID LIB3167-002-Q1-K1-D11

Method BLASTN
NCBI GI g169897
BLAST score 34
E value 1.0e-09
Match length 133
% identity 82

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 41835

Seq. ID LIB3167-002-Q1-K1-D5

Method BLASTN
NCBI GI g403326
BLAST score 68
E value 7.0e-30
Match length 136
% identity 88



T.repens TrMT1A mRNA for metallothionein-like protein

Seq. No. 41836

NCBI Description

Seq. ID LIB3167-002-Q1-K1-D9

Method BLASTX
NCBI GI g4337200
BLAST score 344
E value 1.0e-32
Match length 102
% identity 60

NCBI Description (AC006403) putative NAM protein [Arabidopsis thaliana]

Seq. No. 41837

Seq. ID LIB3167-002-Q1-K1-H10

Method BLASTX
NCBI GI g584929
BLAST score 149
E value 6.0e-10
Match length 70
% identity 37

NCBI Description BASIC ENDOCHITINASE CHB4 PRECURSOR >gi 17799 emb_CAA43708_

(X61488) chitinase [Brassica napus]

Seq. No. 41838

Seq. ID LIB3167-002-Q1-K1-H4

Method BLASTX
NCBI GI g4033429
BLAST score 291
E value 2.0e-26
Match length 87
% identity 67

NCBI Description PYRUVATE KINASE (PK) >gi 2854033 (AF043910) pyruvate kinase

[Eimeria tenella]

Seq. No. 41839

Seg. ID LIB3167-004-P1-K1-A4

Method BLASTX
NCBI GI g4512651
BLAST score 170
E value 4.0e-12
Match length 95
% identity 39

NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis

thaliana]

Seq. No. 41840

Seq. ID LIB3167-004-P1-K1-A5

Method BLASTN
NCBI GI g399619
BLAST score 35
E value 4.0e-10
Match length 59
% identity 90

NCBI Description Lycopersicon esculentum (DB164) meloidogyne-induced giant

cell protein mRNA, 3' end

Seq. No. 41841

6603



Seq. ID LIB3167-004-P1-K1-C10

Method BLASTX
NCBI GI g1655679
BLAST score 198
E value 2.0e-15
Match length 92
% identity 58

NCBI Description (X96386) 3-hydroxy-3-methylglutaryl-CoA-synthase [Pinus

sylvestris]

Seq. No. 41842

Seq. ID LIB3167-004-P1-K1-C2

Method BLASTX
NCBI GI g3913641
BLAST score 153
E value 2.0e-10
Match length 49
% identity 69

NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)

>gi 3041777 dbj BAA25423 (AB007194)

fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 41843

Seq. ID LIB3167-004-P1-K1-D1

Method BLASTX
NCBI GI g2764941
BLAST score 156
E value 2.0e-10
Match length 74
% identity 42

NCBI Description (X98255) transcriptionally stimulated by gibberellins;

expressed in meristematic region, and style [Arabidopsis

thaliana]

Seq. No. 41844

Seq. ID LIB3167-004-P1-K1-D5

Method BLASTX
NCBI GI g2494275
BLAST score 152
E value 2.0e-10
Match length 73
% identity 42

NCBI Description ELONGATION FACTOR P (EF-P) >gi_1399829 (U59235) elongation

factor P [Synechococcus PCC7942]

Seq. No. 41845

Seq. ID LIB3167-004-P1-K1-H5

Method BLASTX
NCBI GI g1458228
BLAST score 239
E value 4.0e-20
Match length 109
% identity 48

NCBI Description (U63329) mutY homolog [Homo sapiens]

Seq. No. 41846



```
LIB3167-010-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3947725
BLAST score
                  145 -
E value
                  4.0e-09
Match length
                  61
% identity
                  57
                  (AJ012656) ribosomal protein S28 [Prunus persica]
NCBI Description
Seq. No.
                  41847
                  LIB3167-010-P1-K1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18551
BLAST score
                  55
E value
                  3.0e-22
Match length
                  134
                  92
% identity
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                  protein
Seq. No.
                  41848
Seq. ID
                  LIB3167-010-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g4056477
BLAST score
                  355
                  9.0e-34
E value
Match length
                  81
                  45
% identity
                   (AC005896) putative RNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  41849
Seq. ID
                  LIB3167-010-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  227
                  3.0e-19
E value
Match length
                  67
                  72
% identity
NCBI Description
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                  41850
Seq. ID
                  LIB3167-010-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q3335359
BLAST score
                  308
                  3.0e-28
E value
                  122
% identity
                  58
                  (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Match length

Seq. No. 41851

LIB3167-010-P1-K1-G2 Seq. ID

Method BLASTX NCBI GI g1351033 BLAST score 153 7.0e-17 E value

6605



Match length 79 % identity 62

NCBI Description STEM 31 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE PROTEIN VSP25) >gi 170088 (M20037) vegetative storage

protein [Glycine max]

Seq. No. 41852

Seq. ID LIB3167-010-P1-K1-G7

Method BLASTX
NCBI GI g2499967
BLAST score 209
E value 1.0e-16
Match length 99
% identity 53

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E

B) >gi_632724_bbs_151002 (S72358) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,

143 aa] [Nicotiana sylvestris]

Seq. No. 41853

Seq. ID LIB3167-010-P1-K1-H12

Method BLASTX
NCBI GI g2505874
BLAST score 269
E value 1.0e-23
Match length 72
% identity 76

NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]

Seq. No. 41854

Seq. ID LIB3167-013-P1-K1-A12

Method BLASTX
NCBI GI g129867
BLAST score 121
E value 9.0e-14
Match length 79
% identity 62

NCBI Description CYTOCHROME B6-F COMPLEX SUBUNIT 4 (17 KD POLYPEPTIDE)

>gi 2924273 emb CAA77425_ (Z00044) cytochrome b/f complex

subunit IV [Nicotiana tabacum]

Seq. No. 41855

Seq. ID LIB3167-013-P1-K1-D4

Method BLASTN
NCBI GI g19701
BLAST score 38
E value 4.0e-12
Match length 58
% identity 91

NCBI Description N.plumbaginifolia mRNA NeIF-5A2 for initiation factor 5A(2)

Seq. No. 41856

Seq. ID LIB3167-013-P1-K1-F10

Method BLASTN
NCBI GI g1055367
BLAST score 302
E value 1.0e-169



Match length 377 % identity 95

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 41857

Seq. ID LIB3167-013-P1-K1-F11

Method BLASTX
NCBI GI g132086
BLAST score 136
E value 6.0e-11
Match length 74
% identity 61

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR

(RUBISCO SMALL SUBUNIT 1) >gi 68053 pir RKSYS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor SRS1 - soybean >gi_18742_emb_CAA23736_ (V00458)

rubpcase [Glycine max]

Seq. No. 41858

Seq. ID LIB3167-013-P1-K1-G6

Method BLASTX
NCBI GI g1170568
BLAST score 205
E value 2.0e-16
Match length 62
% identity 63

NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)

>gi 2147316 pir S60302 D-myo-inositol-3-phosphate synthase

(EC 5.5.1.4) - Spirodela polyrrhiza >gi 558648 emb CAA77751 (Z11693)

D-myo-inositol-3-phosphate synthase [Spirodela polyrrhiza]

Seq. No. 41859

Seq. ID LIB3167-017-P1-K1-B2

Method BLASTX
NCBI GI g4469005
BLAST score 190
E value 2.0e-14
Match length 67
% identity 48

NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 41860

Seq. ID LIB3167-017-P1-K1-E2

Method BLASTX
NCBI GI g282994
BLAST score 189
E value 3.0e-14
Match length 95
% identity 45

NCBI Description Sip1 protein - barley >gi_167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No. 41861

Seq. ID LIB3167-017-P1-K1-E5

Method BLASTX



NCBI GI g3834310 BLAST score 236 E value 3.0e-20 Match length 54 % identity 85

NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,

gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122

come from this gene. [Arabidopsis thaliana]

Seq. No. 41862

Seq. ID LIB3167-017-P1-K1-F4

Method BLASTX
NCBI GI g1228074
BLAST score 180
E value 9.0e-14
Match length 51
% identity 78

NCBI Description (X95763) histone h2a homologue [Allium cepa]

Seq. No. 41863

Seq. ID LIB3167-017-P1-K1-F5

Method BLASTN
NCBI GI g20657
BLAST score 50
E value 4.0e-19
Match length 113
% identity 87

NCBI Description P.sativum Cab II gene for chlorophyll a/b-binding protein

Seq. No. 41864

Seq. ID LIB3167-017-P1-K1-G2

Method BLASTN
NCBI GI g170091
BLAST score 213
E value 1.0e-116
Match length 249
% identity 97

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 41865

Seq. ID LIB3167-017-P1-K1-G6

Method BLASTN
NCBI GI g1165321
BLAST score 111
E value 2.0e-55
Match length 292
% identity 16

NCBI Description Glycine max extensin (SbHRGP3) gene, complete cds

Seq. No. 41866

Seq. ID LIB3167-017-P1-K1-H4

Method BLASTN
NCBI GI g296444
BLAST score 181
E value 2.0e-97



```
Match length
                   94
% identity
```

NCBI Description G.max ADR6 mRNA

41867 Seq. No.

Seq. ID LIB3167-019-P1-K1-A1

BLASTN Method g4098966 NCBI GI 33 BLAST score 6.0e-09 E value

33 Match length 100 % identity

Glycine max putative reistance gene analog genomic sequence NCBI Description

41868 Seq. No.

LIB3167-019-P1-K1-F7 Seq. ID

BLASTN Method g1262439 NCBI GI 396 BLAST score 0.0e + 00E value 396 Match length 100 % identity

NCBI Description Glycine max lipoxygenase (vlxC) mRNA, complete cds

41869 Seq. No.

LIB3167-019-P1-K1-H1 Seq. ID

BLASTX Method g1619300 NCBI GI 238 BLAST score 5.0e-20 E value 58 Match length 72 % identity

(X95269) LRR protein [Lycopersicon esculentum] NCBI Description

Seq. No.

Seq. ID LIB3167-019-P1-K1-H8

41870

Method BLASTX g567893 NCBI GI 164 BLAST score 2.0e-11 E value Match length 70 47 % identity

(L37382) beta-galactosidase-complementation protein NCBI Description

[Cloning vector]

41871 Seq. No.

Seq. ID LIB3167-023-P4-K4-A8

BLASTN Method g1277165 NCBI GI BLAST score 155 1.0e-81 E value Match length 187 96 % identity

Glycine max cysteine proteinase inhibitor mRNA, partial cds NCBI Description

Seq. No.

41872 LIB3167-023-P4-K4-C10 Seq. ID

6609

```
BLASTX
Method
NCBI GI
                  g3212867
BLAST score
                  201
                  5.0e-16
E value
                  71
Match length
                  58
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  41873
Seq. ID
                  LIB3167-023-P4-K4-D5
                  BLASTX
Method
                  g4204306
NCBI GI
BLAST score
                  139
                  5.0e-09
E value
                   42
Match length
                  74
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   41874
                  LIB3167-023-P4-K4-D7
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                  35
                   2.0e-10
E value
Match length
                   48
% identity
                   48
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   41875
Seq. No.
Seq. ID
                  LIB3167-023-P4-K4-G8
                  BLASTX
Method
NCBI GI
                   g282929
BLAST score
                   244
                   1.0e-20
E value
Match length
                   112
                   53
% identity
NCBI Description carbonate dehydratase (EC 4.2.1.1) - garden pea
Seq. No.
                   41876
Seq. ID
                   LIB3167-027-P1-K1-A7
Method
                  BLASTX
NCBI GI
                   g4508078
BLAST score
                   203
                   5.0e-16
E value
                   74
Match length
                   59
% identity
NCBI Description (AC005882) 64134 [Arabidopsis thaliana]
```

Seq. No. 41877

Seq. ID LIB3167-027-P1-K1-C1

Method BLASTN
NCBI GI g18644
BLAST score 347
E value 0.0e+00
Match length 359
% identity 99

6610

BLAST score

Match length

% identity

E value

154

278 90

2.0e-81



NCBI Description Soybean mRNA for HMG-1 like protein

```
41878
Seq. No.
                   LIB3167-027-P1-K1-C7
Seq. ID
                   BLASTX
Method
                   g3152731
NCBI GI
BLAST score
                   226
                   9.0e-19
E value
                   86
Match length
                   56
% identity
                   (AF056325) myo-inositol 1-phosphate synthase; INO1 [Hordeum
NCBI Description
                   vulgare]
                   41879
Seq. No.
Seq. ID
                   LIB3167-027-P1-K1-D12
                   BLASTN
Method
                   g1055367
NCBI GI
                   61
BLAST score
                   7.0e-26
E value
                   65
Match length
                   98
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   41880
Seq. No.
                   LIB3167-027-P1-K1-F2
Seq. ID
                   BLASTX
Method
                   g3776031
NCBI GI
BLAST score
                   548
                   2.0e-56
E value
                   122
Match length
                   86
% identity
                  (AJ010477) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   41881
Seq. No.
Seq. ID
                   LIB3167-027-P1-K1-F6
                   BLASTX
Method
                   g130011
NCBI GI
BLAST score
                   156
                   5.0e-11
E value
Match length
                   73
% identity
                   45
                   LEUCOAGGLUTINATING PHYTOHEMAGGLUTININ PRECURSOR (PHA-L)
NCBI Description
                   >gi 81879 pir_ A25701 phytohemagglutinin chain L precursor
                   - kidney bean >gi_21023 emb_CAA28362_ (X04659) precursor
                   polypeptide (AA -\overline{2}1 to \overline{2}52) [Phaseolus vulgaris]
                   >gi 225351_prf__1301226A phytohemagglutinin [Phaseolus
                   vulgaris]
                   41882
Seq. No.
                   LIB3167-027-P1-K1-H11
Seq. ID
Method
                   BLASTN
                   q169974
NCBI GI
```



NCBI Description Glycine max vspA gene, complete cds 41883 Seq. No. Seq. ID LIB3167-027-P1-K1-H8 BLASTN Method g2055227 NCBI GI BLAST score 232 1.0e-128 E value 324 Match length % identity 100 NCBI Description Glycine max mRNA for SRC1, complete cds 41884 Seq. No. LIB3167-027-P1-K1-H9 Seq. ID Method BLASTX q4415912 NCBI GI BLAST score 288 6.0e-26 E value Match length 77 % identity 70 (AC006282) putative protease [Arabidopsis thaliana] NCBI Description Seq. No. 41885 LIB3167-029-P1-K1-A11 Seq. ID Method BLASTN NCBI GI q871769 BLAST score 42 E value 1.0e-14 Match length 59 % identity NCBI Description V.unguiculata mRNA for glycin-rich protein Seq. No. 41886 Seq. ID LIB3167-029-P1-K1-B12 Method BLASTX g4325371 NCBI GI BLAST score 293 1.0e-26 E value 74 Match length 74 % identity (AF128396) contains similarity to Medicago truncatula N7 NCBI Description protein (GB:Y17613) [Arabidopsis thaliana] 41887 Seq. No. Seq. ID LIB3167-029-P1-K1-D10

Method BLASTX
NCBI GI g129915
BLAST score 203
E value 5.0e-16
Match length 74
% identity 61

NCBI Description PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR

>gi_66912_pir__TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
precursor, chloroplast - wheat >gi_21833_emb_CAA33303_
(X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum

aestivum] >gi_3293043_emb_CAA51931_ (X73528)
phosphoglycerate kinase [Triticum aestivum]



```
Seq. No.
                  41888
                  LIB3167-029-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334150
BLAST score
                  250
                  2.0e-21
E value
Match length
                  102
% identity
                  57
                  MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
NCBI Description
                  (MG-PROTOPORPHYRIN IX CHELATASE) >gi 2129847 pir JC4312
                  chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean
                  chloroplast >gi 1732469 dbj BAA08291_ (D45857) Mg chelatase
                  subunit (46 kD) [Glycine max]
                  41889
Seq. No.
                  LIB3167-029-P1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q534971
BLAST score
                  233
                  1.0e-128
E value
                  329
Match length
% identity
                  93
                  V.faba (var. minor) mRNA for alpha 1,4-glucan phosphorylase
NCBI Description
                  L isoform
                  41890
Seq. No.
                  LIB3167-029-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1916809
BLAST score
                  319
                  1.0e-29
E value
Match length
                  103
                   60
% identity
NCBI Description
                  (U81163) auxin-binding protein [Prunus persica]
Seq. No.
                  41891
                  LIB3167-029-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1399306
BLAST score
                  190
E value
                  1.0e-103
Match length
                  238
% identity
                   95
                  Glycine max phosphoinositide-specific phospholipase C P25
NCBI Description
                  mRNA, complete cds
                   41892
Seq. No.
                  LIB3167-029-P1-K1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170091
```

Method BLASTN
NCBI GI g170091
BLAST score 156
E value 2.0e-82
Match length 272
% identity 90

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Match length

NCBI Description

% identity

Seq. No.

121 87

41898



```
Seq. No.
                  41893
Seq. ID
                  LIB3167-029-P1-K1-H8
                  BLASTX
Method
NCBI GI
                  g2764941
BLAST score
                  147
                  2.0e-09
E value
                  60
Match length
% identity
                  50
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  41894
Seq. No.
                  LIB3167-031-P1-K1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2435517
BLAST score
                  175
E value
                  1.0e-12
Match length
                  74
% identity
                  50
                   (AF024504) contains similarity to peptidase family A1
NCBI Description
                   [Arabidopsis thaliana]
                  41895
Seq. No.
                  LIB3167-031-P1-K1-A6
Seq. ID
                  BLASTN
Method
                  g2160155
NCBI GI
BLAST score
                   40
                   4.0e-13
E value
Match length
                  76
                   88
% identity
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   41896
Seq. ID
                   LIB3167-031-P1-K1-A9
                   BLASTN
Method
NCBI GI
                   q3510347
BLAST score
                   37
E value
                   2.0e-11
Match length
                   117
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   41897
Seq. ID
                   LIB3167-031-P1-K1-B9
                   BLASTN
Method
NCBI GI
                   g170087
BLAST score
                   47
E value
                   2.0e-17
```

6614

G.max vegetative storage protein mRNA (VSP25 gene)



```
LIB3167-031-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2582822
BLAST score
                  235
E value
                   1.0e-19
Match length
                   66
% identity
                   (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                  Protein of 32kDa) [Solanum tuberosum]
                   41899
Seq. No.
                  LIB3167-031-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2342727
BLAST score
                   381
                   9.0e-37
E value
                   130
Match length
% identity
                   58
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41900
Seq. ID
                  LIB3167-031-P1-K1-E2
                  BLASTX
Method
                   g2340166
NCBI GI
BLAST score
                   468
E value
                   6.0e-47
Match length
                   141
                   63
% identity
                   (AF008124) glutathione S-conjugate transporting ATPase
NCBI Description
                   [Arabidopsis thaliana] >gi 2459949 (AF008125) multidrug
                   resistance-associated protein homolog [Arabidopsis
                   thaliana]
                   41901
Seq. No.
                   LIB3167-031-P1-K1-F4
Seq. ID
Method
                   BLASTX
                   g2293301
NCBI GI
BLAST score
                   145
                   5.0e-09
E value
Match length
                   72
% identity
                   (AF008220) YtqB [Bacillus subtilis]
NCBI Description
                   >gi_2635533_emb_CAB15027_ (Z99119) ytqB [Bacillus subtilis]
Seq. No.
                   41902
Seq. ID
                   LIB3167-037-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g2129636
BLAST score
                   148
                   1.0e-09
E value
Match length
                   109
                   36
% identity
```

NCBI Description

lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

41903 Seq. No.

LIB3167-037-P1-K1-E12 Seq. ID



```
BLASTX
Method
                  q4432840
NCBI GI
                  190
BLAST score
                  3.0e-14
E value
                  97
Match length
                  39
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                  41904
Seq. No.
                  LIB3167-038-P1-K1-B12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2689634
                  56
BLAST score
                   6.0e-23
E value
Match length
                   176
                   81
% identity
NCBI Description Expression vector pESP-3, complete sequence
                   41905
Seq. No.
                   LIB3167-038-P1-K1-C7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1262439
BLAST score
                   44
E value
                   1.0e-15
Match length
                   222
                   74
% identity
NCBI Description Glycine max lipoxygenase (vlxC) mRNA, complete cds
Seq. No.
                   41906
                   LIB3167-038-P1-K1-D6
Seq. ID
                   BLASTN
Method
                   g1055367
NCBI GI
BLAST score
                   84
                   2.0e-39
E value
Match length
                   353
% identity
                   76
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   41907
Seq. No.
                   LIB3167-038-P1-K1-E10
Seq. ID
                   BLASTX
Method
                   g1483218
NCBI GI
                   140
BLAST score
                   1.0e-08
E value
                   71
Match length
% identity
                   (X99793) induced upon wounding stress [Arabidopsis
NCBI Description
                   thaliana]
                   41908
Seq. No.
Seq. ID
                   LIB3167-038-P1-K1-F4
                   BLASTN
Method
                   g18725
NCBI GI
BLAST score
                   110
```

7.0e-55

229

E value Match length



% identity 87

NCBI Description Soybean (G. max) mRNA for proliferating cell nuclear antigen (PCNA), partial

Seq. No. 41909

Seq. ID LIB3167-038-P1-K1-G10

Method BLASTX
NCBI GI g3334113
BLAST score 141
E value 7.0e-09
Match length 86
% identity 42

NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015)

acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No. 41910

Seq. ID LIB3167-042-P1-K1-H6

Method BLASTN
NCBI GI g1055367
BLAST score 403
E value 0.0e+00
Match length 435
% identity 98

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 41911

Seq. ID LIB3167-049-P1-K1-B12

Method BLASTX
NCBI GI g100347
BLAST score 439
E value 2.0e-43
Match length 150
% identity 57

NCBI Description monosaccharide transport protein MST1 - common tobacco

>gi 19885 emb CAA47324 (X66856) monosaccharid transporter

[Nicotiana tabacum]

Seq. No. 41912

Seq. ID LIB3167-049-P1-K1-B4

Method BLASTX
NCBI GI g2506211
BLAST score 306
E value 5.0e-28
Match length 115
% identity 54

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) (VAA3-1) >gi 849136 (U26709) vacuolar H+-ATPase

subunit A [Vigna radiata]

Seq. No. 41913

Seq. ID LIB3167-049-P1-K1-B7

Method BLASTN
NCBI GI g217868
BLAST score 335
E value 0.0e+00
Match length 471



% identity

Arabidopsis thaliana mRNA for putative transmenbrane NCBI Description

channel protein

41914 Seq. No.

Seq. ID

LIB3167-049-P1-K1-C10

Method

BLASTX

NCBI GI

g2245006

BLAST score

139

E value

1.0e-08

Match length

52 58

% identity NCBI Description

(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.

41915

Seq. ID

LIB3167-049-P1-K1-C12

Method NCBI GI BLASTN

BLAST score

g19655 59

E value Match length

1.0e-24 135

% identity NCBI Description M.sativa 26S rRNA

86

Seq. No.

41916

Seq. ID

LIB3167-049-P1-K1-C7

Method NCBI GI BLASTN g1495254

BLAST score

394 0.0e+00

E value Match length

462 97

% identity

NCBI Description A.thaliana mRNA for unknown protein, ORF02

Seq. No.

41917

Seq. ID

LIB3167-049-P1-K1-E11

Method NCBI GI BLASTN g1236948

BLAST score

189

E value

1.0e-102

Match length % identity

373 88

NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds

Seq. No.

41918

Seq. ID Method

LIB3167-049-P1-K1-F10 BLASTN

NCBI GI

q430946

BLAST score

100

E value

6.0e-49

Match length

% identity

268 85

NCBI Description Arabidopsis thaliana PSI type III chlorophyll a/b-binding

protein (Lhca3*1) mRNA, complete cds

Seq. No.

41919

Seq. ID

LIB3167-050-P1-K1-A1



```
BLASTX
Method
NCBI GI
                  g3885511
BLAST score
                  161
                  2.0e-17
E value
                  81
Match length
                  67
% identity
NCBI Description
                  (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
Seq. No.
                  41920
                  LIB3167-050-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351033
BLAST score
                  237
E value
                  4.0e-24
                  114
Match length
                  54
% identity
                  STEM 31 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE
NCBI Description
                  PROTEIN VSP25) >gi 170088 (M20037) vegetative storage
                  protein [Glycine max]
                  41921
Seq. No.
Seq. ID
                  LIB3167-050-P1-K1-D6
Method
                  BLASTN
                  q170091
NCBI GI
BLAST score
                  311
                  1.0e-175
E value
                  414
Match length
                  94
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                  41922
Seq. No.
                  LIB3167-050-P1-K1-F6
Seq. ID
                  BLASTN
Method
NCBI GI
                  q829118
BLAST score
                  137
                  5.0e-71
E value
Match length
                  313
                  86
% identity
NCBI Description P.vulgaris gene for cyclophilin
Seq. No.
                  41923
Seq. ID
                  LIB3167-050-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q627650
BLAST score
                  218
E value
                  2.0e-17
Match length
                  78
% identity
                  53
NCBI Description transcription factor BTF2 chain p34 - human
```

Seq. No.

41924

Seq. ID LIB3167-050-P1-K1-H6

Method BLASTX NCBI GI g1709825 BLAST score 331

% identity

NCBI Description

50



```
0e-31
E value
                  70
Match length
                   81
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
                   41925
Seq. No.
                  LIB3167-077-P1-K1-A10
Seq. ID
                  BLASTX
Method
                   g3493172
NCBI GI
                   282
BLAST score
                   4.0e-25
E value
                   110
Match length
                   57
% identity
                  (U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
Seq. No.
                   41926
                   LIB3167-077-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   g3789952
NCBI GI
BLAST score
                   164
E value
                   3.0e-11
Match length
                   73
% identity
                   51
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   41927
Seq. No.
                   LIB3167-077-P1-K1-A3
Seq. ID
                   BLASTX
Method
                   g3927838
NCBI GI
                   142
BLAST score
                   7.0e-09
E value
                   39
Match length
                   67
% identity
                  (AC005727) unknown protein [Arabidopsis thaliana]
NCBI Description
                   41928
Seq. No.
                   LIB3167-077-P1-K1-B10
Seq. ID
                   BLASTX
Method
                   g2832680
NCBI GI
BLAST score
                   206
                   3.0e-16
E value
                   104
Match length
% identity
                  (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                   41929
Seq. No.
Seq. ID
                   LIB3167-077-P1-K1-B4
                   BLASTX
Method
                   q1076316
NCBI GI
BLAST score
                   158
                   1.0e-10
E value
                   60
Match length
```

drought-induced protein Di19 - Arabidopsis thaliana

>gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis

Seq. ID



thaliana]

```
41930
Seq. No.
                  LIB3167-077-P1-K1-B6
Seq. ID
                  BLASTX
Method
                  g4191782
NCBI GI
                  288
BLAST score
E value
                  7.0e-26
                  136
Match length
                  50
% identity
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
                  41931
Seq. No.
Seq. ID
                  LIB3167-077-P1-K1-B9
                  BLASTX
Method
                  g3482967
NCBI GI
BLAST score
                  268
                  1.0e-23
E value
                  70
Match length
                  73
% identity
                   (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4559345_gb_AAD23006.1 AC006585 1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
                  41932
Seq. No.
                  LIB3167-077-P1-K1-C10
Seq. ID
                  BLASTN
Method
                  g441205
NCBI GI
BLAST score
                   44
                  1.0e-15
E value
Match length
                   108
% identity
                   85
                  Soybean lox1gm4 gene encoding lipxygenase L-4
NCBI Description
                   41933
Seq. No.
Seq. ID
                  LIB3167-077-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g4510389
BLAST score
                   180
                   4.0e-13
E value
Match length
                   131
% identity
                   43
                   (AC007017) putative solute carrier protein [Arabidopsis
NCBI Description
                   thaliana]
                   41934
Seq. No.
Seq. ID
                   LIB3167-077-P1-K1-D11
                   BLASTX
Method
NCBI GI
                   g2789660
BLAST score
                   170
                   2.0e-12
E value
Match length
                   79
% identity
                   (AF040102) p105 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   41935
```

LIB3167-077-P1-K1-D5

```
Method-
                  BLASTN
                  g170087
NCBI GI
BLAST score
                  103
                  1.0e-50
E value
                  276
Match length
                  84
% identity
NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)
                  41936
Seq. No.
                  LIB3167-077-P1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3021374
BLAST score
                  151
                  2.0e-79
E value
                  339
Match length
% identity
                  86
NCBI Description Glycine max mRNA for profilin, PRO1
Seq. No.
                  41937
Seq. ID
                  LIB3167-077-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q2760330
BLAST score
                  262
                  8.0e-23
E value
Match length
                  112
% identity
                  49
NCBI Description (AC002130) F1N21.15 [Arabidopsis thaliana]
                  41938
Seq. No.
Seq. ID
                  LIB3167-077-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q512400
BLAST score
                  245
                  5.0e-21
E value
                  108
Match length
% identity
                  53
NCBI Description (X74947) annexin [Medicago sativa]
Seq. No.
                  41939
Seq. ID
                  LIB3167-077-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2689631
BLAST score
                  146
                  3.0e-09
E value
Match length
                  87
% identity
NCBI Description (AF022389) ADP-ribosylation factor [Vigna unguiculata]
                  41940
Seq. No.
                  LIB3167-077-P1-K1-E12
Seq. ID
```

Method BLASTX
NCBI GI g1705677
BLAST score 356
E value 8.0e-34
Match length 145
% identity 32

* 1200

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG



>qi 2118115 pir S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi 1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No. 41941 Seq. ID LIB3167-077-P1-K1-E5 Method BLASTX NCBI GI g2501189 BLAST score 155 2.0e-16 E value 90 Match length

54

% identity THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR NCBI Description

>gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

41942 Seq. No.

Seq. ID LIB3167-077-P1-K1-E6

Method BLASTN NCBI GI g3560095 BLAST score 34 7.0e-10 E value 118 Match length 82 % identity

Cloning vector pEH1 NCBI Description

41943 Seq. No.

Seq. ID LIB3167-077-P1-K1-E9

BLASTN Method g170087 NCBI GI BLAST score 62 3.0e-26 E value 122 Match length % identity

G.max vegetative storage protein mRNA (VSP25 gene) NCBI Description

41944 Seq. No.

LIB3167-077-P1-K1-F1 Seq. ID

BLASTN Method NCBI GI q1277165 87 BLAST score E value 2.0e-41 Match length 155 89 % identity

Glycine max cysteine proteinase inhibitor mRNA, partial cds NCBI Description

Seq. No. 41945

Seq. ID LIB3167-077-P1-K1-F11

BLASTN Method NCBI GI g169897 BLAST score 139 3.0e-72 E value Match length 427 % identity 83

NCBI Description G.max 28 kDa protein, complete cds



Seq. No. Seq. ID LIB3167-077-P1-K1-F12 BLASTX Method NCBI GI g2459435 BLAST score 178 5.0e-13 E value Match length 88 44 % identity (AC002332) putative serine carboxypeptidase [Arabidopsis NCBI Description thaliana] 41947 Seq. No. Seq. ID LIB3167-077-P1-K1-F3 BLASTN Method NCBI GI g1055367 123 BLAST score 1.0e-62 E value 368 Match length 83 % identity Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description subunit mRNA, complete cds 41948 Seq. No. Seq. ID LIB3167-077-P1-K1-F4 BLASTX Method g1237250 NCBI GI BLAST score 162 5.0e-11E value 120 Match length 33 % identity NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum] 41949 Seq. No. Seq. ID LIB3167-077-P1-K1-F6 BLASTN Method NCBI GI q537626 BLAST score 129 3.0e-66 E value Match length 366 % identity 84 Glycine max inducible nitrate reductase 2 (INR2) mRNA, NCBI Description complete cds Seq. No. 41950 LIB3167-077-P1-K1-G10 Seq. ID BLASTX Method NCBI GI q3335378 BLAST score 337 1.0e-31 E value Match length 145 52 % identity (ACO03028) Myb-related transcription activator [Arabidopsis NCBI Description thaliana]

Seq. No. 41951

Seq. ID LIB3167-077-P1-K1-G11

Method BLASTN

6624

```
NCBI GI
                  87
BLAST score
                  3.0e-41
E value
                  275
Match length
% identity
NCBI Description Soybean calmodulin (SCaM-1) mRNA, complete cds
                  41952
Seq. No.
                  LIB3167-077-P1-K1-G3
Seq. ID
                  BLASTX
Method
                  g4371290
NCBI GI
                  248
BLAST score
                  4.0e-21
E value
                  108
Match length
```

45 % identity (AC006260) unknown protein [Arabidopsis thaliana] NCBI Description

41953 Seq. No. LIB3167-077-P1-K1-G6 Seq. ID BLASTX Method q1709358 NCBI GI 196 BLAST score 4.0e-15

E value 134 Match length % identity 25

NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE NCBI Description

PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859

nucleoside triphosphatase - garden pea

>gi_2129890_pir__S65147 nucleoside triphosphatase

precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase

[Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

41954 Seq. No.

LIB3167-077-P1-K1-G7 Seq. ID

Method BLASTX q2191136 NCBI GI BLAST score 217 1.0e-17 E value 115 Match length 37 % identity

(AF007269) Similar to UTP-Glucose Glucosyltransferase; NCBI Description

coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

41955 Seq. No.

LIB3167-077-P1-K1-G8 Seq. ID

Method BLASTN g169897 NCBI GI 153 BLAST score 1.0e-80 E value 301 Match length 88 % identity

NCBI Description G.max 28 kDa protein, complete cds



```
Seq. No.
                   41956
Seq. ID
                  LIB3167-077-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3747050
BLAST score
                  217
E value
                  1.0e-17
Match length
                  102
% identity
                  49
NCBI Description
                  (AF093540) ribosomal protein L26 [Zea mays]
Seq. No.
                  41957
Seq. ID
                  LIB3167-077-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2500354
BLAST score
                  214
E value
                  3.0e-17
Match length
                  96
% identity
                  49
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
Seq. No.
                  41958
Seq. ID
                  LIB3167-077-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q130011
BLAST score
                  205
E value
                  4.0e-16
Match length
                  106
% identity
                  46
NCBI Description
                  LEUCOAGGLUTINATING PHYTOHEMAGGLUTININ PRECURSOR (PHA-L)
                  >gi 81879 pir A25701 phytohemagglutinin chain L precursor
                  - kidney bean >gi_21023_emb_CAA28362 (X04659) precursor
                  polypeptide (AA -21 to 252) [Phaseolus vulgaris]
                  >gi 225351 prf 1301226A phytohemagglutinin [Phaseolus
                  vulgaris]
Seq. No.
                  41959
Seq. ID
                  LIB3167-077-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3560266
BLAST score
                  155
E value
                  3.0e-11
Match length
                  125
% identity
                  41
NCBI Description
                  (AL031535) putative n-terminal acetyltransferase complex su
                  bunit [Schizosaccharomyces pombe]
Seq. No.
                  41960
                  LIB3167-077-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1055368
BLAST score
                  475
E value
                  8.0e-48
```

Match length 130 % identity 71

(U39567) ribulose-1,5-bisphosphate carboxylase small NCBI Description

subunit [Glycine max]



```
41961
Seq. No.
                  LIB3167-077-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g2443755
NCBI GI
BLAST score
                  160
                  8.0e-11
E value
Match length
                  56
% identity
                  61
                  (AF020433) cyclophilin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  41962
                  LIB3167-077-P1-K2-B4
Seq. ID
Method
                  BLASTX
                  g2191171
NCBI GI
BLAST score
                  123
E value
                  1.0e-08
Match length
                  41
                  68
% identity
                   (AF007270) similar to A. thaliana DI19 mRNA (NID:g469110)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  41963
                  LIB3167-077-P1-K2-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q441205
BLAST score
                  48
E value
                   4.0e-18
                  72
Match length
                   92
% identity
NCBI Description Soybean lox1gm4 gene encoding lipxygenase L-4
Seq. No.
                   41964
                  LIB3167-077-P1-K2-C3
Seq. ID
Method
                  BLASTX
                   q3336912
NCBI GI
BLAST score
                   141
                   7.0e-09
E value
                   85
Match length
                   44
% identity
                  (Y13784) Calmodulin [Mougeotia scalaris]
NCBI Description
                   41965
Seq. No.
                   LIB3167-077-P1-K2-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4510389
                   285
BLAST score
                   9.0e-26
E value
                   98
Match length
                   55
% identity
                   (AC007017) putative solute carrier protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   41966
Seq. ID
                   LIB3167-077-P1-K2-D4
```

6627

BLASTN

g296442

Method NCBI GI

NCBI Description



```
BLAST score
                  7.0e-12
E value
Match length
                  182
                  91
% identity
NCBI Description G.max ADR11 mRNA
Seq. No.
                   41967
                  LIB3167-078-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4098517
BLAST score
                   280
E value
                   8.0e-25
Match length
                   124
                   51
% identity
                  (U79114) auxin-binding protein ABP19 [Prunus persica]
NCBI Description
                   41968
Seq. No.
                   LIB3167-078-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g951449
BLAST score
                   219
                   7.0e-18
E value
Match length
                   94
% identity
                   45
                   (L46681) aspartic protease precursor [Lycopersicon
NCBI Description
                   esculentum]
                   41969
Seq. No.
Seq. ID
                   LIB3167-078-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g4337027
                   347
BLAST score
E value
                   9.0e-33
                   133
Match length
% identity
                   53
                  (AF123254) MFP2 [Arabidopsis thaliana]
NCBI Description
                   41970
Seq. No.
                   LIB3167-078-P1-K1-E4
Seq. ID
                   BLASTN
Method
                   g439856
NCBI GI
                   85
BLAST score
                   4.0e-40
E value
                   280
Match length
                   82
% identity
                  Glycine max Williams 82 lipoxygenase mRNA, complete cds
NCBI Description
                   41971
Seq. No.
                   LIB3167-078-P1-K1-E6
Seq. ID
                   BLASTN
Method
                   g242461
NCBI GI
                   110
BLAST score
E value
                   7.0e-55
                   290
Match length
                   84
% identity
```

mRNA, 1897 nt]

loxA=lipoxygenase [Glycine max=soybeans, Merr.cv.Williams,

% identity

NCBI Description



```
41972
Seq. No.
Seq. ID
                  LIB3167-078-P1-K1-E8
                  BLASTX
Method
NCBI GI
                  g116908
                  306
BLAST score
                  5.0e-28
E value
                  117
Match length
                  54
% identity
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                  (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                  3-O-METHYLTRANSFERASE) (COMT) >gi_166420 (M63853)
                  S-adenosyl-L-methionine: caffeic acid 3-0-methyltransferase
                  [Medicago sativa]
                  41973
Seq. No.
                  LIB3167-078-P1-K1-F12
Seq. ID
                  BLASTN
Method
                  g1262439
NCBI GI
BLAST score
                  112
                  4.0e-56
E value
Match length
                  347
% identity
                  84
                  Glycine max lipoxygenase (vlxC) mRNA, complete cds
NCBI Description
                   41974
Seq. No.
                  LIB3167-078-P1-K1-F4
Seq. ID
Method
                  BLASTX
                  g3901012
NCBI GI
                   270
BLAST score
                   8.0e-24
E value
                   93
Match length
% identity
                   59
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                   sylvatica]
                   41975
Seq. No.
                   LIB3167-078-P1-K1-F7
Seq. ID
                   BLASTX
Method
                   g3560529
NCBI GI
                   269
BLAST score
E value
                   1.0e-23
                   131
Match length
                   46
% identity
                   (AF039598) light harvesting chlorophyll A/B binding protein
NCBI Description
                   [Prunus persica]
                   41976
Seq. No.
Seq. ID
                   LIB3167-078-P1-K1-F9
                   BLASTX
Method
NCBI GI
                   g3860277
BLAST score
                   289
                   5.0e-26
E value
                   118
Match length
```

(AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative





ribosomal protein L10A [Arabidopsis thaliana]

```
41977
Seq. No.
Seq. ID
                  LIB3167-078-P1-K1-G12
                  BLASTX
Method
                  g4539301
NCBI GI
                  197
BLAST score
                  3.0e-15
E value
                  115
Match length
% identity
                  41
                   (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                  thaliana]
                  41978
Seq. No.
                  LIB3167-078-P1-K1-H10
Seq. ID
                  BLASTN
Method
                  g439856
NCBI GI
                  163
BLAST score
                  2.0e-86
E value
                  372
Match length
% identity
                   85
NCBI Description Glycine max Williams 82 lipoxygenase mRNA, complete cds
                   41979
Seq. No.
                  LIB3167-078-P1-K1-H3
Seq. ID
                  BLASTX
Method
                   g4185511
NCBI GI
BLAST score
                   200
                   5.0e-16
E value
Match length
                   76
% identity
                   53
                   (AF102822) actin depolymerizing factor 4 [Arabidopsis
NCBI Description
                   thaliana]
                   41980
Seq. No.
Seq. ID
                   LIB3167-078-P1-K2-B11
                   BLASTX
Method
                   g2499613
NCBI GI
                   192
BLAST score
                   3.0e-19
E value
                   83
Match length
                   64
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG MMK2
NCBI Description
                   >gi_1204129_emb_CAA57719_ (X82268) protein kinase [Medicago
                   sativa]
                   41981
Seq. No.
Seq. ID
                   LIB3167-078-P1-K2-B8
                   BLASTX
Method
                   g1418984
NCBI GI
                   185
BLAST score
                   7.0e-14
E value
Match length
                   62
                   60
% identity
                  (Z75521) photosystem II 10 kD polypeptide [Lycopersicon
NCBI Description
```

esculentum]

Seq. No. LIB3167-078-P1-K2-C9 Seq. ID BLASTX Method g2827992 NCBI GI BLAST score 119 1.0e-14 E value 106 Match length 45 % identity (AF034743) UDP-glucuronosyltransferase [Pisum sativum] NCBI Description 41983 Seq. No. LIB3167-078-P1-K2-D8 Seq. ID Method BLASTX NCBI GI q2497486 BLAST score 209 4.0e-17 E value Match length 49 % identity 88 URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP NCBI Description KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana] Seq. No. 41984 LIB3167-078-P1-K2-E11 Seq. ID Method BLASTX NCBI GI g140207 BLAST score 204 E value 3.0e-16 69 Match length % identity 55 PROBABLE 40S RIBOSOMAL PROTEIN S9 >gi 102109 pir__S12674 NCBI Description ribosomal protein S9.e - Trypanosoma brucei >gi_10399_emb_CAA36818_ (X52586) ald orfU protein (AA 1 -190) [Trypanosoma brucei] 41985 Seq. No. LIB3167-078-P1-K2-G5 Seq. ID Method BLASTX g465975 NCBI GI 179 BLAST score

4.0e-13 E value 62 Match length 56 % identity

PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME NCBI Description

III >gi_482102_pir__S40731 ATP-dependent RNA helicase

homolog T26G10.1 - Caenorhabditis elegans

>gi_3880293_emb_CAA82362_ (Z29115) similar to RNA

helicases, deleted exon 1397-1495 which introduced stop codon at 3' splice; 5' splice looks v. good; ?possible alternate final exon.; cDNA EST yk368a4.3 comes from this

gene; cDNA EST yk368a4.5 comes fr

Seq. No. 41986

LIB3170-001-Q1-J1-B1 Seq. ID

Method BLASTX NCBI GI g2583135 BLAST score 201



E value 2.0e-15
Match length 51
% identity 76

NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

>qi 3822216 (AF074948) FIL [Arabidopsis thaliana]

>gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs

protein [Arabidopsis thaliana]

Seq. No. 41987

Seq. ID LIB3170-001-Q1-K1-B7

Method BLASTX
NCBI GI g70654
BLAST score 216
E value 9.0e-18
Match length 83
% identity 54

NCBI Description ubiquitin / ribosomal protein CEP52 - Chlamydomonas

reinhardtii >gi_18244_emb_CAA43216_ (X60826) ubiquitin extension protein (UbCEP52) [Chlamydomonas reinhardtii] >gi_18246_emb_CAA33466_ (X15427) ubiquitin/ribosomal

protein [Chlamydomonas reinhardtii]

Seq. No. 41988

Seq. ID LIB3170-001-Q1-K1-C12

Method BLASTX
NCBI GI g3024020
BLAST score 241
E value 1.0e-32
Match length 124
% identity 58

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No. 41989

Seq. ID LIB3170-001-Q1-K1-C3

Method BLASTX
NCBI GI g2462834
BLAST score 176
E value 1.0e-12
Match length 116
% identity 34

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 41990

Seq. ID LIB3170-001-Q1-K1-C8

Method BLASTN
NCBI GI g1575730
BLAST score 123
E value 1.0e-62
Match length 476
% identity 87

NCBI Description Glycine max 14-3-3 related protein SGF14D mRNA, complete

cds

Seq. No. 41991

Seq. ID LIB3170-001-Q1-K1-D2

```
Method
                  g3182981
NCBI GI
BLAST score
                  154
E value
                  2.0e-10
                  59
Match length
                  51
% identity
NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_
                  (D86494) diminuto [Pisum sativum]
Seq. No.
                  41992
                  LIB3170-001-Q1-K1-E8
Seq. ID
                  BLASTN
Method
                  g531828
NCBI GI
                  37
BLAST score
                  1.0e-11
E value
                  73
Match length
                  88
% identity
NCBI Description Cloning vector pSport1, complete cds
                  41993
Seq. No.
Seq. ID
                  LIB3170-001-Q1-K1-G2
Method
                  BLASTX
                  g2500354
NCBI GI
                  286
BLAST score
                  1.0e-25
E value
                  103
Match length
                  57
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj_BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                  41994
Seq. No.
Seq. ID
                  LIB3170-001-Q1-K1-G8
                  BLASTX
Method
NCBI GI
                  a1703375
                  149
BLAST score
                   5.0e-19
E value
Match length
                  81
                  77
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                  DcARF1 [Daucus carota]
                   41995
Seq. No.
Seq. ID
                  LIB3170-002-Q1-J1-A9
Method
                  BLASTX
```

Method BLASTX
NCBI GI g400247
BLAST score 161
E value 4.0e-11
Match length 43
% identity 72

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_169667 (M62757) S-adenosylmethionine synthetase [Petroselinum

crispum]

Seq. No.

41996

Seq. ID LIB3170-002-Q1-J1-G2

Method BLASTN



g2565339 NCBI GI 37 BLAST score 8.0e-12 E value 53 Match length 92 % identity Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete NCBI Description cds 41997 Seq. No. Seq. ID LIB3170-002-Q1-J1-G8 BLASTN Method

NCBI GI g4580381 BLAST score 41 E value 5.0e-14 Match length 69 % identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC T11P11 genomic

sequence, complete sequence

Seq. No. 41998 Seq. ID LIB3170-002-Q1-K1-B4

Method BLASTX
NCBI GI g2499967
BLAST score 277
E value 2.0e-24
Match length 123
% identity 53

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E

B) >gi_632724 bbs_151002 (S72358) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,

143 aa] [Nicotiana sylvestris]

Seq. No. 41999

Seq. ID LIB3170-002-Q1-K1-F8

Method BLASTX
NCBI GI g730645
BLAST score 185
E value 7.0e-14
Match length 77
% identity 55

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi 313152_emb_CAA80679_

(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 42000

Seq. ID LIB3170-003-Q1-J1-A4

Method BLASTX
NCBI GI g3885884
BLAST score 246
E value 5.0e-21
Match length 75
% identity 69



(AF093630) 60S ribosomal protein L21 [Oryza sativa] NCBI Description

42001 Seq. No.

LIB3170-003-Q1-J1-C9 Seq. ID

BLASTN Method g170053 NCBI GI BLAST score 45 E value 4.0e-16 150 Match length

% identity Soybean ribosomal protein S11 mRNA, 3' end NCBI Description

42002 Seq. No.

LIB3170-003-Q1-J1-E7 Seq. ID

86

BLASTX Method g3868758 NCBI GI 271 BLAST score 6.0e-24E value 74 Match length 70 % identity

(D89802) elongation factor 1B gamma [Oryza sativa] NCBI Description

42003 Seq. No.

Seq. ID LIB3170-003-Q1-K1-B6

BLASTN Method g2995835 NCBI GI 53 BLAST score 3.0e-21 E value 57 Match length 98 % identity

Trifolium ornithopodioides 18S ribosomal RNA gene, partial NCBI Description

sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;

and 26S ribosomal RNA gene, partial sequence

42004 Seq. No.

Seq. ID LIB3170-003-Q1-K1-F2

BLASTN Method g531828 NCBI GI 37 BLAST score 1.0e-11 E value Match length 89 85 % identity

Cloning vector pSport1, complete cds NCBI Description

42005 Seq. No.

Seq. ID LIB3170-003-Q1-K1-F4

BLASTX Method q531829 NCBI GI 154 BLAST score E value 3.0e-10 Match length 72 % identity

(U12390) beta-galactosidase alpha peptide [cloning vector NCBI Description

pSport1]

Seq. No. 42006

```
LIB3170-004-Q1-K1-B2
Seq. ID
Method
                  BLASTX
                  q3894191
NCBI GI
BLAST score
                  180
                  2.0e-13
E value
Match length
                  47
% identity
                  72
NCBI Description (AC005662) unknown protein [Arabidopsis thaliana]
                  42007
Seq. No.
                  LIB3170-004-Q1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3893118
BLAST score
                  179
                   6.0e-21
E value
Match length
                   121
% identity
                  (Y18419) t-complex polypeptide 20 [Drosophila virilis]
NCBI Description
                   42008
Seq. No.
                  LIB3170-004-Q1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1150683
BLAST score
                   73
                   7.0e - 33
E value
                   152
Match length
                   90
% identity
NCBI Description V.radiata atpB, rbcL and trnK genes
Seq. No.
                   42009
                   LIB3170-005-Q1-J1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2739371
                   257
BLAST score
E value
                   3.0e-22
Match length
                   61
% identity
                   84
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                   42010
Seq. No.
                   LIB3170-005-Q1-J1-C7
Seq. ID
                   BLASTN
Method
                   g169954
NCBI GI
                   42
BLAST score
                   2.0e-14
E value
                   175
Match length
% identity
                   84
                   Glycine max iron superoxide dismutase (FeSOD) mRNA,
NCBI Description
```

NCBI Description

Seq. No.

42011

complete cds

Seq. ID LIB3170-005-Q1-J1-F10

Method BLASTN
NCBI GI g12139
BLAST score 39
E value 8.0e-13
Match length 63



```
% identity
                  Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and
NCBI Description
                  trnG coding for ribosomal protein S2, one CF(1) and three
                  CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly
Seq. No.
                  42012
                  LIB3170-005-Q1-J1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g303900
                  70
BLAST score
E value
                  3.0e - 31
Match length
                  202
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                  42013
Seq. No.
                  LIB3170-005-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3482966
BLAST score
                  272
                  6.0e-24
E value
                  114
Match length
% identity
                  (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                  42014
Seq. No.
                  LIB3170-005-Q1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                   41
                   3.0e-14
E value
Match length
                   81
                  88
% identity
NCBI Description Cloning vector pSport1, complete cds
                   42015
Seq. No.
                  LIB3170-006-Q1-J1-C1
Seq. ID
                  BLASTX
Method
                   g2344897
NCBI GI
                   304
BLAST score
                   1.0e-27
E value
                   83
Match length
                   75
% identity
                  (AC002388) unknown protein [Arabidopsis thaliana]
NCBI Description
                   42016
Seq. No.
```

LIB3170-006-Q1-J1-E4 Seq. ID

BLASTX Method g2062167 NCBI GI BLAST score 225 1.0e-19 E value 81 Match length 62 % identity

(AC001645) Proline-rich protein APG isolog [Arabidopsis NCBI Description

thaliana]

Seq. No. 42017

BLAST score

E value

175 1.0e-12



```
LIB3170-006-Q1-J1-F10
Seq. ID
                  BLASTN
Method
                  g11772
NCBI GI
                   35
BLAST score
                   3.0e-10
E value
Match length
                  109
% identity
                   89
                  Tobacco chloroplast tRNA-Ser and tRNA-Gln genes
NCBI Description
Seq. No.
                   42018
Seq. ID
                   LIB3170-006-Q1-J1-H7
Method
                   BLASTX
NCBI GI
                   g2829910
BLAST score
                   327
                   3.0e-30
E value
Match length
                   77
                   81
% identity
                   (AC002291) Unknown protein, contains regulator of
NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
                   42019
Seq. No.
                   LIB3170-006-Q1-K1-H1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g310575
                   257
BLAST score
                   1.0e-142
E value
                   404
Match length
                   93
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
Seq. No.
                   42020
                   LIB3170-007-Q1-J1-E1
Seq. ID
Method
                   BLASTX
                   q4160280
NCBI GI
BLAST score
                   508
                   1.0e-51
E value
                   110
Match length
% identity
                   81
                  (AJ006224) purple acid phosphatase [Ipomoea batatas]
NCBI Description
                   42021
Seq. No.
                   LIB3170-007-Q1-J1-F3
Seq. ID
                   {\tt BLASTX}
Method
                   g4376509
NCBI GI
                   148
BLAST score
                   3.0e-09
E value
Match length
                   86
                   41
% identity
                   (AE001609) deoxyoctulonosic Acid Synthetase [Chlamydia
NCBI Description
                   pneumoniae]
                   42022
Seq. No.
                   LIB3170-007-Q1-K1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2507421
```

20

6638



```
Match length
                  58
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
NCBI Description
                  (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi 4490709 emb CAB38843.1 (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
                  42023
Seq. No.
                  LIB3170-007-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201554
BLAST score
                  205
                  3.0e-16
E value
                  93
Match length
                  53
% identity
NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]
                  42024
Seq. No.
                  LIB3170-009-Q1-J1-D10
Seq. ID
                  BLASTN
Method
                  g531055
NCBI GI
BLAST score
                  61
E value
                  6.0e-26
                  109
Match length
                  89
% identity
NCBI Description Wheat mRNA for protein H2B-6, complete cds
                  42025
Seq. No.
Seq. ID
                  LIB3170-009-Q2-J1-G3
Method
                  BLASTX
                  g1170567
NCBI GI
BLAST score
                  237
                  6.0e-20
E value
Match length
                  62
                  76
% identity
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                  >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi
                  >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi]
                  42026
Seq. No.
Seq. ID
                  LIB3170-009-Q2-K1-D9
Method
                  BLASTX
NCBI GI
                  g1052973
BLAST score
                  174
E value
                  8.0e-13
Match length
                  71
% identity
                  55
                  (U37838) fructokinase [Beta vulgaris]
NCBI Description
```

42027 Seq. No.

LIB3170-009-Q2-K1-F11 Seq. ID

Method BLASTX NCBI GI q4056469 BLAST score 194 E value 3.0e-22 Match length 93 % identity 65



NCBI Description (AC005990) Strong similarity to gb_M95166 ADP-ribosylation

factor from Arabidopsis thaliana. ESTs gb_Z25826,

gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,

gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and

gb Z25043 come from t

Seq. No. 42028

Seq. ID LIB3170-009-Q2-K1-F2

Method BLASTX
NCBI GI g4090257
BLAST score 265
E value 3.0e-23
Match length 85
% identity 65

NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No. 42029

Seq. ID LIB3170-009-Q2-K1-H1

Method BLASTX
NCBI GI g488573
BLAST score 320
E value 1.0e-29
Match length 88
% identity 73

NCBI Description (U09463) histone H3.2 [Medicago sativa]

Seq. No. 42030

Seq. ID LIB3170-009-Q2-K2-A3

Method BLASTX
NCBI GI g289920
BLAST score 222
E value 3.0e-18
Match length 102
% identity 52

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No. 42031

Seq. ID LIB3170-009-Q2-K2-F11

Method BLASTX
NCBI GI g728881
BLAST score 157
E value 4.0e-11
Match length 71
% identity 34

NCBI Description ADP-RIBOSYLATION FACTOR 2 >gi 1079047 pir A53859

ADP-ribosylation factor 2 - fruit fly (Drosophila

melanogaster) >gi_507232 (L25062) ADP ribosylation factor 2

[Drosophila melanogaster]

Seq. No. 42032

Seq. ID LIB3170-009-Q2-K2-G6

Method BLASTN
NCBI GI g1431621
BLAST score 43
E value 4.0e-15
Match length 182

6640



```
% identity
NCBI Description T.repens mRNA for protein kinase
                   42033
Seq. No.
Seq. ID
                  LIB3170-009-Q2-K2-H1
Method
                  BLASTX
                  g1053057
NCBI GI
                  180
BLAST score
                   2.0e-13
E value
Match length
                  81
% identity
                  (U38422) histone H3 [Triticum aestivum]
NCBI Description
Seq. No.
                   42034
                   LIB3170-010-Q1-J1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g730557
BLAST score
                   167
                   9.0e-12
E value
                   96
Match length
                   44
% identity
                   60S RIBOSOMAL PROTEIN L34 >gi_2119150_pir__S60476 ribosomal
NCBI Description
                   protein L34 - garden pea >gi_{4}98908 (\overline{U}100\overline{47}) ribosomal
                   protein L34 homolog [Pisum sativum]
                   42035
Seq. No.
                   LIB3170-010-Q1-K1-D7
Seq. ID
Method
                   BLASTX
                   g730557
NCBI GI
                   139
BLAST score
                   1.0e-19
E value
                   89
Match length
% identity
                   64
                   60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal
NCBI Description
                   protein L34 - garden pea >gi 498908 (U10047) ribosomal
                   protein L34 homolog [Pisum sativum]
                   42036
Seq. No.
                   LIB3170-010-Q1-K1-F8
Seq. ID
                   BLASTN
Method
                   g2281054
NCBI GI
                   54
BLAST score
                   1.0e-21
E value
                   66
Match length
                   95
% identity
                   Phreatamoeba balamuthi UBI1 sequence, putative
NCBI Description
                   polyubiquitin gene
                   42037
Seq. No.
                   LIB3170-011-Q1-J1-F2
Seq. ID
                   BLASTX
Method
                   g453128
NCBI GI
BLAST score
                   165
                   1.0e-11
E value
                   77
Match length
                   48
% identity
NCBI Description (S67284) petD [corn, seedlings, Peptide Chloroplast, 160
```



aa] [Zea mays]

```
42038
Seq. No.
                   LIB3170-011-Q1-K1-A9
Seq. ID
                   BLASTX
Method
                   g3122673
NCBI GI
                   140
BLAST score
                   1.0e-08
E value
                   92
Match length
% identity
                   42
                   60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   42039
Seq. No.
                   LIB3170-012-Q1-J1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g464621
                   171
BLAST score
                   4.0e-12
E value
Match length
                   46
                   74
% identity
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
                   42040
Seq. No.
                   LIB3170-012-Q1-K1-A2
Seq. ID
                   BLASTX
Method
                   g2500354
NCBI GI
                   358
BLAST score
                   3.0e - 34
E value
Match length
                   74
                   88
% identity
                   60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj_BAA19462_
NCBI Description
                    (AB001891) QM family protein [Solanum melongena]
                   42041
Seq. No.
                   LIB3170-012-Q1-K1-D1
Seq. ID
                   BLASTN
Method
                   g456713
NCBI GI
BLAST score
                   81
                   7.0e-38
E value
Match length
                   182
                    35
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
                    42042
Seq. No.
Seq. ID
                   LIB3170-012-Q1-K1-E12
                    BLASTN
Method
                    g531828
NCBI GI
BLAST score
                    38
                    3.0e-12
E value
                    90
Match length
% identity
```

NCBI Description Cloning vector pSport1, complete cds

BLAST score

E value

1.0e-20



```
Seq. No.
Seq. ID
                  LIB3170-013-Q1-J1-B1
Method
                  BLASTX
                  q170920
NCBI GI
                  236
BLAST score
                  7.0e-20
E value
Match length
                  59
                  78
% identity
                  (M62396) ribosomal protein L41 [Candida maltosa]
NCBI Description
                  42044
Seq. No.
                  LIB3170-013-Q1-J1-G5
Seq. ID
Method
                  BLASTX
                  g3309117
NCBI GI
BLAST score
                  143
                  7.0e-09
E value
                  86
Match length
                  36
% identity
                  (AF051899) 1,8-cineole synthase [Salvia officinalis]
NCBI Description
                  42045
Seq. No.
                  LIB3170-013-Q1-K1-A11
Seq. ID
                  BLASTX
Method
                  g3158476
NCBI GI
BLAST score
                  390
E value
                  6.0e-38
                  110
Match length
                  75
% identity
                  (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
                  42046
Seq. No.
                  LIB3170-013-Q1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4417266
BLAST score
                   223
E value
                   2.0e-18
Match length
                   109
                   47
% identity
                  (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   42047
Seq. No.
                   LIB3170-013-Q1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122753
BLAST score
                   156
                   1.0e-10
E value
Match length
                   67
                   52
% identity
                   60S RIBOSOMAL PROTEIN L44 >gi 2244789 emb CAB10211.1_
NCBI Description
                   (Z97336) ribosomal protein [Arabidopsis thaliana]
                   42048
Seq. No.
                   LIB3170-013-Q1-K1-C10
Seq. ID
                   BLASTN
Method
                   g2995831
NCBI GI
                   52
```

6643



Match length 56 % identity 98

NCBI Description Trifolium michelianum 18S ribosomal RNA gene, partial

sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;

and 26S ribosomal RNA gene, partial sequence

Seq. No. 42049

Seq. ID LIB3170-013-Q1-K1-G9

Method BLASTX
NCBI GI g4163997
BLAST score 282
E value 4.0e-25
Match length 96

% identity 60

NCBI Description (AF087483) alpha-xylosidase precursor [Arabidopsis

thaliana]

Seq. No.

Seq. ID LIB3170-014-Q1-J1-E8

42050

Method BLASTX
NCBI GI g1172597
BLAST score 159
E value 1.0e-10
Match length 47
% identity 70

NCBI Description WOUND-INDUCED BASIC PROTEIN >gi_81888_pir__JS0731

wound-inducible basic protein - kidney bean >gi_169365

(L00625) basic protein [Phaseolus vulgaris]

>gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein

[Phaseolus vulgaris]

Seq. No. 42051

Seq. ID LIB3170-014-Q1-K1-A4

Method BLASTX
NCBI GI g2500354
BLAST score 377
E value 4.0e-48
Match length 122
% identity 80

NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_

(AB001891) QM family protein [Solanum melongena]

Seq. No. 42052

Seq. ID LIB3170-014-Q1-K1-B12

Method BLASTN
NCBI GI g3687405
BLAST score 75
E value 5.0e-34
Match length 155
% identity 87

NCBI Description Lycopersicon esculentum mRNA for hypothetical protein

Seq. No. 42053

Seq. ID LIB3170-014-Q1-K1-B6

Method BLASTX NCBI GI g3687251



```
BLAST score
                  2.0e-16
E value
                  61
Match length
                  66
% identity
                  (AC005169) unknown protein [Arabidopsis thaliana]
NCBI Description
                  42054
Seq. No.
                  LIB3170-014-Q1-K1-E2
Seq. ID
                  BLASTN
Method
                  g3168839
NCBI GI
                  73
BLAST score
                  1.0e-32
E value
                  145
Match length
                  88
% identity
                  Arabidopsis thaliana copper homeostasis factor (CCH) mRNA,
NCBI Description
                  complete cds
                  42055
Seq. No.
                  LIB3170-014-Q1-K1-E4
Seq. ID
                  BLASTN
Method
                  g313026
NCBI GI
                  82
BLAST score
                  4.0e-38
E value
                  194
Match length
                  86
% identity
                  L.esculentum rpl38 mRNA for ribosomal protein L38
NCBI Description
                   42056
Seq. No.
                  LIB3170-014-Q1-K1-E9
Seq. ID
                   BLASTX
Method
                   g3913008
NCBI GI
                   374
BLAST score
                   3.0e-58
E value
                   138
Match length
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                   >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic
                   fructose-1,6-bisphosphate aldolase [Cicer arietinum]
Seq. No.
                   42057
                   LIB3170-014-Q1-K1-F6
Seq. ID
                   BLASTN
Method
                   q18747
NCBI GI
                   239
BLAST score
E value
                   1.0e-132
                   266
Match length
                   98
 % identity
                   G.max mRNA for a protein similar to potato tuber protein
NCBI Description
                   p322 homolgous to Bowman-Birk Proteinase Inhibitor
 Seq. No.
                   42058
                   LIB3170-014-Q1-K1-F8
 Seq. ID
                   BLASTX
 Method
                   g2961300
 NCBI GI
```

97

2.0e-17

BLAST score

Match length

E value



```
% identity
                  (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
                  42059
Seq. No.
                  LIB3170-014-Q1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264317
                  45
BLAST score
                  5.0e-16
E value
                  93
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUG13, complete sequence [Arabidopsis thaliana]
                   42060
Seq. No.
                  LIB3170-014-Q1-K1-H8
Seq. ID
                  BLASTN
Method
NCBI GI
                   q4102691
                   74
BLAST score
                   2.0e-33
E value
Match length
                   98
                   94
% identity
NCBI Description
                  Glycine max late-embryogenesis abundant protein mRNA,
                   complete cds
                   42061
Seq. No.
                   LIB3170-015-Q1-J1-B5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2924257
                   68
BLAST score
                   5.0e-30
E value
                   172
Match length
% identity
                  Tobacco chloroplast genome DNA
NCBI Description
Seq. No.
                   42062
                   LIB3170-015-Q1-J1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1778051
BLAST score
                   152
                   2.0e-14
E value
Match length
                   85
% identity
                   52
                   (U62583) Prt1 homolog [Homo sapiens]
NCBI Description
                   >gi 4503527_ref_NP_003742.1_pEIF3S9__UNKNOWN
Seq. No.
                   42063
                   LIB3170-015-Q1-K1-H4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g531828
                   39
BLAST score
                   5.0e-13
E value
                   79
Match length
                   87
% identity
NCBI Description Cloning vector pSport1, complete cds
```

42064

Seq. No.



```
LIB3170-016-Q1-K1-B12
Seq. ID
                  BLASTX
Method
                  g2443836
NCBI GI
                  269
BLAST score
                  8.0e-24
E value
Match length
                  85
% identity
                   68
                   (AF020793) tonoplast intrinsic protein homolog MSMCP1
NCBI Description
                   [Medicago sativa]
Seq. No.
                   42065
Seq. ID
                  LIB3170-016-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                   g3831452
BLAST score
                   275
                   2.0e-24
E value
Match length
                   80
% identity
                   60
                  (AC005700) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   42066
Seq. No.
Seq. ID
                   LIB3170-016-Q1-K1-C5
Method
                   BLASTX
                   g3204129
NCBI GI
BLAST score
                   191
                   4.0e-15
E value
                   59
Match length
                   69
% identity
                  (AJ006768) histone H2A [Cicer arietinum]
NCBI Description
                   42067
Seq. No.
                   LIB3170-016-Q1-K1-F10
Seq. ID
Method
                   BLASTN
                   g18747
NCBI GI
                   58
BLAST score
                   6.0e-24
E value
Match length
                   125
                   93
% identity
                   G.max mRNA for a protein similar to potato tuber protein
NCBI Description
                   p322 homolgous to Bowman-Birk Proteinase Inhibitor
                   42068
Seq. No.
Seq. ID
                   LIB3170-016-Q1-K1-H10
                   BLASTX
Method
NCBI GI
                   q531829
                   157
BLAST score
                   4.0e-11
E value
Match length
                   58
                   52
% identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
Seq. No.
                   42069
Seq. ID
                   LIB3170-017-Q1-J1-A2
                   BLASTN
Method
NCBI GI
                   g303900
```

367

BLAST score



```
E value
                  371
Match length
% identity
                  40
                  Soybean gene for ubiquitin, complete cds
NCBI Description
                  42070
Seq. No.
Seq. ID
                  LIB3170-017-Q1-J1-C1
Method
                  BLASTX
NCBI GI
                  q1350983
                  275
BLAST score
                2.0e-24
E value
                  107
Match length
                  60
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  42071
Seq. No.
Seq. ID
                  LIB3170-017-Q1-J1-H1
Method
                  BLASTX
NCBI GI
                  g2507106
BLAST score
                  162
E value
                  2.0e-11
Match length
                  84
                  40
% identity
                  SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ >gi 887842
NCBI Description
                  (U28375) single-stranded DNA-specific exonuclease
                  [Escherichia coli] >gi 1789259 (AE000373) ssDNA
                  exonuclease, 5' --> 3' specific [Escherichia coli]
                  42072
Seq. No.
                  LIB3170-017-Q1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3176098
                  344
BLAST score
                  2.0e-32
E value
                  113
Match length
                  59
% identity
NCBI Description (Y15036) annexin [Medicago truncatula]
                  42073
Seq. No.
Seq. ID
                  LIB3170-017-Q1-K1-B1
                  BLASTX
Method
NCBI GI
                  g548852
BLAST score
                  267
E value
                  2.0e-23
Match length
                  82
                  66
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal
                  protein S21 - rice >gi_303839_dbj_BAA02158 (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
                  42074
Seq. No.
```

Seq. ID LIB3170-017-Q1-K1-E7

Method BLASTX
NCBI GI g1350720
BLAST score 233
E value 1.0e-19
Match length 84



```
% identity
                      60S RIBOSOMAL PROTEIN L32
 NCBI Description
                      42075
    Seq. No.
    Seq. ID
                      LIB3170-017-Q1-K1-F12
    Method
                      BLASTN
                      g18764
    NCBI GI
                      111
    BLAST score
                      2.0e-55
    E value
    Match length
                      342
    % identity
                      83
    NCBI Description G.max tefS1 gene for elongation factor EF-la
                      42076
    Seq. No.
    Seq. ID
                      LIB3170-017-Q1-K1-H8
    Method
                      BLASTX
    NCBI GI
                      g122003
    BLAST score
                      309
                      3.0e-28
    E value
                      111
    Match length
                      62
    % identity
                      HISTONE H2A >gi 82089 pir JQ1182 histone H2A.1 - tomato
    NCBI Description
                      42077
    Seq. No.
                      LIB3170-018-Q1-J1-D6
    Seq. ID
                      BLASTX
    Method
    NCBI GI
                      q4510348
    BLAST score
                      101
                      9.0e-10
    E value
                      74
    Match length
                      42
    % identity
    NCBI Description
                      (AC006921) unknown protein [Arabidopsis thaliana]
                      42078
    Seq. No.
    Seq. ID
                      LIB3170-018-Q1-J1-F10
    Method
                      BLASTX
    NCBI GI
                      g2760362
    BLAST score
                      168
                      8.0e-12
    E value
    Match length
                      62
                      55
    % identity
                      (AF016511) 15.9 kDa subunit of RNA polymerase II
    NCBI Description
                      [Arabidopsis thaliana]
                      42079
    Seq. No.
    Seq. ID
                      LIB3170-018-Q1-K1-F10
    Method
                      BLASTN
    NCBI GI
                      q2760361
    BLAST score
                      60
                      4.0e-25
    E value
    Match length
                      196
    % identity
                      83
                      Arabidopsis thaliana 15.9 kDa subunit of RNA polymerase II
    NCBI Description
```

Seq. No. 42080

Seq. ID LIB3170-019-Q1-J1-A3

(RPB15.9) mRNA, complete cds



```
BLASTN
                                                  1 4 1 24
Method
                                   q508602
NCBI GI
                   32
BLAST score
                   8.0e-09
E value
                   69
Match length
% identity
                   96
                   Glycine max stearoyl-acyl carrier protein desaturase
NCBI Description
                   (SACPD) mRNA, complete cds
Seq. No.
                   42081
                   LIB3170-019-Q1-J1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4115371
                   164
BLAST score
                    4.0e-11
E value
                   110
Match length
                    43
% identity
                   (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                    42082
Seq. No.
                   LIB3170-019-Q1-J1-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                    g266945
BLAST score
                    180
                    3.0e-13
E value
                    65
Match length
                    54
% identity
                    60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                    >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                    >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
>gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                    [Pisum sativum]
                    42083
Seq. No.
                    LIB3170-019-Q1-J1-G10
Seq. ID
                    BLASTX
Method
                    q4544453
NCBI GI
                    363
BLAST score
                    1.0e-34
E value
                    106
Match length
                    70
% identity
                    (AC006592) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    42084
Seq. No.
                    LIB3170-020-Q1-J1-F1
Seq. ID
                    BLASTX
Method
                    g266945
NCBI GI
BLAST score
                    288
                    8.0e-26
E value
                    106
Match length
                    57
 % identity
                    60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                    >gi 100065 pir S19978 ribosomal protein L9 - garden pea
```

[Pisum sativum]

>gi_20727_emb_CAA46273 (X65155) GA [Pisum sativum]
>gi_1279645_emb_CAA65987 (X97322) ribosomal protein L9



```
Seq. No.
                  LIB3170-020-Q1-J1-H3
Seq. ID
                  BLASTX
Method
                  g70772
NCBI GI
                   294
BLAST score
                  1.0e-26
E value
                  88
Match length
                  73
% identity
                  histone H4 - wheat >gi 70773 pir HSPM4 histone H4 - garden
NCBI Description
                  pea
                   42086
Seq. No.
Seq. ID
                  LIB3170-020-Q1-K1-C12
                  BLASTN
Method
NCBI GI
                   g2292935
BLAST score
                   43
                   2.0e-15
E value
                   63
Match length
                   92
% identity
                  M.musculus genes encoding histone H4, histone H3 and
NCBI Description
                  histone H1.1
                   42087
Seq. No.
Seq. ID
                   LIB3170-021-Q1-J1-B8
                   BLASTX
Method
                   g4490316
NCBI GI
BLAST score
                   146
                   2.0e-09
E value
                   37
Match length
                   68
% identity
                  (AL035678) nucellin-like protein [Arabidopsis thaliana]
NCBI Description
                   42088
Seq. No.
Seq. ID
                   LIB3170-021-Q1-J1-E5
Method
                   BLASTX
NCBI GI
                   g4567215
BLAST score
                   406
E value
                   1.0e-39
Match length
                   91
                   89
% identity
                  (AC007113) putative presenilin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   42089
                   LIB3170-021-Q1-K1-B1
Seq. ID
Method
                   BLASTX
                   q3377797
NCBI GI
BLAST score
                   217
                   9.0e-18
E value
                   73
Match length
                   66
```

% identity

(AF075597) Similar to 60S ribosome protein L19; coded for NCBI Description by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by

A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 42090

```
LIB3170-021-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  q2618688
NCBI GI
                  222
BLAST score
                  2.0e-18
E value
                   79
Match length
% identity
                  (AC002510) putative esterase D [Arabidopsis thaliana]
NCBI Description
                  42091
Seq. No.
                  LIB3170-022-Q1-J1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4105697
                   607
BLAST score
                   3.0e-63
E value
                   141
Match length
                   76
% identity
                  (AF049870) thaumatin-like protein [Arabidopsis thaliana]
NCBI Description
                   42092
Seq. No.
                   LIB3170-022-Q1-J1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2346970
BLAST score
                   232
                   4.0e-19
E value
                   103
Match length
                   50
% identity
                   (AB006597) ZPT2-10 [Petunia x hybrida]
NCBI Description
                   42093
Seq. No.
                   LIB3170-022-Q1-J1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244964
BLAST score
                   171
E value
                   3.0e-12
                   39
Match length
% identity
                   77
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   42094
                   LIB3170-022-Q1-J1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3204100
BLAST score
                   86
                   2.0e-40
E value
Match length
                   118
                   93
% identity
NCBI Description Cicer arietinum mRNA for hypothetical protein, clone Can107
                   42095
Seq. No.
                   LIB3170-022-Q1-J1-F4
Seq. ID
Method
                   BLASTN
                   g547507
NCBI GI
                   79
BLAST score
                   1.0e-36
E value
                   115
Match length
```

. P.

6652

92

% identity



NCBI Description G.max mRNA for glutamine synthetase 42096 Seq. No. Seq. ID LIB3170-022-Q1-J1-G11 Method BLASTX g3202042 NCBI GI 357 BLAST score 9.0e-34 E value 121 Match length % identity 66 (AF069324) 26S proteasome regulatory subunit S5A NCBI Description [Mesembryanthemum crystallinum] 42097 Seq. No. LIB3170-022-Q1-J1-G8 Seq. ID Method BLASTX NCBI GI g2129698 280 BLAST score 7.0e-25 E value Match length 100 % identity 61 protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana NCBI Description >gi 1054633 emb CAA63387 (X92728) protein kinase [Arabidopsis thaliana] 42098 Seq. No. Seq. ID LIB3170-022-Q1-J1-H9 Method BLASTX g3287696 NCBI GI 506 BLAST score 3.0e-51 E value 122 Match length % identity 73 (AC003979) Strong similarity to phosphoribosylanthranilate NCBI Description transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana] 42099 Seq. No. Seq. ID LIB3170-022-Q1-K1-C9 BLASTX Method g729669 NCBI GI BLAST score 287 7.0e-26 E value Match length 98 59 % identity HISTONE H2A >gi 2118992 pir S60474 histone H2A - garden NCBI Description pea >gi_498896 (U10041) histone H2A homolog [Pisum sativum] 42100 Seq. No. Seq. ID LIB3170-023-Q1-J1-A11 Method BLASTN NCBI GI q493019

Method BLASTN
NCBI GI 9493019
BLAST score 203
E value 1.0e-110
Match length 292
% identity 93



NCBI Description Glycine max delta-aminolevulinic acid dehydratase (Alad) mRNA, complete cds

Seq. No. 42101

Seq. ID LIB3170-023-Q1-J1-D1

Method BLASTX
NCBI GI g1172874
BLAST score 193
E value 1.0e-14
Match length 88
% identity 42

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi_479589_pir__S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 42102

Seq. ID LIB3170-023-Q1-J1-D5

Method BLASTX
NCBI GI 94337187
BLAST score 255
E value 7.0e-22
Match length 82
% identity 60

NCBI Description (AC006403) putative prolylcarboxypeptidase, 5' partial

[Arabidopsis thaliana]

Seq. No. 42103

Seq. ID LIB3170-023-Q1-J1-F2

Method BLASTX
NCBI GI 94508073
BLAST score 355
E value 1.0e-33
Match length 104
% identity 62

NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No. 42104

Seq. ID LIB3170-023-Q1-J1-F6

Method BLASTX
NCBI GI g3482971
BLAST score 454
E value 3.0e-45
Match length 97
% identity 82

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No.

42105

Seq. ID LIB3170-023-Q1-J1-F9

Method BLASTX
NCBI GI g3023271
BLAST score 532
E value 2.0e-54
Match length 108
% identity 90

NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)

NCBI GI

E value

BLAST score

Match length

NCBI Description

% identity

g3269285

236 7.0e-20

56

80

```
(FALDH) (GSH-FDH) >gi_1675394 (U77637) class III ADH enzyme
                  [Oryza sativa]
                  42106
Seq. No.
                  LIB3170-023-Q1-J1-H12
Seq. ID
Method
                  BLASTX
                  g4454480
NCBI GI
                  191
BLAST score
                  1.0e-14
E value
Match length
                  94
% identity
                  39
                  (AC006234) putative (1-4)-beta-mannan endohydrolase
NCBI Description
                  [Arabidopsis thaliana]
                  42107
Seq. No.
                  LIB3170-023-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541943
BLAST score
                  339
                   6.0e-32
E value
                  78
Match length
                  73
% identity
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                   42108
Seq. No.
                  LIB3170-023-Q1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1778374
BLAST score
                   171
                   3.0e-12
E value
Match length
                   67
                   51
% identity
                   (U81287) glycine-rich RNA-binding protein PsGRBP [Pisum
NCBI Description
                   sativum]
                   42109
Seq. No.
                   LIB3170-024-Q1-J1-A10
Seq. ID
Method
                   BLASTN
                   g556557
NCBI GI
                   101
BLAST score
                   2.0e-49
E value
                   236
Match length
                   86
% identity
                  Rice mRNA for homologue of Tat binding protein, complete
NCBI Description
                   cds
                   42110
Seq. No.
                   LIB3170-024-Q1-J1-A11
Seq. ID
                   BLASTX
Method
```

6655

(AL030978) hypothetical protein [Arabidopsis thaliana]

Method

NCBI GI

BLASTN

g468055



```
Seq. No.
                    42111
                   LIB3170-024-Q1-J1-A5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q3157950
 BLAST score
                   233
 E value
                   1.0e-19
Match length
                   81
 % identity
                   59
                   (AC002131) Contains similarity to hypothetical protein
NCBI Description
                   C18b11.05 gb_Z50728 from S. pombe. EST gb_H76601 comes
                   from this gene. [Arabidopsis thaliana]
 Seq. No.
                   42112
Seq. ID
                   LIB3170-024-Q1-J1-A7
Method
                   BLASTX
NCBI GI
                   g1684913
BLAST score
                   225
E value
                   2.0e-18
Match length
                   83
% identity
                   53
NCBI Description
                   (U77888) receptor-like protein kinase [Ipomoea nil]
Seq. No.
                   42113
                   LIB3170-024-Q1-J1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1150932
BLAST score
                   123
E value
                   4.0e-11
Match length
                   91
% identity
                   52
NCBI Description
                   (X88864) cyclin [Medicago sativa]
Seq. No.
                   42114
Seq. ID
                   LIB3170-024-Q1-K1-D10
Method
                   BLASTN
NCBI GI
                   g531832
BLAST score
                   34
E value
                   1.0e-09
Match length
                   101
% identity
                   85
NCBI Description
                  Cloning vector pSport2, complete sequence
Seq. No.
                   42115
Seq. ID
                  LIB3170-024-Q1-K1-F10
Method
                  BLASTN
NCBI GI
                  g4204373
BLAST score
                  96
E value
                  8.0e-47
Match length
                  107
% identity
                  98
NCBI Description Zea mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA,
                  partial cds
Seq. No.
                  42116
Seq. ID
                  LIB3170-024-Q1-K1-G10
```

```
BLAST score
                   1.0e-157
E value
                   301
Match length
                   99
% identity
                  Zea mays B73 QM protein mRNA, complete cds
NCBI Description
                   42117
Seq. No.
                  LIB3170-024-Q1-K1-G12
Seq. ID
                   BLASTN
Method
                   g998429
NCBI GI
                   247
BLAST score
                   1.0e-137
E value
                   263
Match length
                   98
% identity
                   GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                   5348 nt]
                   42118
Seq. No.
                   LIB3170-024-Q1-K1-G9
Seq. ID
                   BLASTN
Method
                   g2599091
NCBI GI
BLAST score
                   48
                   3.0e-18
E value
Match length
                   128
% identity
                   84
                   Arabidopsis thaliana WD-40 repeat protein MSI4 (MSI4) mRNA,
NCBI Description
                   complete cds
                   42119
Seq. No.
                   LIB3170-024-Q1-K1-H10
Seq. ID
                   BLASTN
Method
                   g1498596
NCBI GI
                   328
BLAST score
                   0.0e + 00
E value
                   338
Match length
                   99
% identity
                   Zea mays phospholipid transfer protein mRNA, complete cds
NCBI Description
Seq. No.
                   42120
                   LIB3170-025-Q1-J1-C5
Seq. ID
                   BLASTX
Method
                   g3980384
NCBI GI
                   155
BLAST score
                   4.0e-10
E value
                   87
Match length
                   48
% identity
                   (AC004561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   42121
Seq. No.
                   LIB3170-025-Q1-J1-C9
Seq. ID
Method
                   BLASTX
                   q3024859
NCBI GI
                   203
BLAST score
                   1.0e-15
E value
                   90
Match length
```

NCBI Description HYPOTHETICAL PROTEIN AF0130 >gi_2650515 (AE001097)

43

% identity



acetylpolyamine aminohydrolase (aphA) [Archaeoglobus fulgidus]

42122 Seq. No.

LIB3170-025-Q1-J1-D6 Seq. ID

Method BLASTX g4454043 NCBI GI 259 BLAST score 2.0e-22 E value 84 Match length 68 % identity

(AL035394) putative receptor kinase [Arabidopsis thaliana] NCBI Description

Seq. No. 42123

LIB3170-025-Q1-J1-E12 Seq. ID

BLASTX Method g4185143 NCBI GI 435 BLAST score E value 6.0e-43132 Match length 65 % identity

(AC005724) putative signal recognition particle receptor NCBI Description

beta subunit [Arabidopsis thaliana]

Seq. No. 42124

LIB3170-025-Q1-J1-G1 Seq. ID

BLASTX Method g3668081 NCBI GI BLAST score 223 E value 3.0e-18 125 Match length 37 % identity

NCBI Description (AC004667) putative peptidase [Arabidopsis thaliana]

Seq. No.

42125

Seq. ID LIB3170-025-Q1-J1-H6

Method BLASTX q833835 NCBI GI BLAST score 164 E value 2.0e-11 72 Match length % identity 46

(U26025) amygdalin hydrolase isoform AH I precursor [Prunus NCBI Description

serotina]

42126 Seq. No.

LIB3170-025-Q1-K1-B4 Seq. ID

Method BLASTX NCBI GIq3341443 BLAST score 236 E value 8.0e-20 Match length 92 51 % identity

(AJ223074) acid phosphatase [Glycine max] NCBI Description

Seq. No. 42127

LIB3170-025-Q1-K1-D5 Seq. ID

```
BLASTN
Method
NCBI GI
                   q310575
                   146
BLAST score
                   2.0e-76
E value
                   274
Match length
                   91
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   42128
Seq. No.
                  LIB3170-025-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827715
BLAST score
                   180
                   3.0e-13
E value
                   67
Match length
                   52
% identity
                   (AL021684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   42129
Seq. No.
                   LIB3170-025-Q1-K1-F8
Seq. ID
                   BLASTX
Method
                   g4105798
NCBI GI
BLAST score
                   152
                   5.0e-10
E value
Match length
                   28
                   79
% identity
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   42130
Seq. No.
                   LIB3170-026-Q1-J1-C5
Seq. ID
                   BLASTN
Method
                   g3982595
NCBI GI
BLAST score
                   295
                   1.0e-165
E value
Match length
                   327
% identity
                   97
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                   42131
                   LIB3170-026-Q1-J1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1663724
                   284
BLAST score
E value
                   3.0e-25
Match length
                   93
 % identity
                   (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
NCBI Description
                   42132
 Seq. No.
                   LIB3170-026-Q1-K1-B11
 Seq. ID
Method
                   BLASTX
                   g3319774
 NCBI GI
 BLAST score
                   150
```

8.0e-10

41

66

E value

Match length

% identity



NCBI Description (Y16228) TOM7 protein [Solanum tuberosum] 42133 Seq. No. LIB3170-026-Q1-K1-D4 Seq. ID Method BLASTN NCBI GI g3510343 BLAST score 36 9.0e-11 E value 100 Match length % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MJC20, complete sequence [Arabidopsis thaliana] 42134 Seq. No. LIB3170-027-Q2-K1-A8 Seq. ID Method BLASTX g3108053 NCBI GI BLAST score 271 3.0e-24E value 84 Match length % identity (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea NCBI Description mays] 42135 Seq. No. LIB3170-027-Q2-K1-C10 Seq. ID BLASTN Method q339596 NCBI GI BLAST score 157 5.0e-83 E value 365 Match length 86 % identity Human triglyceride lipase mRNA, complete cds NCBI Description 42136 Seq. No. LIB3170-027-Q2-K1-C4 Seq. ID Method BLASTX q144832 NCBI GI BLAST score 155 3.0e-10 E value 56 Match length 48 % identity (M74569) dnaJ [Clostridium acetobutylicum] NCBI Description 42137 Seq. No. LIB3170-027-Q2-K1-F5 Seq. ID BLASTN Method

g20657 NCBI GI BLAST score 76 1.0e-34 E value

124 Match length 90 % identity

NCBI Description P.sativum Cab II gene for chlorophyll a/b-binding protein

Seq. No.

42138

Seq. ID

LIB3170-027-Q2-K1-H8

Method

BLASTX

Match length

% identity

58



```
q2129579
NCBI GI
                                              æ-
  BLAST score
                    167
                    4.0e-12
  E value
                    64
  Match length
  % identity
                    Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
  NCBI Description
                    Dwarf1 [Arabidopsis thaliana]
                    42139
  Seq. No.
                    LIB3170-028-Q1-J1-C11
  Seq. ID
  Method
                    BLASTX
                    g1346871
  NCBI GI
  BLAST score
                    143
                    8.0e-09
  E value
                    70
  Match length
                    47
  % identity
                    PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi 967968
  NCBI Description
                     (L31936) photosystem II 10kDa polypeptide [Brassica
                    campestris]
                    42140
  Seq. No.
                    LIB3170-028-Q1-J1-D12
  Seq. ID
                    BLASTX
  Method
                    g119143
  NCBI GI
  BLAST score
                     181
                     5.0e-22
  E value
                     119
  Match length
                     57
  % identity
                    ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
  NCBI Description
                     >gi_81606_pir__S06724 translation elongation factor eEF-1
                     alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                     (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                     >gi_1369927_emb_CAA34454_ (X16431) elongation factor
                     1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                     (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                     >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                     >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                     >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
   Seq. No.
                     42141
                     LIB3170-028-Q1-J1-E9
   Seq. ID
                     BLASTX
  Method
                     g1806146
  NCBI GI
                     289
  BLAST score
                     4.0e-26
  E value
                     67
  Match length
                     79
   % identity
                    (X97317) cdc2MsF [Medicago sativa]
   NCBI Description
                     42142
   Seq. No.
                     LIB3170-028-Q1-J1-H9
   Seq. ID
                     BLASTX
   Method
                     g3650030
   NCBI GI
                     235
   BLAST score
                     1.0e-19
   E value
                     71
```





```
(AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
                  42143
Seq. No.
                  LIB3170-028-Q1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982289
                  222
BLAST score
                  3.0e-18
E value
                  102
Match length
                  47
% identity
                  (AF051229) 60S ribosomal protein L17 [Picea mariana]
NCBI Description
Seq. No.
                  LIB3170-028-Q1-K1-D3
Seq. ID
                  BLASTX
Method
                   g2723477
NCBI GI
                   313
BLAST score
                   8.0e-29
E value
                   116
Match length
                   61
% identity
                  (D89824) GTP-binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   42145
                   LIB3170-028-Q1-K1-E4
Seq. ID
                   BLASTX
Method
                   q1076485
NCBI GI
                   289
BLAST score
                   4.0e-26
E value
Match length
                   68
                   82
% identity
                   SAM-synthetase - chickpea (fragment)
NCBI Description
                   >gi 732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer
                   arietinum]
                   42146
Seq. No.
                   LIB3170-029-Q1-K1-A11
Seq. ID
                   BLASTN
Method
                   g12307
NCBI GI
                   69
BLAST score
                   2.0e-30
E value
                   177
Match length
                   85
% identity
                   Spinach plastid genes rps3, rps19, rpl14, rpl16 and rpl22
NCBI Description
                   for ribosomal proteins S3, S19, L14, L16 and L22
                   42147
Seq. No.
                   LIB3170-029-Q1-K1-D6
Seq. ID
Method
                   BLASTX
                   g515377
NCBI GI
                   174
BLAST score
                   8.0e-13
E value
                   54
Match length
                   72
 % identity
                   (X79715) histone H4 [Lolium temulentum]
NCBI Description
```

LIB3170-030-Q1-J1-G11

Seq. No.

Seq. ID

```
Method BLASTN
NCBI GI g166421
BLAST score 105
E value 7.0e-52
Match length 161
% identity 92
NCBI Description Medicago sativa ubiquitin carrier protein mRNA, complete cds
```

Seq. No. 42149
Seq. ID LIB3170-030-Q1-J1-G4

Method BLASTX
NCBI GI g3264759
BLAST score 181
E value 2.0e-13
Match length 70
% identity 54

NCBI Description (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]

Seq. No. 42150

Seq. ID LIB3170-030-Q1-J1-G5

Method BLASTX
NCBI GI g1732515
BLAST score 165
E value 4.0e-12
Match length 73
% identity 58

NCBI Description (U62744) myosin heavy chain-like protein [Arabidopsis

thaliana]

Seq. No. 42151

Seq. ID LIB3170-030-Q1-K1-C7

Method BLASTX
NCBI GI g4220477
BLAST score 174
E value 1.0e-12
Match length 85
% identity 46

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 42152

Seq. ID LIB3170-030-Q1-K1-D6

Method BLASTX
NCBI GI g132825
BLAST score 153
E value 3.0e-10
Match length 83
% identity 46

NCBI Description 50S RIBOSOMAL PROTEIN CL25, CHLOROPLAST PRECURSOR

>gi_71308_pir__R5PM25 ribosomal protein PsCL25 precursor,
chloroplast - garden pea >gi_20877_emb_CAA32187_ (X14022)
PsCL25 ribosomal preprotein (AA -30 to 74) [Pisum sativum]

Seq. No. 42153

Seq. ID LIB3170-030-Q1-K1-G1

Method BLASTN NCBI GI g11576



BLAST score 0.0e + 00E value 361 Match length 98 % identity Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NCBI Description NADH dehydrogenase and ORF Seq. No. 42154 LIB3170-031-Q1-J1-C6 Seq. ID Method BLASTX NCBI GI g132521 BLAST score 206 4.0e-16 E value Match length 96 46 % identity RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN NCBI Description RGP1) >gi 100684_pir__S16554 GTP-binding protein rgp1 rice >gi 20356 emb CAA41966 (X59276) GTP-binding protein [Oryza sativa] >gi 228209 prf 1718315A GTP-binding protein [Oryza sativa] Seq. No. 42155 Seq. ID LIB3170-031-Q1-J1-G4 Method BLASTN NCBI GI q3695058 BLAST score 35 4.0e-10 E value 105 Match length % identity 91 Lotus japonicus rac GTPase activating protein 1 mRNA, NCBI Description complete cds Seq. No. 42156 LIB3170-031-Q1-K1-A11 Seq. ID Method BLASTX q464621 NCBI GI 185 BLAST score 5.0e-14 E value Match length 85 44 % identity 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 NCBI Description ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum] 42157 Seq. No. LIB3170-031-Q1-K1-A6 Seq. ID

Method BLASTX g643469 NCBI GI 308 BLAST score 3.0e-28 E value 85 Match length 71 % identity

(U19886) unknown [Lycopersicon esculentum] NCBI Description

42158 Seq. No.

LIB3170-031-Q1-K1-C7 Seq. ID

```
Method BLASTX
NCBI GI g2959767
BLAST score 153
E value 3.0e-10
Match length 99
% identity 40
NCBI Description (AJ00258
(AC00530
```

(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

 Seq. No.
 42159

 Seq. ID
 LIB3170-031-Q1-K1-C8

 Method
 BLASTN

 NCBI GI
 g18644

 BLAST score
 187

BLAST score 187 E value 1.0e-101 Match length 267 % identity 93

NCBI Description Soybean mRNA for HMG-1 like protein

 Seq. No.
 42160

 Seq. ID
 LIB3170-031-Q1-K1-D12

 Method
 BLASTN

 NCBI GI
 q2852444

NCBI GI g285244
BLAST score 49
E value 1.0e-18
Match length 129
% identity 84

NCBI Description Salix bakko mRNA for SUI1 homolog, complete cds

 Seq. No.
 42161

 Seq. ID
 LIB3170-032-Q1-K1-A8

 Method
 BLASTX

 MODI GI
 C417103

NCBI GI g417103
BLAST score 371
E value 1.0e-35
Match length 101
% identity 77
NCBI Description HISTONE

HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >qi 16324 emb CAA42957 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] $>gi_488567$ ($\overline{U}09460$) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2 [Medicago sativa] >gi 488577 (U09465) histone H3.2 [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi 1435157_emb_CAA58445_ histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] $>gi_3885890$ (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Method

BLASTX



```
42162
Seq. No.
Seq. ID
                  LIB3170-033-Q1-J1-D7
                  BLASTX
Method
NCBI GI
                  g2347208
                  142
BLAST score
                  1.0e-08
E value
                  74
Match length
                   39
% identity
                  (AC002338) APG protein isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   42163
                  LIB3170-033-Q1-J1-E5
Seq. ID
                  BLASTX
Method
                   g129613
NCBI GI
                   309
BLAST score
                   2.0e-28
E value
Match length
                   61
                   85
% identity
                   CYSTEINE PROTEINASE (CLONE PLBPC13) >gi_81562_pir__B26074
NCBI Description
                   cysteine proteinase (EC 3.4.22.-) 13 - papaya (fragment)
                   >gi 18086 emb_CAA27609_ (X03971) pot. cysteine proteinase
                   [Carica papaya]
                   42164
Seq. No.
                   LIB3170-033-Q1-K1-C8
Seq. ID
Method
                   BLASTX
                   g2708532
NCBI GI
BLAST score
                   241
                   3.0e-20
E value
Match length
                   82
                   29
% identity
                   (AF029351) putative RNA binding protein [Nicotiana tabacum]
NCBI Description
Seq. No.
                   42165
                   LIB3170-033-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   q4056503
NCBI GI
BLAST score
                   169
                   3.0e-12
E value
                   36
Match length
                   86
% identity
                   (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
                   42166
Seq. No.
                   LIB3170-033-Q1-K1-F2
Seq. ID
                   BLASTX
Method
                   g1053045
NCBI GI
                   224
BLAST score
                   1.0e-18
E value
                   62
Match length
                   79
% identity
                  (U38424) histone H3 [Glycine max]
NCBI Description
                   42167
Seq. No.
Seq. ID
                   LIB3170-034-Q1-J1-F1
```

```
q1806146
NCBI GI
                  313
BLAST score
                  9.0e-29
E value
                  70
Match length
                  80
% identity
NCBI Description (X97317) cdc2MsF [Medicago sativa]
                  42168
Seq. No.
                  LIB3170-034-Q1-J1-F4
Seq. ID
                  BLASTX
Method
                  g2462744
NCBI GI
                  289
BLAST score
                  7.0e-26
E value
                  93
Match length
                  58
% identity
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
                  42169
Seq. No.
                  LIB3170-034-Q1-J1-G8
Seq. ID
                  BLASTN
Method
                  g3341442
NCBI GI
                   43
BLAST score
                   6.0e-15
E value
                   135
Match length
                   83
% identity
NCBI Description Glycine max mRNA for root nodule acid phosphatase
                   42170
Seq. No.
                   LIB3170-034-Q1-J1-H1
Seq. ID
                   BLASTX
Method
                   g3641870
NCBI GI
                   153
BLAST score
                   5.0e-10
E value
                   62
Match length
                   50
% identity
NCBI Description (AJ011013) hypothetical protein [Cicer arietinum]
                   42171
Seq. No.
                   LIB3170-034-Q1-K1-F7
 Seq. ID
                   BLASTX
Method
                   q3056595
NCBI GI
                   162
BLAST score
                   6.0e-11
 E value
                   46
Match length
                   72
 % identity
NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]
                   42172
 Seq. No.
                   LIB3170-034-Q1-K1-G2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2827630
                   300
 BLAST score
                   4.0e-27
 E value
                   79
 Match length
                   68
 % identity
 NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
```

```
Seq. No. 42173
Seq. ID LIB3170-035-Q1-J1-A9
Method BLASTN
```

Method BLASTN
NCBI GI g2407799
BLAST score 34

E value 1.0e-09 Match length 62 % identity 89

NCBI Description Arabidopsis thaliana mRNA for histone H2A.F/Z

Seq. No. 42174

Seq. ID LIB3170-035-Q1-J1-B12

Method BLASTN
NCBI GI g3452086
BLAST score 296
E value 1.0e-166
Match length 335
% identity 98

NCBI Description Glycine max mRNA for 14-3-3 protein, partial

Seq. No. 42175

Seq. ID LIB3170-035-Q1-J1-B8

Method BLASTX
NCBI GI g2252634
BLAST score 148
E value 1.0e-09
Match length 58
% identity 45

NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No. 42176

Seq. ID LIB3170-035-Q1-K1-A11

Method BLASTN
NCBI GI g2407789
BLAST score 33
E value 3.0e-09
Match length 49
% identity 92

NCBI Description Glycine max grr1 (grr1) mRNA, complete cds

Seq. No. 42177

Seq. ID LIB3170-035-Q1-K1-D9

Method BLASTX
NCBI GI g3281869
BLAST score 158
E value 9.0e-11
Match length 70
% identity 51

NCBI Description (AL031004) RSZp22 splicing factor [Arabidopsis thaliana]

>qi 3435094 (AF033586) 9G8-like SR protein [Arabidopsis

thaliana]

Seq. No. 42178

Seq. ID LIB3170-035-Q1-K1-E1

Method BLASTX NCBI GI g113361 BLAST score 227



4.0e-19 E value Match length 71 % identity ALCOHOL DEHYDROGENASE 1 >gi_81891_pir__S00912 alcohol NCBI Description dehydrogenase (EC 1.1.1.1) 1 (clone lambda-PG8) - garden pea >gi 20639 emb CAA29609 (X06281) alcohol dehydrogenase [Pisum sativum] 42179 Seq. No. LIB3170-035-Q1-K1-F4 Seq. ID Method BLASTX NCBI GI q4415908 BLAST score 195 E value 7.0e-15 109 Match length 55 % identity (AC006282) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 42180 LIB3170-035-Q1-K1-G10 Seq. ID BLASTX Method g1172558 NCBI GI BLAST score 172 E value 9.0e-13 46 Match length 74 % identity OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT NCBI Description ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_480122_pir__S36454 porin porl - garden pea
>gi_396819_emb_CAA80988_ (Z25540) Porin [Pisum sativum] Seq. No. 42181 LIB3170-035-Q1-K1-G4 Seq. ID Method BLASTX q3341443 NCBI GI BLAST score 402 E value 4.0e-39 130 Match length 60 % identity (AJ223074) acid phosphatase [Glycine max] NCBI Description 42182 Seq. No. LIB3170-035-Q1-K1-G5 Seq. ID Method BLASTX g548740 NCBI GI 174 BLAST score 1.0e-12 E value Match length 81 % identity 38 50S RIBOSOMAL PROTEIN L11 >gi 144456 (M94319) ribosomal NCBI Description

protein L11 [Citrus greening disease-associated

bacterium-like organism] >gi_739023_prf__2002224B ribosomal protein L11 [Citrus greening disease-associated bacterium]

Seq. No. 42183

Seq. ID LIB3170-036-Q1-K1-B3

BLASTX Method



```
g3182915
NCBI GI .
                  141
BLAST score
                  7.0e-09
E value
Match length
                  64
                  53
% identity
                  ADP-RIBOSYLATION FACTOR >gi 1842150 dbj BAA19225
NCBI Description
                   (AB001051) ADP-ribosylation factor [Dugesia japonica]
                  42184
Seq. No.
                  LIB3170-036-Q1-K1-B9
Seq. ID
                  BLASTN
Method
                  g456567
NCBI GI
                   95
BLAST score
                   5.0e-46
E value
Match length
                   209
% identity
                   89
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                   42185
Seq. No.
                   LIB3170-036-Q1-K1-E10
Seq. ID
                   BLASTX
Method
                   q3341443
NCBI GI
BLAST score
                   142
                   5.0e-09
E value
Match length
                   61
% identity
                   54
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                   42186
Seq. No.
                   LIB3170-036-Q1-K1-E5
Seq. ID
                   BLASTN
Method
                   g1336081
NCBI GI
                   119
BLAST score
                   2.0e-60
E value
                   211
Match length
                   89
% identity
                  Glycine max var. Century ascorbate peroxidase 2 (APx2)
NCBI Description
                   mRNA, complete cds
                   42187
Seq. No.
                   LIB3170-036-Q1-K2-B9
Seq. ID
                   BLASTN
Method
                   q456567
NCBI GI
                   102
BLAST score
                   3.0e-50
E value
                   209
Match length
                   89
 % identity
                   Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                   42188
 Seq. No.
                   LIB3170-036-Q1-K2-E10
 Seq. ID
                   BLASTN
 Method
                   g3341442
 NCBI GI
 BLAST score
                    47
```

3.0e-17

E value



Match length 59 % identity 95

NCBI Description Glycine max mRNA for root nodule acid phosphatase

Seq. No.

Seq. ID LIB3170-036-Q1-K2-E6

42189

Method BLASTN
NCBI GI g1336081
BLAST score 161
E value 2.0e-85
Match length 313
% identity 88

NCBI Description Glycine max var. Century ascorbate peroxidase 2 (APx2)

mRNA, complete cds

Seq. No. 42190

Seq. ID LIB3170-036-Q1-K2-G8

Method BLASTN
NCBI GI g2502086
BLAST score 138
E value 9.0e-72
Match length 190
% identity 93

NCBI Description Vigna radiata adenosine triphosphatase mRNA, complete cds

Seq. No. 42191

Seq. ID LIB3170-037-Q1-J1-C6

Method BLASTN
NCBI GI g169930
BLAST score 92
E value 3.0e-44
Match length 221
% identity 85

NCBI Description Glycine max calcium dependent protein kinase mRNA

Seq. No. 42192

Seq. ID LIB3170-037-Q1-J1-D4

Method BLASTN
NCBI GI g1143318
BLAST score 298
E value 1.0e-167
Match length 390
% identity 98

NCBI Description Glycine max biotin carboxyl carrier protein precursor

(accB-1) mRNA, complete cds

Seq. No. 42193

Seq. ID LIB3170-037-Q1-J1-G5

Method BLASTX
NCBI GI g3242787
BLAST score 234
E value 1.0e-19
Match length 66
% identity 68

NCBI Description (AF055356) respiratory burst oxidase protein E [Arabidopsis

thaliana]



```
42194
Seq. No.
                  LIB3170-037-Q1-K1-B3
Seq. ID
                  BLASTN
Method
                  q1928978
NCBI GI
                  200
BLAST score
                  1.0e-108
E value
                  314
Match length
                  91
% identity
NCBI Description Vigna unguiculata phospholipase D mRNA, complete cds
                  42195
Seq. No.
                  LIB3170-037-Q1-K1-C7
Seq. ID
                  BLASTX
Method
                  g1169128
NCBI GI
BLAST score
                  526
                  1.0e-53
E value
                  159
Match length
                  65
% identity
NCBI Description SERINE/THREONINE-PROTEIN KINASE CTR1 >gi_166680 (L08789)
                  protein kinase [Arabidopsis thaliana] >gi_166682 (L08790)
                  protein kinase [Arabidopsis thaliana]
                   42196
Seq. No.
                  LIB3170-037-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g3242787
NCBI GI
BLAST score
                   544
                   1.0e-55
E value
                   195
Match length
                   56
% identity
                   (AF055356) respiratory burst oxidase protein E [Arabidopsis
NCBI Description
                   thaliana]
                   42197
Seq. No.
                   LIB3170-038-Q1-J1-F11
Seq. ID
                   BLASTX
Method
                   q3334665
NCBI GI
                   158
BLAST score
                   9.0e-11
E value
                   66
Match length
% identity
                   52
                  (Y10492) putative cytochrome P450 [Glycine max]
NCBI Description
                   42198
Seq. No.
                   LIB3170-038-Q1-J1-F12
Seq. ID
                   BLASTX
Method
                   q3702323
NCBI GI
                   166
BLAST score
E value
                   9.0e-12
                   42
Match length
% identity
                   71
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 42199

Seq. ID LIB3170-038-Q1-K1-A5

Method BLASTN NCBI GI g3821780

NCBI Description



```
BLAST score
                  1.0e-09
E value
                  34
Match length
                  42
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  42200
Seq. No.
                  LIB3170-038-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  g2052029
NCBI GI
                  160
BLAST score
                   3.0e-11
E value
                   54
Match length
                   59
% identity
NCBI Description (Y10820) glutathione transferase [Glycine max]
                   42201
Seq. No.
                   LIB3170-038-Q1-K1-H3
Seq. ID
                   BLASTX
Method
                   g2462760
NCBI GI
                   139
BLAST score
                   7.0e-09
E value
                   75
Match length
                   41
% identity
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   42202
Seq. No.
                   LIB3170-039-Q1-J1-C1
Seq. ID
                   BLASTX
Method
                   g3769673
NCBI GI
                   326
BLAST score
                   3.0e-30
E value
                   81
Match length
                   72
% identity
                   (AF095285) Tic20 [Pisum sativum]
NCBI Description
                   42203
 Seq. No.
                   LIB3170-039-Q1-J1-C11
 Seq. ID
                   BLASTN
Method
                   a2687434
NCBI GI
                   87
 BLAST score
                   2.0e-41
 E value
                   269
 Match length
                   82
 % identity
                   Eucryphia lucida large subunit 26S ribosomal RNA gene,
 NCBI Description
                   partial sequence
                   42204
 Seq. No.
                   LIB3170-039-Q1-J1-D2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g1888485
                    222
 BLAST score
                    2.0e-35
 E value
                    115
 Match length
                    66
 % identity
```

(Y11749) dihydroflavonol 4-reductase [Vitis vinifera]



```
42205
Seq. No.
                   LIB3170-039-Q1-J1-F10
 Seq. ID
                   BLASTN
 Method
                   g210811
 NCBI GI
                   50
 BLAST score
                   4.0e-19
 E value
                   267
 Match length
                   82
 % identity
 NCBI Description Bean pod mottle virus coat protein gene, complete cds,
                   complete middle component (M) RNA
                    42206
 Seq. No.
                   LIB3170-039-Q1-J1-G2
 Seq. ID
                   BLASTX
 Method
                   g2832700
 NCBI GI
                    212
 BLAST score
                    9.0e-17
 E value
                    81
 Match length
                    56
 % identity
                   (AL021713) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    42207
 Seq. No.
                    LIB3170-039-Q1-J2-B4
 Seq. ID
                    BLASTX
 Method
                    g2653879
 NCBI GI
                    155
 BLAST score
                    3.0e-20
 E value
                    113
 Match length
                    53
 % identity
 NCBI Description (AF026389) adenyl cyclase [Nicotiana tabacum]
                    42208
 Seq. No.
                    LIB3170-039-Q1-J2-C11
 Seq. ID
                    BLASTN
 Method
 NCBI GI
                    g2687434
                    136
 BLAST score
                    1.0e-70
 E value
                    299
 Match length
                    87
  % identity
                    Eucryphia lucida large subunit 26S ribosomal RNA gene,
  NCBI Description
                    partial sequence
                    42209
  Seq. No.
                    LIB3170-039-Q1-J2-D11
  Seq. ID
  Method
                    BLASTX
                    q1403522
  NCBI GI
                    182
  BLAST score
                    2.0e-13
  E value
  Match length
                    57
                    60
  % identity
  NCBI Description (X57187) chitinase [Phaseolus vulgaris]
                     42210
  Seq. No.
                    LIB3170-039-Q1-J2-D2
  Seq. ID
  Method
                    BLASTX
```

q1706369

166

NCBI GI

BLAST score



E value 1.0e-11 Match length 42 % identity 67 DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL NCBI Description 4-REDUCTASE) >gi 1066451 emb CAA91922 (Z67981) dihydroflavonol 4-reductase [Callistephus chinensis] 42211 Seq. No. LIB3170-039-Q1-J2-F10 Seq. ID Method BLASTN NCBI GI q210811 BLAST score 58 E value 7.0e-24 Match length 183 82 % identity Bean pod mottle virus coat protein gene, complete cds, NCBI Description complete middle component (M) RNA Seq. No. 42212 Seq. ID LIB3170-039-Q1-J2-F9 Method BLASTX NCBI GI q485110 BLAST score 248 5.0e-21 E value 81 Match length 59 % identity (U00050) similarity across entire gene to DNA-directed RNA NCBI Description polymerase [Caenorhabditis elegans] Seq. No. 42213 Seq. ID LIB3170-039-Q1-K1-B6 Method BLASTN q170009 NCBI GI BLAST score 44 8.0e-16 E value Match length 44 100 % identity NCBI Description Soybean late embryogenesis abundant (LEA) protein mRNA, complete cds Seq. No. 42214 Seq. ID LIB3170-039-Q1-K2-A3 Method BLASTX NCBI GI g3790441 BLAST score 244 8.0e-21 E value 78 Match length % identity 64 NCBI Description (AF030515) chaperonin 60 alpha subunit [Canavalia lineata] Seq. No. 42215 Seq. ID LIB3170-040-Q1-J1-A1

Method BLASTN

NCBI GI g1044867 BLAST score 93 E value 3.0e-45 Match length 101

Seq. ID Method



```
% identity
NCBI Description Glycine max mRNA for cinnamic acid 4-hydroxylase (CYP73)
                  42216
Seq. No.
Seq. ID
                  LIB3170-040-Q1-J1-B11
Method
                  BLASTX
NCBI GI
                  q3367574
BLAST score
                  302
E value
                  2.0e-27
Match length
                  119
% identity
                  52
                  (AL031135) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  42217
Seq. ID
                  LIB3170-040-Q1-J1-D10
Method
                  BLASTX
                  q2244974
NCBI GI
BLAST score
                  165
                  2.0e-11
E value
Match length
                  101
                  43
% identity
                  (Z97340) similarity to pore protein Pisum sativum
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  42218
Seq. ID
                  LIB3170-040-Q1-J1-G4
Method
                  BLASTX
                  q3395441
NCBI GI
BLAST score
                  184
E value
                  2.0e-13
Match length
                  60
                   63
% identity
NCBI Description
                  (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   42219
                  LIB3170-040-Q1-K1-A11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g18653
BLAST score
                  73
                   9.0e-33
E value
Match length
                  77
                  99
% identity
NCBI Description Soybean gene for heat shock protein Gmhspl8.5-C (class I)
Seq. No.
                   42220
Seq. ID
                   LIB3170-040-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3169719
BLAST score
                   415
                   1.0e-40
E value
Match length
                  98
                  83
% identity
NCBI Description
                  (AF007109) similar to yeast dcpl [Arabidopsis thaliana]
                   42221
Seq. No.
```

LIB3170-040-Q1-K1-E12

BLASTX

NCBI GI

E value

BLAST score

q567893

5.0e-09



```
g4455274
NCBI GI
BLAST score
                  469
E value
                  4.0e-47
Match length
                  122
                  74
% identity
                  (AL035527) spliceosome associated protein-like [Arabidopsis
NCBI Description
                  thaliana]
                  42222
Seq. No.
                  LIB3170-040-Q1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g407800
BLAST score
                  43
E value
                  5.0e-15
                  79
Match length
                  89
% identity
                  G.hirsutum mRNA for ribosomal protein 41, large subunit
NCBI Description
                   (RL41)
Seq. No.
                  42223
Seq. ID
                  LIB3170-040-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  q3158476
BLAST score
                  418
                  6.0e-41
E value
Match length
                  105
% identity
                  82
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
                  42224
Seq. No.
Seq. ID
                  LIB3170-040-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4204303
BLAST score
                  454
E value
                  3.0e-45
Match length
                  90
% identity
                  (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  42225
Seq. ID
                  LIB3170-040-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3894158
BLAST score
                  155
E value
                  1.0e-10
                  84
Match length
                  35
% identity
NCBI Description
                  (AC005312) similar to phloem-specific lectin [Arabidopsis
                  thaliana]
                  42226
Seq. No.
Seq. ID
                  LIB3170-040-Q1-K1-H5
Method
                  BLASTX
```

```
93
```

```
Match length 92
% identity 38
NCBI Description (L37382) beta-galactosidase-complementation protein [Cloning vector]
```

 Seq. No.
 42227

 Seq. ID
 LIB3170-041-Q1-J1-B5

 Method
 BLASTX

 NCBI GI
 g3608133

 BLAST score
 265

 E value
 4.0e-23

E value 4.0e
Match length 80
% identity 57

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 42228

Seq. ID LIB3170-041-Q1-J1-E11

Method BLASTX
NCBI GI g1877279
BLAST score 311
E value 2.0e-28
Match length 132
% identity 49

NCBI Description (Z92770) fadE2 [Mycobacterium tuberculosis]

Seq. No. 42229

Seq. ID LIB3170-041-Q1-J1-F6

Method BLASTX
NCBI GI g4115923
BLAST score 160
E value 3.0e-11
Match length 52
% identity 60

NCBI Description (AF118222) contains similarity to ubiquitin

carboxyl-terminal hydrolase family 2 (Pfam: PF00443,

score=40.0, E=5.2e-08, N=1) and (Pfam: PF00442, Score=37.9

E=5.3e-10, N=1) [Arabidopsis thaliana]

Seq. No. 42230

Seq. ID LIB3170-041-Q1-J1-F8

Method BLASTN
NCBI GI g218264
BLAST score 170
E value 1.0e-90
Match length 347
% identity 87

NCBI Description Glycine max mRNA for glycinin A2Bla subunit, complete cds

Seq. No.

42231

Seq. ID LIB3170-041-Q1-K1-B2

Method BLASTN
NCBI GI g1430886
BLAST score 56
E value 9.0e-23
Match length 68
% identity 96

NCBI Description M.sativa mRNA for 70 kD heat shock protein



```
42232
Seq. No.
                  LIB3170-041-Q1-K1-C11
Seq. ID
                  BLASTX
Method
                  g2459573
NCBI GI
                  161
BLAST score
                  8.0e-11
E value
                  100
Match length
                  15
% identity
NCBI Description (U75345) envelope protein [Chlamydomonas reinhardtii]
                  42233
Seq. No.
                  LIB3170-041-Q1-K1-D9
Seq. ID
                  BLASTN
Method
                  g21012
NCBI GI
BLAST score
                   213
                   1.0e-116
E value
                   325
Match length
                   92
% identity
NCBI Description Phaseolus vulgaris mRNA (pR-2) for glutamine synthetase
                   (GS, EC 6.3.1.2)
                   42234
Seq. No.
                   LIB3170-041-Q1-K1-E2
Seq. ID
                   BLASTX
Method
                   g3386621
NCBI GI
                   160
BLAST score
                   5.0e-11
E value
Match length
                   64
                   48
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                   42235
Seq. No.
                   LIB3170-041-Q1-K1-F3
Seq. ID
                   BLASTX
Method
                   g2827141
NCBI GI
                   303
BLAST score
                   9.0e-28
E value
                   100
Match length
                   53
 % identity
                   (AF027173) cellulose synthase catalytic subunit
 NCBI Description
                   [Arabidopsis thaliana]
                   42236
 Seq. No.
                   LIB3170-042-Q1-J1-A3
 Seq. ID
                   BLASTN
 Method
                   g296442
 NCBI GI
                   41
 BLAST score
                   8.0e-14
 E value
                   170
 Match length
                   88
 % identity
 NCBI Description G.max ADR11 mRNA
                    42237
 Seq. No.
                   LIB3170-042-Q1-J1-B10
 Seq. ID
 Method
                   BLASTX
```

g3687249

NCBI GI

BLAST score

Match length

E value

70

155

4.0e-31



```
BLAST score
                  2.0e-17
E value
                   48
Match length
% identity
                  88
                   (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana]
                   42238
Seq. No.
                  LIB3170-042-Q1-J1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730538
BLAST score
                   301
E value
                   1.0e-27
                   98
Match length
                   60
% identity
                   60S RIBOSOMAL PROTEIN L18A >gi 401845 (L05093) ribosomal
NCBI Description
                   protein L18a [Homo sapiens] >gi 3702270 (AC005796)
                   ribosomal protein L18a [Homo sapiens]
Seq. No.
                   42239
                   LIB3170-042-Q1-J1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3851636
BLAST score
                   522
E value
                   4.0e-53
                   153
Match length
% identity
                   (AF098519) unknown [Avicennia marina] >gi 4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   42240
Seq. No.
Seq. ID
                   LIB3170-042-Q1-J1-E5
Method
                   BLASTX
                   g3935142
NCBI GI
BLAST score
                   144
                   6.0e-09
E value
                   61
Match length
                   49
% identity
NCBI Description (AC005106) T25N20.6 [Arabidopsis thaliana]
                   42241
Seq. No.
Seq. ID
                   LIB3170-042-Q1-J1-F5
                   BLASTN
Method
NCBI GI
                   g164047
BLAST score
                   342
                   0.0e + 00
E value
                   434
Match length
                   95
% identity
NCBI Description Canine lipase mRNA, complete cds
                   42242
Seq. No.
Seq. ID
                   LIB3170-042-Q1-J1-F6
Method
                   BLASTN
                   g1885372
NCBI GI
```



% identity NCBI Description

Glycine max small subunit ribosomal RNA gene, partial sequence, internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence,

and large subunit ribosomal RNA gene, partial seq

42243 Seq. No.

Seq. ID LIB3170-042-Q1-J1-F7

Method BLASTX NCBI GI q4097880 BLAST score 671 1.0e-70 E value 183 Match length % identity 66

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No. 42244

Seq. ID LIB3170-042-Q1-K1-A4

Method BLASTN NCBI GI g2511688 BLAST score 76 E value 1.0e-34 Match length 145 % identity 89

NCBI Description Phaseolus vulgaris Moldavian encoding cysteine proteinase

precursor (clone cp6a)

Seq. No. 42245

Seq. ID LIB3170-042-Q1-K1-B4

Method BLASTX NCBI GI g3063448 BLAST score 208 2.0e-16 E value Match length 109 36 % identity

NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]

Seq. No. 42246

Seq. ID LIB3170-042-Q1-K1-F10

Method BLASTX NCBI GI g3738312 BLAST score 184 8.0e-14 E value Match length 49 % identity

NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]

42247 Seq. No.

LIB3170-042-Q1-K1-G8 Seq. ID

Method BLASTX NCBI GI q2501432 BLAST score 180 E value 1.0e-13 Match length 72 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >qi 2146981 pir JC4894 ubiquitin-conjugating enzyme (EC 6.3.2.-) E2 - human >gi_1181558_dbj_BAA11675_ (D83004) ubiquitin-conjugating enzyme E2 UbcH-ben [Homo sapiens] >gi_4507793_ref_NP_003339.1_pUBE2N_ ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)

Seq. ID LIB3170-042-Q1-K1-H1 Method BLASTX NCBI GI g4567245 BLAST score 238 E value 6.0e-20 Match length 97 % identity 49

42248

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. Seq. ID

Seq. No.

42249 LIB3170-043-Q1-J1-A12

Method BLASTX
NCBI GI g133405
BLAST score 199
E value 5.0e-16
Match length 61
% identity 61

NCBI Description DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN

>gi 81956 pir S04384 DNA-directed RNA polymerase (EC

2.7.7.6) alpha chain - garden pea chloroplast

>gi_12180_emb_CAA33668 (X15645) RNA polymerase alpha

subunit (AA 1-334) [Pisum sativum]

Seq. No.

42250

Seq. ID LIB3170-043-Q1-J1-A8 Method BLASTN

NCBI GI g1794171 BLAST score 67 E value 7.0e-30 Match length 95 % identity 93

NCBI Description Glycine max lipoxygenase-3 mRNA, complete cds

Seq. No.

42251

Seq. ID LIB3170-043-Q1-J1-B1

Method BLASTN
NCBI GI g999395
BLAST score 63
E value 6.0e-27
Match length 122
% identity 88

NCBI Description HSP81-3=heat-shock Protein [Arabidopsis thaliana=thale-cress, Genomic, 3094 nt]

Seq. No.

42252

Seq. ID LIB3170-043-Q1-J1-B7

Method BLASTN
NCBI GI g1431744
BLAST score 34
E value 1.0e-09



```
Match length
% identity
                  93
NCBI Description
                  Glycine max sucrose binding protein (sbp) mRNA, complete
                  cds
Seq. No.
                  42253
```

Seq. ID LIB3170-043-Q1-J1-B9 Method BLASTN NCBI GI g170009 BLAST score 66 1.0e-28 E value Match length 221

% identity 72

NCBI Description Soybean late embryogenesis abundant (LEA) protein mRNA, complete cds

Seq. No. 42254

Seq. ID LIB3170-043-Q1-J1-C9

Method BLASTN NCBI GI g18614 BLAST score 171 E value 3.0e-91 Match length 327 % identity 88

NCBI Description Soybean mRNA for glycinin AlaBx precursor

>gi_2170694_dbj_E02463_E02463 cDNA encoding glycinine

subunit AlaBlb precursor

Seq. No. 42255

Seq. ID LIB3170-043-Q1-J1-H8

Method BLASTX NCBI GI g4097880 BLAST score 351 E value 2.0e-33 Match length 113 % identity 64

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 42256

Seq. ID LIB3170-043-Q1-K1-C5

Method BLASTX NCBI GI g1514643 BLAST score 440 E value 1.0e-43 Match length 139 % identity 27

(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza] NCBI Description

Seq. No.

42257

Seq. ID LIB3170-043-Q1-K1-E10

Method BLASTX NCBI GI q3668092 BLAST score 186 E value 9.0e-14 Match length 109 % identity 49

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

% identity

Seq. No.



```
Seq. No.
                  42258
Seq. ID
                  LIB3170-043-Q1-K1-H6
Method
                  BLASTX
                  g138364
NCBI GI
BLAST score
                  185
E value
                  5.0e-14
Match length
                  50
% identity
                  74
NCBI Description
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  42259
Seq. ID
                  LIB3170-044-Q1-J1-A3
Method
                  BLASTN
                  g4469002
NCBI GI
BLAST score
                  48
E value
                  7.0e-18
Match length
                  164
% identity
                  82
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
                  (ESSA project)
                  42260
Seq. No.
Seq. ID
                  LIB3170-044-Q1-J1-C1
Method
                  BLASTN
                  g170009
NCBI GI
BLAST score
                  42
E value
                  7.0e-15
Match length
                  61
% identity
                  93
NCBI Description
                  Soybean late embryogenesis abundant (LEA) protein mRNA,
                  complete cds
Seq. No.
                  42261
Seq. ID
                  LIB3170-044-Q1-J1-C10
Method
                  BLASTX
NCBI GI
                  q3850630
BLAST score
                  246
E value
                  6.0e-21
Match length
                  72
% identity
                  56
NCBI Description (AJ012581) cytochrome P450 [Cicer arietinum]
Seq. No.
                  42262
Seq. ID
                  LIB3170-044-Q1-J1-H6
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  373
E value
                  9.0e-36
Match length
                  121
```

6684

NCBI Description (AJ223074) acid phosphatase [Glycine max]

42263

NCBI GI

BLAST score



```
LIB3170-044-Q1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g56539
BLAST score
                   52
E value
                   3.0e-20
Match length
                   155
                   92
% identity
NCBI Description
                  R.norvegicus gene encoding prolactin, exon 5
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
Seq. No.
                   42264
Seq. ID
                  LIB3170-044-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                   q531829
BLAST score
                   158
E value
                   1.0e-10
Match length
                   81
% identity
                   47
NCBI Description
                  (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
Seq. No.
                   42265
Seq. ID
                   LIB3170-044-Q1-K1-G10
Method
                  BLASTN
NCBI GI
                   q18655
BLAST score
                   103
E value
                   5.0e-51
Match length
                   111
                   99
% identity
NCBI Description Soybean heat-shock gene hs6871 sequence
Seq. No.
                   42266
                  LIB3170-045-Q1-J1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                   q732912
BLAST score
                   82
                   2.0e-38
E value
                   202
Match length
                   85
% identity
NCBI Description P.vulgaris mRNA for pectinesterase
Seq. No.
                   42267
Seq. ID
                  LIB3170-045-Q1-J1-F6
Method
                  BLASTX
NCBI GI
                  g4468812
BLAST score
                   370
E value
                  1.0e-35
                  124
Match length
                   55
% identity
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                  42268
Seq. ID
                  LIB3170-045-Q1-J1-F8
Method
                  BLASTX
```

6685

g2244898

154



E value 4.0e-10 Match length 63 % identity 51 (Z97338) strong similarity to protein phosphatase 2A NCBI Description regulatory chain, 74K [Arabidopsis thaliana] Seq. No. Seq. ID LIB3170-045-Q1-K1-A8 Method BLASTX NCBI GI q113965 250

BLAST score 250 E value 2.0e-21 Match length 140 % identity 18

NCBI Description ANNEXIN VII (SYNEXIN) >gi_71775_pir__LUD07 annexin VII -

slime mold (Dictyostelium discoideum)

>gi_829171_emb_CAA42815_ (X60269) annexin 7 [Dictyostelium

discoideum]

Seq. No. 42270

Seq. ID LIB3170-045-Q1-K1-B9

Method BLASTX
NCBI GI g1946360
BLAST score 183
E value 2.0e-13
Match length 79
% identity 57

NCBI Description (U93215) elicitor response element binding protein WRKY3

isolog [Arabidopsis thaliana]

Seq. No. 42271

Seq. ID LIB3170-045-Q1-K1-D6

Method BLASTX
NCBI GI g629692
BLAST score 198
E value 2.0e-15
Match length 42
% identity 88

NCBI Description hypothetical protein - common tobacco

>gi_506471_emb_CAA56189_ (X79794) unnamed protein product

[Nicotiana tabacum]

Seq. No. 42272

Seq. ID LIB3170-045-Q1-K1-F6

Method BLASTX
NCBI GI 94468812
BLAST score 219
E value 6.0e-18
Match length 53
% identity 68

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 42273

Seq. ID LIB3170-046-Q1-J1-A10

Method BLASTX NCBI GI g3341672 BLAST score 168



```
8.0e-12
E value
                  100
Match length
                   40
% identity
                   (AC003672) putative heme A: farnesyltransferase, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
                   42274
Seq. No.
Seq. ID
                  LIB3170-046-Q1-J1-G7
                  BLASTX
Method
NCBI GI
                   g1914683
                  160
BLAST score
E value
                  8.0e-11
                  53
Match length
                   60
% identity
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]
Seq. No.
                   42275
Seq. ID
                  LIB3170-046-Q1-K1-C12
Method
                   BLASTN
                   q169980
NCBI GI
BLAST score
                   411
E value
                   0.0e + 00
Match length
                   426
                   99
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   42276
Seq. No.
                   LIB3170-046-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   g2444176
NCBI GI
                   151
BLAST score
E value
                   7.0e-10
                   97
Match length
                   37
% identity
NCBI Description (U94782) unconventional myosin [Helianthus annuus]
                  42277
Seq. No.
                   LIB3170-046-Q1-K1-F8
Seq. ID
                   BLASTN
Method
                   g169980
NCBI GI
BLAST score
                   52
E value
                   8.0e-21
                   77
Match length
                   95
% identity
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   42278
Seq. No.
Seq. ID
                   LIB3170-046-Q1-K1-H8
                   BLASTN
Method
                   g2062705
NCBI GI
BLAST score
                   36
                   3.0e-11
E value
Match length
                   37
                   38
% identity
                  Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
```

6687

42279

Seq. No.



```
LIB3170-047-Q1-J1-A9
Seq. ID
Method
                   BLASTX
                   q1362047
NCBI GI
                   200
BLAST score
                   1.0e-15
E value
                   58
Match length
% identity
                   cysteine proteinase (EC 3.4.22.-) precursor - soybean
NCBI Description
                   >gi 479060 emb_CAA83673 (Z32795) cysteine proteinase
                   [Glycine max] >gi_1096153_prf__2111244A Cys protease
                   [Glycine max]
                   42280
Seq. No.
                   LIB3170-047-Q1-J1-D8
Seq. ID
                   BLASTX
Method
                   q1502430
NCBI GI
BLAST score
                   330
                   1.0e-30
E value
                   97
Match length
                   69
% identity
                   (U62331) phosphate transporter [Arabidopsis thaliana]
NCBI Description
                   >gi_2564661 (AF022872) phosphate transporter [Arabidopsis
                   thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate
Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                   phosphate transporter, AtPT2 [Arabidopsis thaliana]
                   42281
Seq. No.
                   LIB3170-047-Q1-J1-F5
Seq. ID
                   BLASTN
Method
                    q2905771
NCBI GI
                    144
BLAST score
E value
                    4.0e-75
                    156
Match length
% identity
                    98
                   Glycine max glyceraldehyde-3 phosphate dehydrogenase
NCBI Description
                    (GAPDH) mRNA, partial cds
                    42282
Seq. No.
                    LIB3170-047-Q1-J1-F8
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3367594
BLAST score
                    221
                    3.0e-18
E value
                    54
Match length
% identity
                    67
                    (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                    42283
Seq. No.
Seq. ID
                    LIB3170-047-Q1-J1-G11
Method
                    BLASTX
                    g2653885
NCBI GI
                    274
BLAST score
                    3.0e-24
E value
                    71
Match length
                    72
 % identity
                    (AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis
NCBI Description
```

thaliana]



```
42284
Seq. No.
                  LIB3170-047-Q1-J1-H7
Seq. ID
                  BLASTN
Method
                  q1053215
NCBI GI
                  181
BLAST score
                  3.0e-97
E value
                  373
Match length
                  87
% identity
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
                  42285
Seq. No.
                  LIB3170-047-Q1-K1-B12
Seq. ID
                  BLASTN
Method
                  q170071
NCBI GI
                   203
BLAST score
                  1.0e-110
E value
                   207
Match length
                   100
% identity
NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds
                   42286
Seq. No.
                   LIB3170-048-Q1-J1-C1
Seq. ID
Method
                   BLASTN
                   g457572
NCBI GI
                   58
BLAST score
                   7.0e-24
E value
                   122
Match length
                   87
% identity
                  V.angularis mRNA for endo-xyloglucan transferase, complete
NCBI Description
                   42287
Seq. No.
                   LIB3170-048-Q1-J1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3168840
                   168
BLAST score
                   1.0e-11
E value
Match length
                   39
                   77
% identity
                   (U88711) copper homeostasis factor [Arabidopsis thaliana]
NCBI Description
                   42288
Seq. No.
                   LIB3170-048-Q1-J1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1695182
                   44
BLAST score
                   2.0e-15
E value
Match length
                   68
% identity
                   91
NCBI Description N.tabacum mRNA for isopentenyl pyrophosphate isomerase
                   42289
Seq. No.
                   LIB3170-048-Q1-J1-G9
 Seq. ID
```

BLASTX

g4262230

Method

NCBI GI



```
BLAST score
                  6.0e-22
E value
                  64
Match length
                  73
% identity
                  (AC006200) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  42290
Seq. ID
                  LIB3170-048-Q1-J1-H5
Method
                  BLASTN
                  g18555
NCBI GI
BLAST score
                  33
E value
                  4.0e-09
Match length
                  61
                  89
% identity
NCBI Description G.max DNA for Cab4
                  42291
Seq. No.
                  LIB3170-049-Q1-J1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4530126
                   198
BLAST score
E value
                   3.0e-15
Match length
                   80
% identity
                   55
                   (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
                   42292
Seq. No.
                   LIB3170-049-Q1-J1-B5
Seq. ID
Method
                   BLASTN
                   g999189
NCBI GI
                   58
BLAST score
E value
                   8.0e-24
                   82
Match length
                   93
% identity
                   dihydrofolate reductase-thymidylate synthase=bifunctional
NCBI Description
                   enzyme [Glycine max, seedling, mRNA, 1794 nt]
Seq. No.
                   42293
                   LIB3170-049-Q1-J1-C8
Seq. ID
                   BLASTN
Method
                   g1220521
NCBI GI
BLAST score
                   80
                   5.0e-37
E value
                   104
Match length
                   94
% identity
                   Glycine max TATA-box binding protein (STBP1) mRNA, complete
NCBI Description
                   cds
                   42294
Seq. No.
                   LIB3170-049-Q1-J1-E10
Seq. ID
                   BLASTX
Method
                   g3023713
NCBI GI
BLAST score
                   210
                   1.0e-16
E value
                   43
Match length
```

95

% identity



ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372

(U09450) enolase [Oryza sativa]

Seq. No. 42295

LIB3170-049-Q1-J1-F1 Seq. ID

BLASTX Method g2347056 NCBI GI 171 BLAST score 5.0e-12 E value 123 Match length 31 % identity

NCBI Description (AJ000085) Nedd4 protein [Xenopus laevis]

Seq. No.

LIB3170-049-Q1-K1-D4 Seq. ID

42296

BLASTN Method g168650 NCBI GI 174 BLAST score 4.0e-93 E value 302 Match length % identity 89

NCBI Description Zea mays ubiquitin fusion protein (UBF9) gene, complete cds

42297 Seq. No.

LIB3170-049-Q1-K2-B11 Seq. ID

Method BLASTX g1352363 NCBI GI BLAST score 265 3.0e-23 E value 111 Match length 50 % identity

NCBI Description ELASTASE IIIA PRECURSOR (PROTEASE E)

>gi_220014_dbj_BAA00212_ (D00306) pancreatic protease E
precursor [Homo sapiens] >gi_361780_prf__1410241A

pancreatic protease E isozyme [Homo sapiens]

42298 Seq. No.

LIB3170-049-Q1-K2-B6 Seq. ID

BLASTX Method g2244998 NCBI GI 384 BLAST score 4.0e-37 E value 115 Match length 63 % identity

(Z97341) similarity to probable transcriptional adaptor NCBI Description

ADA2 [Arabidopsis thaliana]

42299 Seq. No.

LIB3170-049-Q1-K2-C11 Seq. ID

BLASTX Method NCBI GI q136406 130 BLAST score 1.0e-14 E value 95 Match length % identity 56

NCBI Description TRYPSINOGEN, CATIONIC PRECURSOR >gi 67551 pir TRDGC





trypsin (EC 3.4.21.4) precursor, cationic - dog >gi_164097 (M11590) cationic trypsinogen precursor [Canis sp.]

 Seq. No.
 42300

 Seq. ID
 LIB3170-049-Q1-K2-C4

 Method
 BLASTX

 NCBI GI
 g2129605

 BLAST score
 274

 E value
 3.0e-24

 Match length
 74

% identity 76
NCBI Description GTP-binding protein 2 - Arabidopsis thaliana

>gi_2129702_pir__S71585 Rab2 homolog GTP-binding protein
ATGB2 - Arabidopsis thaliana >gi_1184983 (U46925) ATGB2
[Arabidopsis thaliana] >gi_3805852_emb_CAA21472_ (AL031986)

GTP-binding protein GB2 [Arabidopsis thaliana]

Seq. No. 42301

Seq. ID LIB3170-049-Q1-K2-D11

Method BLASTN
NCBI GI g164094
BLAST score 227
E value 1.0e-124
Match length 419
% identity 89

NCBI Description Dog pancreatic anionic trypsinogen mRNA

Seq. No. 42302

Seq. ID LIB3170-049-Q1-K2-F11

Method BLASTN
NCBI GI g163925
BLAST score 51
E value 1.0e-19
Match length 180
% identity 86

NCBI Description Dog pancreatic colipase gene, complete cds

Seq. No. 42303

Seq. ID LIB3170-049-Q1-K2-G6

Method BLASTX
NCBI GI g416873
BLAST score 171
E value 9.0e-13
Match length 49
% identity 61

NCBI Description 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (HIBADH)

>gi_111295_pir__A32867 3-hydroxyisobutyrate dehydrogenase
(EC 1.1.1.31) precursor - rat (fragment) >gi_556389

(EC 1.1.1.31) precursor - rat (fragment) 291_556569 (J04628) 3-hydroxyisobutyrate dehydrogenase [Rattus

norvegicus]

Seq. No. 42304

Seq. ID LIB3170-049-Q1-K2-H12

Method BLASTN
NCBI GI g164094
BLAST score 288
E value 1.0e-161



Match length % identity 97

NCBI Description Dog pancreatic anionic trypsinogen mRNA

Seq. No.

42305

Seq. ID

LIB3170-050-Q1-J1-B6

Method NCBI GI BLASTN g456713

BLAST score

43

E value Match length 5.0e-15

% identity

151 57

NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No.

42306

Seq. ID

LIB3170-050-Q1-J1-D7

Method

BLASTX g1050956

NCBI GI

BLAST score E value

179 6.0e-13

Match length

% identity

132 36

NCBI Description

(U26160) 43 kDa secreted glycoprotein precursor

2208385A [Paracoccidioides brasiliensis] >gi_1588394_prf

glycoprotein gp43 [Paracoccidioides brasiliensis]

Seq. No.

42307

Seq. ID

LIB3170-050-Q1-J1-E4

Method

BLASTX g3859548

NCBI GI

139

BLAST score E value

1.0e-08

Match length

31

% identity NCBI Description

81 (AF097182) protein phosphatase 2A catalytic subunit [Oryza

sativa]

Seq. No.

42308

Seq. ID

LIB3170-050-Q1-J1-F10

Method NCBI GI BLASTX q3738302

BLAST score E value

145 5.0e-09

Match length

59 53

% identity NCBI Description

(AC005309) tubby-like protein [Arabidopsis thaliana]

>gi_4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

Seq. No.

42309

Seq. ID

LIB3170-050-Q1-K1-B11 BLASTX

Method NCBI GI BLAST score

q4325338

E value

222 4.0e-18

Match length % identity

93 52



NCBI Description (AF128392) No definition line found [Arabidopsis thaliana]

 Seq. No.
 42310

 Seq. ID
 LIB3170-050-Q1-K1-C4

 Method
 BLASTX

 NCBI GI
 g136636

 BLAST score
 235

E value 7.0e-20 Match length 77 % identity 64

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK__Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK__Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 42311

Seq. ID LIB3170-050-Q1-K1-F10

Method BLASTX
NCBI GI g4309738 BLAST score 164
E value 4.0e-13
Match length 95
% identity 44

NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3170-050-Q1-K1-H3

Method BLASTX
NCBI GI g2119719
BLAST score 266
E value 2.0e-23
Match length 81
% identity 67

NCBI Description heat-shock cognate protein 70-3 - tomato >gi_762844

(L41253) Hsc70 [Lycopersicon esculentum]

Seq. No. 42313

Seq. ID LIB3170-051-Q1-J1-A7

Method BLASTX
NCBI GI g3776579
BLAST score 233
E value 3.0e-19
Match length 86
% identity 56

NCBI Description (AC005388) Strong similarity to F22013.22 gi_3063460 myosin

homolog from A. thaliana BAC gb_AC003981. [Arabidopsis

thaliana]

Seq. No. 42314

Seq. ID LIB3170-051-Q1-J1-D1

Method BLASTN NCBI GI g450544

BLAST score

Match length

E value

166 2.0e-11

40

```
BLAST score
                    2.0e-78
 E value
                    289
 Match length
                    88
  % identity
                    Mitochondrion Glycine max gene for ATPase proteolipid
 NCBI Description
                    subunit
                    42315
  Seq. No.
                    LIB3170-051-Q1-K1-G10
  Seq. ID
                    BLASTX
  Method
                    g3924596
  NCBI GI
                    222
  BLAST score
                    3.0e-18
  E value
                    90
  Match length
                    53
  % identity
                     (AF069442) putative phospho-ser/thr phosphatase
  NCBI Description
                   [Arabidopsis thaliana]
                     42316
  Seq. No.
                    LIB3170-051-Q1-K1-G9
  Seq. ID
                    BLASTX
  Method
                     q4467128
  NCBI GI
                     200
  BLAST score
                     1.0e-15
  E value
  Match length
                     69
                     51
  % identity
                    (AL035538) putative protein [Arabidopsis thaliana]
  NCBI Description
                     42317
  Seq. No.
                     LIB3170-051-Q1-K2-B3
  Seq. ID
                     BLASTX
  Method
                     q3355474
  NCBI GI
                     283
  BLAST score
  E value
                     2.0e-25
                     97
  Match length
                     58
  % identity
                    (AC004218) unknown protein [Arabidopsis thaliana]
  NCBI Description
                     42318
  Seq. No.
                     LIB3170-052-Q1-J1-A3
  Seq. ID
                     BLASTN
  Method
                     g460933
  NCBI GI
                     33
  BLAST score
  E value
                     5.0e-09
  Match length
                     109
                     83
  % identity
                     Cloning vector pUCP18, Escherichia-Pseudomonas shuttle
  NCBI Description
                     vector with beta-lactamase (bla) and LacZ alpha peptide
                      (lacZ alpha) genes, complete sequence
   Seq. No.
                     42319
                     LIB3170-052-Q1-J1-B8
   Seq. ID
                     BLASTX
  Method
                     g2618731
   NCBI GI
```



```
% identity
NCBI Description (U49077) IAA21 [Arabidopsis thaliana]
                  42320
Seq. No.
                  LIB3170-052-Q1-J1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3850630
                  313
BLAST score
E value
                  9.0e-29
                  87
Match length
                  63
% identity
NCBI Description (AJ012581) cytochrome P450 [Cicer arietinum]
Seq. No.
                  42321
                  LIB3170-052-Q1-J1-C5
Seq. ID
                  BLASTX
Method
                  g1150406
NCBI GI
BLAST score
                  254
                  1.0e-21
E value
                   117
Match length
                   46
% identity
                  (Z46868) exo-1,3-beta-glucanase/1,3-beta-D-glucan
NCBI Description
                   glucanohydrolase [Pichia angusta]
                   42322
Seq. No.
                   LIB3170-052-Q1-J1-D6
Seq. ID
                   BLASTX
Method
                   g3334219
NCBI GI
BLAST score
                   158
                   1.0e-10
E value
                   68
Match length
                   47
% identity
                   4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)
NCBI Description
                   >gi_2231615 (U87257) 4-hydroxyphenylpyruvate dioxygenase
                   [Daucus carota]
Seq. No.
                   42323
                   LIB3170-052-Q1-J1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1545805
BLAST score
                   256
                   2.0e-22
E value
                   88
Match length
                   39
% identity
NCBI Description (D64052) cytochrome P450 like_TBP [Nicotiana tabacum]
                   42324
Seq. No.
                   LIB3170-052-Q1-J1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4262224
BLAST score
                   287
                   1.0e-25
E value
Match length
                   129
                   46
 % identity
                   (AC006200) putative amino acid or GABA permease
NCBI Description
```

[Arabidopsis thaliana]



```
Seq. No.
                  LIB3170-052-Q1-J1-F3
Seq. ID
                  BLASTN
Method
                  g1399304
NCBI GI
                  61
BLAST score
                  7.0e-26
E value
                  105
Match length
                  90
% identity
                  Glycine max phosphoinositide-specific phospholipase C P13
NCBI Description
                  mRNA, complete cds
                  42326
Seq. No.
                  LIB3170-052-Q1-J1-G3
Seq. ID
                  BLASTX
Method
                  g2529663
NCBI GI
                  164
BLAST score
                   3.0e-11
E value
                   69
Match length
                   49
% identity
                   (AC002535) putative lysophospholipase [Arabidopsis
NCBI Description
                   thaliana] >gi_3738277 (AC005309) putative lysophospholipase
                   [Arabidopsis thaliana]
                   42327
Seq. No.
                   LIB3170-052-Q1-K1-C4
Seq. ID
                   BLASTX
Method
                   g3250695
NCBI GI
                   222
BLAST score
                   3.0e-21
E value
                   80
Match length
                   53
% identity
                   (AL024486) putative protein [Arabidopsis thaliana]
NCBI Description
                   42328
Seq. No.
                   LIB3170-052-Q1-K1-D6
Seq. ID
                   BLASTX
Method
                   q3334219
NCBI GI
BLAST score
                   224
                   1.0e-18
E value
                   97
Match length
                   53
% identity
                   4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)
NCBI Description
                   >gi_2231615 (U87257) 4-hydroxyphenylpyruvate dioxygenase
                   [Daucus carota]
                   42329
 Seq. No.
                   LIB3170-052-Q1-K1-G4
 Seq. ID
                   BLASTX
Method
NCBI GI
                   q2244904
                   193
BLAST score
E value
                   6.0e-15
                   99
Match length
 % identity
                   (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
 NCBI Description
                    [Arabidopsis thaliana]
```

Seq. No. 42330

Seq. ID

Method



```
Seq. ID
                   LIB3170-052-Q1-K1-H7
Method
                   BLASTN
NCBI GI
                   g1389896
BLAST score
                   80
E value
                   4.0e-37
Match length
                   108
% identity
                   94
NCBI Description
                   Glycine max 68 kDa LEA protein mRNA, complete cds
Seq. No.
                   42331
Seq. ID
                   LIB3170-053-Q1-J1-A3
Method
                   BLASTN
NCBI GI
                   g1142620
BLAST score
                   48
E value
                   5.0e-18
Match length
                   208
% identity
                   84
NCBI Description
                   Phaseolus vulgaris phaseolin G-box binding protein PG2
                   (PG2) mRNA, partial cds
Seq. No.
                   42332
Seq. ID
                   LIB3170-053-Q1-J1-A4
Method
                   BLASTX
NCBI GI
                   g4006899
BLAST score
                   243
E value
                   2.0e-20
Match length
                   83
% identity
                   57
NCBI Description
                   (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   42333
Seq. ID
                  LIB3170-053-Q1-J1-A6
Method
                  BLASTN
NCBI GI
                   q2583106
BLAST score
                   53
E value
                  8.0e-21
Match length
                  105
                  88
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4L23 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  42334
Seq. ID
                  LIB3170-053-Q1-J1-C5
Method
                  BLASTX
NCBI GI
                  g1362047
BLAST score
                  164
E value
                  2.0e-11
Match length
                  89
% identity
                  46
NCBI Description
                  cysteine proteinase (EC 3.4.22.-) precursor - soybean
                  >gi 479060 emb CAA83673 (Z32795) cysteine proteinase
                  [Glycine max] >gi_1096153_prf__2111244A Cys protease
                   [Glycine max]
Seq. No.
                  42335
```

LIB3170-053-Q1-J1-G11

BLASTX



```
g3395441
NCBI GI
                  244
BLAST score
                  1.0e-20
E value
                  74
Match length
                  68
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  42336
Seq. No.
                  LIB3170-053-Q1-K1-A3
Seq. ID
                  BLASTX
Method
                  g2244974
NCBI GI
                  424
BLAST score
                  1.0e-41
E value
                  159
Match length
                  58
% identity
                   (Z97340) similarity to pore protein Pisum sativum
NCBI Description
                   [Arabidopsis thaliana]
                   42337
Seq. No.
                  LIB3170-053-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4415933
BLAST score
                   395
                   3.0e-38
E value
Match length
                   124
                   67
% identity
                   (AC006418) putative cellular apoptosis susceptibility
NCBI Description
                   protein [Arabidopsis thaliana]
                   >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative
                   cellular apoptosis susceptibility protein [Arabidopsis
                   thaliana]
Seq. No.
                   42338
                   LIB3170-053-Q1-K1-C7
Seq. ID
Method
                   BLASTX
                   q531829
NCBI GI
                   166
BLAST score
                   1.0e-11
E value
                   79
Match length
                   49
% identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
                   42339
Seq. No.
                   LIB3170-053-Q1-K1-E3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2708744
BLAST score
                   141
                   6.0e-09
E value
Match length
                   88
% identity
                   36
                   (AC003952) putative Bop-like zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   42340
Seq. No.
Seq. ID
                   LIB3170-054-Q1-J1-A3
```

6699

BLASTX

Method

```
q2346988
NCBI GI
BLAST score
                  218
E value
                  1.0e-17
Match length
                  121
% identity
                  45
                 (AB006606) ZPT4-4 [Petunia x hybrida]
NCBI Description
                  42341
Seq. No.
                  LIB3170-054-Q1-J1-C1
Seq. ID
Method
                  BLASTN
                  g22075
NCBI GI
BLAST score
                  91
E value
                  1.0e-43
Match length
                  187
% identity
                  87
NCBI Description Vigna unguiculata cDNA for stored cotyledon mRNA
                  42342
Seq. No.
                  LIB3170-054-Q1-J1-E1
Seq. ID
Method
                  BLASTN
                  g18743
NCBI GI
BLAST score
                  47
E value
                  2.0e-17
Match length
                  178
                  83
% identity
NCBI Description G.max mRNA from stress-induced gene (SAM22)
Seq. No.
                  42343
                  LIB3170-054-Q1-J1-F1
Seq. ID
Method
                  BLASTX
                  g4490743
NCBI GI
BLAST score
                  385
                  4.0e-37
E value
                  96
Match length
% identity
                  74
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
                  42344
Seq. No.
                  LIB3170-054-Q1-J1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3122703
BLAST score
                  176
E value
                  6.0e-13
Match length
```

59 % identity 64

NCBI Description 60S RIBOSOMAL PROTEIN L23A >qi 2641201 (AF031542) ribosomal

protein L23a [Fritillaria agrestis]

Seq. No. 42345

Seq. ID LIB3170-054-Q1-J1-H9

Method BLASTX NCBI GI g4204268 BLAST score 152 E value 3.0e-10 Match length 71 48 % identity

NCBI Description (AC005223) 62134 [Arabidopsis thaliana]

Method

NCBI GI

BLASTN

g392820



```
42346
Seq. No.
Seq. ID
                  LIB3170-054-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  g4510339
BLAST score
                  234
E value
                  1.0e-19
Match length
                  103
% identity
                  46
                  (AC006921) putative ABC transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  42347
Seq. No.
Seq. ID
                  LIB3170-054-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1931645
BLAST score
                  465
E value
                  2.0e-46
                  155
Match length
% identity
                  61
NCBI Description (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
Seq. No.
                  42348
Seq. ID
                  LIB3170-054-Q1-K1-F1
Method
                  BLASTX
NCBI GI
                  g4490743
BLAST score
                  144
                  5.0e-09
E value
                  74
Match length
                  50
% identity
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                  42349
Seq. ID
                  LIB3170-054-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g531829
BLAST score
                  142
                  5.0e-09
E value
Match length
                  76
% identity
                  47
NCBI Description (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
Seq. No.
                  42350
Seq. ID
                  LIB3170-054-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2262115
BLAST score
                  153
E value
                  5.0e-10
                  94
Match length
                  39
% identity
NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.
                  42351
Seq. ID
                  LIB3170-055-Q1-K1-A11
```

6701



```
BLAST score
                  1.0e-56
E value
                  165
Match length
                  100
% identity
NCBI Description Glycine max Williams cellulase mRNA, partial cds
                  42352
Seq. No.
                  LIB3170-055-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                   g4469009
NCBI GI
                   327
BLAST score
                   2.0e-30
E value
                   126
Match length
                   60
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                   42353
Seq. No.
                   LIB3170-055-Q1-K1-C1
Seq. ID
                   BLASTX
Method
                   q1418990
NCBI GI
                   255
BLAST score
                   3.0e-22
E value
                   72
Match length
                   68
% identity
NCBI Description (Z75524) unknown [Lycopersicon esculentum]
Seq. No.
                   42354
                   LIB3170-055-Q1-K1-D1
Seq. ID
                   BLASTX
Method
                   q531829
NCBI GI
                   147
BLAST score
                   2.0e-09
E value
                   79
Match length
                   42
 % identity
                   (U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                   pSport1]
                   42355
 Seq. No.
                   LIB3170-055-Q1-K1-F10
 Seq. ID
                   BLASTX
 Method
                   g1101770
 NCBI GI
                   200
 BLAST score
                   2.0e-15
 E value
                   77
 Match length
                   75
 % identity
                   (U39448) MYB-like transcriptional factor MBF1 [Picea
 NCBI Description
                   mariana]
                    42356
 Seq. No.
                   LIB3170-055-Q1-K1-F12
 Seq. ID
 Method
                   BLASTX
                    q1653246
 NCBI GI
 BLAST score
                    232
                    2.0e-19
 E value
                    122
 Match length
                    39
 % identity
 NCBI Description (D90912) hypothetical protein [Synechocystis sp.]
```



```
42357
Seq. No.
                  LIB3170-055-Q1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2920665
BLAST score
                  168
                  2.0e-89
E value
Match length
                  284
% identity
                  90
NCBI Description
                  Glycine max 2,4-D inducible glutathione S-transferase
                   (GSTa) mRNA, complete cds
Seq. No.
                  42358
                  LIB3170-055-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212865
                  292
BLAST score
                  7.0e-39
E value
Match length
                  160
% identity
                  59
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   42359
Seq. No.
Seq. ID
                  LIB3170-056-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                   q3258575
BLAST score
                   439
E value
                   2.0e-43
Match length
                   151
% identity
                   59
                  (U89959) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   42360
                  LIB3170-056-Q1-K1-D7
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                   g3004556
BLAST score
                   195
E value
                   7.0e-15
                   99
Match length
                   43
% identity
NCBI Description
                  (AC003673) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   42361
Seq. ID
                   LIB3170-056-Q1-K1-G1
Method
                   BLASTN
NCBI GI
                   g170023
BLAST score
                   60
                   4.0e-25
E value
Match length
                   140
% identity
                   91
NCBI Description
                  Glycine max maturation-associated protein (MAT9) mRNA,
                   complete cds
Seq. No.
                   42362
```

Seq. ID LIB3170-057-Q1-J1-A5

Method BLASTX NCBI GI g2078350



```
BLAST score
E value
                  3.0e-15
Match length
                  118
                  48
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  42363
Seq. ID
                  LIB3170-057-Q1-K1-B2
Method
                  BLASTX
NCBI GI
                  g567893
BLAST score
                  255
E value
                  6.0e-22
Match length
                  95
                  55
% identity
NCBI Description
                  (L37382) beta-galactosidase-complementation protein
                  [Cloning vector]
Seq. No.
                  42364
                  LIB3170-057-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494299
BLAST score
                  219
E value
                  1.0e-17
Match length
                  120
% identity
                  43
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT
NCBI Description
                  (EIF-2-BETA) >gi_1732361 (U80269) translation initiation
                  factor 2 beta [Malus domestica]
Seq. No.
                  42365
Seq. ID
                  LIB3170-057-Q1-K1-F9
Method
                  BLASTX
NCBI GI
                  g567890
BLAST score
                  149
                  1.0e-09
E value
Match length
                  86
% identity
                  41
                  (L37352) beta-galactosidase-complementation protein
NCBI Description
                  [Cloning vector]
Seq. No.
                  42366
Seq. ID
                  LIB3170-057-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1345842
BLAST score
                  138
                  7.0e-09
E value
```

Match length 50 56 % identity

NCBI Description 139 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL PROTOXIN) >gi_80480_pir__S00873 parasporal

crystal protein - Bacillus thuringiensis subsp. thuringiensis >gi_580949_emb_CAA29898_ (X06711) delta-endotoxin (AA 1-1228) [Bacillus thuringiensis]

Seq. No. 42367

Seq. ID LIB3170-057-Q1-K1-H6

Method BLASTX



```
NCBI GI
                  g2801701
BLAST score
                  288
                  1.0e-25
E value
Match length
                  186
% identity
                  33
NCBI Description
                  (AF042379) spindle pole body protein spc97 homolog GCP2
                  [Homo sapiens]
Seq. No.
                  42368
Seq. ID
                  LIB3170-058-Q1-J1-E12
Method
                  BLASTX
NCBI GI
                  g2865394
BLAST score
                  206
                  3.0e-16
E value
Match length
                  57
% identity
                  63
                  (AF036949) basic leucine zipper protein [Zea mays]
NCBI Description
                  42369
Seq. No.
                  LIB3170-058-Q1-J1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q418854
BLAST score
                  587
E value
                  9.0e-61
Match length
                  118
% identity
                  18
                  ubiquitin precursor - parsley >gi 288112 emb CAA45621
NCBI Description
                   (X64344) polyubiquitin [Petroselinum crispum]
                  >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                   [Petroselinum crispum]
                  42370
Seq. No.
                  LIB3170-058-Q1-J1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1199562
BLAST score
                  52
                  2.0e-20
E value
                  88
Match length
% identity
                  Glycine max 34 kDa maturing seed vacuolar thiol protease
NCBI Description
                  mRNA,
                         complete cds
Seq. No.
                  42371
                  LIB3170-058-Q1-J1-G11
Seq. ID
Method
                  BLASTN
                  g2605511
NCBI GI
BLAST score
                  57
                  2.0e-23
E value
Match length
                  105
                  90
% identity
NCBI Description
                  Glycine max mRNA for beta subunit of beta conglycinin,
```

complete cds

Seq. No. 42372 Seq. ID LIB3170-058-Q1-J1-H3

Method BLASTN NCBI GI g511937



```
BLAST score
                  8.0e-66
E value
                  206
Match length
                  91
% identity
NCBI Description
                  Soybean mRNA for cysteine proteinase, complete cds
Seq. No.
                  42373
                  LIB3170-058-Q1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2764574
BLAST score
                  221
                  5.0e-18
E value
                  103
Match length
% identity
                  48
NCBI Description
                  (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]
                  42374
Seq. No.
                  LIB3170-058-Q1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132521
BLAST score
                  366
                  4.0e-35
E value
Match length
                  100
% identity
                  70
                  RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN
NCBI Description
                  RGP1) >gi 100684 pir S16554 GTP-binding protein rgp1 -
                  rice >gi 20356 emb CAA41966 (X59276) GTP-binding protein
                  [Oryza sativa] >gi 228209 prf 1718315A GTP-binding protein
                  [Oryza sativa]
                  42375
Seq. No.
Seq. ID
                  LIB3170-058-Q1-K1-D11
                  BLASTN
Method
NCBI GI
                  q168579
BLAST score
                  122
E value
                  7.0e-62
                  370
Match length
                  87
% identity
NCBI Description Maize pyruvate, orthophosphate dikinase mRNA, complete cds
Seq. No.
                  42376
Seq. ID
                  LIB3170-058-Q1-K1-F9
Method.
                  BLASTN
NCBI GI
                  q303900
BLAST score
                  469
E value
                  0.0e + 00
Match length
                  503
                  32
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
```

42377 Seq. No. Seq. ID LIB3170-059-Q1-J1-C1

Method BLASTN

NCBI GI q1142618 BLAST score 65

E value 4.0e-28 Match length 121



```
% identity
                  Phaseolus vulgaris phaseolin G-box binding protein PG1
NCBI Description
                   (PG1) mRNA, complete cds
Seq. No.
                  42378
                  LIB3170-059-Q1-J1-G4
Seq. ID
                  BLASTN
Method
                  g1399379
NCBI GI
BLAST score
                  53
                  3.0e-21
E value
                  93
Match length
                  89
% identity
                  Glycine max S-adenosyl-L-methionine:delta24-sterol-C-
NCBI Description
                  methyltransferase mRNA, complete cds
                  42379
Seq. No.
                  LIB3170-060-Q1-J1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642154
BLAST score
                  158
E value
                  1.0e-10
Match length
                   50
% identity
                   48
NCBI Description
                   (AC003000) unknown protein [Arabidopsis thaliana]
                  >gi 3790595 (AF079186) RING-H2 finger protein RHC2a
                   [Arabidopsis thaliana]
Seq. No.
                   42380
Seq. ID
                  LIB3170-060-Q1-J1-C7
                  BLASTN
Method
NCBI GI
                  g633598
BLAST score
                   47
E value
                  2.0e-17
                  79
Match length
% identity
                   90
NCBI Description
                  N.tabacum mRNA for inorganic pyrophosphatase (TVP5clone)
                   42381
Seq. No.
Seq. ID
                  LIB3170-060-Q1-K1-A3
Method
                  BLASTX
NCBI GI
                   g4455364
BLAST score
                   330
                   8.0e-31
E value
                  107
Match length
                   60
% identity
                   (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                   thaliana]
                   42382
Seq. No.
                  LIB3170-060-Q1-K1-D11
Seq. ID
```

Method

BLASTX

NCBI GI BLAST score E value

g2191150 385 3.0e-37

Match length % identity

109 38

NCBI Description (AF007269) similar to mitochondrial carrier family

Seq. ID Method



[Arabidopsis thaliana]

```
42383
Seq. No.
Seq. ID
                  LIB3170-060-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q4263790
BLAST score
                  189
E value
                  3.0e-14
Match length
                  130
% identity
                  40
                  (AC006068) putative ch-TOG protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  42384
                  LIB3170-060-Q1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q944814
BLAST score
                  174
                  4.0e-93
E value
Match length
                  270
% identity
                  91
                  Pueraria lobata mRNA for chalcone flavanone isomerase,
NCBI Description
                  complete cds
Seq. No.
                  42385
Seq. ID
                  LIB3170-061-Q1-J1-E12
Method
                  BLASTN
NCBI GI
                  g310579
BLAST score
                  389
E value
                  0.0e + 00
Match length
                  389
                  100
% identity
NCBI Description Glycine max protein kinase 2 (SPK-2) mRNA, complete cds
                  42386
Seq. No.
Seq. ID
                  LIB3170-061-Q1-J1-F2
Method
                  BLASTX
NCBI GI
                  g2459445
BLAST score
                  185
                  6.0e-14
E value
Match length
                  101
                  23
% identity
NCBI Description
                  (AC002332) putative ribonucleoprotein [Arabidopsis
                  thaliana]
                  42387
Seg. No.
Seq. ID
                  LIB3170-061-Q1-J1-F8
Method
                  BLASTX
NCBI GI
                  g3894183
BLAST score
                  273
                  3.0e-24
E value
Match length
                  91
% identity
                  65
                  (AC005662) calmodulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  42388
```

6708

LIB3170-061-Q1-K2-E4

BLASTX

NCBI GI

BLAST score



```
NCBI GI
                   q531829
                  190
BLAST score
E value
                   2.0e-14
Match length
                  79
% identity
                   49
NCBI Description
                  (U12390) beta-galactosidase alpha peptide [cloning vector
                  pSport1]
Seq. No.
                   42389
Seq. ID
                   LIB3170-061-Q1-K2-G3
Method
                  BLASTX
NCBI GI
                   g136125
BLAST score
                   203
                   7.0e-16
E value
Match length
                  79
% identity
                   51
                  PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005_
NCBI Description
                   (X05424) ORFa [Zea mays]
Seq. No.
                   42390
                  LIB3170-062-Q1-J1-A4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g476213
BLAST score
                   69
E value
                   2.0e-30
Match length
                   117
% identity
                   91
                  Glycine max Century 84 p24 oleosin isoform A gene, complete
NCBI Description
                   cds
Seq. No.
                   42391
Seq. ID
                   LIB3170-062-Q1-J1-B5
Method
                   BLASTX
NCBI GI
                   g2828280
BLAST score
                   240
                   2.0e-20
E value
Match length
                   88
% identity
                   58
                   (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_2832633_emb_CAA16762_ (AL021711) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   42392
Seq. ID
                   LIB3170-062-Q1-J1-C12
Method
                   BLASTX
NCBI GI
                   g4455278
BLAST score
                   256
                   5.0e-22
E value
Match length
                   77
                   57
% identity
NCBI Description
                  (AL035527) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   42393
Seq. ID
                   LIB3170-062-Q1-J1-D5
Method
                   BLASTX
```

g4262225

356



E value 1.0e-33 Match length 103 % identity 61

NCBI Description (AC006200) putative phosphatidic acid phosphatase

[Arabidopsis thaliana]

Seq. No. 42394

Seq. ID LIB3170-062-Q1-J1-F10

Method BLASTN
NCBI GI g945059
BLAST score 117
E value 4.0e-59
Match length 173
% identity 92

NCBI Description Vigna unguiculata aminoimidazole ribonucleotide (AIRS)

synthetase (pur5) mRNA, complete cds

Seq. No. 42395

Seq. ID LIB3170-064-Q1-J1-C12

Method BLASTX
NCBI GI g2464864
BLAST score 607
E value 4.0e-63
Match length 179
% identity 36

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 42396

Seq. ID LIB3170-064-Q1-J1-G12

Method BLASTX
NCBI GI g1730172
BLAST score 218
E value 1.0e-17
Match length 54
% identity 80

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 1 (GPI)

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_1364077_pir__S57830 glucose-6-phosphate isomerase (EC 5.3.1.9) isoenzyme 1, cytosolic - Clarkia xantiana >gi_784974_emb_CAA56693_(X80666) glucose-6-phosphate isomerase [Clarkia xantiana] >gi_1370068_emb_CAA61566_(X89386) glucose-6-phosphate isomerase [Clarkia xantiana]

Seq. No. 42397

Seq. ID LIB3170-064-Q1-K1-C7

Method BLASTX
NCBI GI g2651305
BLAST score 198
E value 4.0e-15
Match length 64
% identity 61

NCBI Description (AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 42398

Seq. ID LIB3170-064-Q1-K1-D2

Method BLASTN NCBI GI g18764



BLAST score E value 0.0e + 00Match length 448 100 % identity

NCBI Description G.max tefS1 gene for elongation factor EF-la

42399 Seq. No.

Seq. ID LIB3170-064-Q1-K1-F12

BLASTX Method NCBI GI g2281107 BLAST score 150 2.0e-09 E value 97 Match length 43 % identity

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.

42400 Seq. ID LIB3170-064-Q1-K1-G12

Method BLASTX NCBI GI q462147 BLAST score 442 E value 1.0e-49 Match length 115 % identity 88

GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI) NCBI Description

> (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi 541866 pir_ S41808 glucose-6-phosphate isomerase

(EC 5.3.1.9) - Arabidopsis thaliana

>gi 415923 emb CAA48940 (X69195) glucose-6-phosphate

isomerase [Arabidopsis Thaliana]

Seq. No. 42401

LIB3170-064-Q1-K1-G8 Seq. ID

Method BLASTX NCBI GI g3482967 BLAST score 264 E value 4.0e-23 Match length 119 % identity 47

(AL031369) Protein phosphatase 2C-like protein [Arabidopsis NCBI Description

thaliana] >gi 4559345 gb AAD23006.1 AC006585 1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 42402

Seq. ID LIB3170-064-Q1-K1-H5

Method BLASTN NCBI GI g2815245 BLAST score 86 E value 1.0e-40 Match length 242 % identity 84

C.arietinum mRNA for class I type 2 metallothionein (clone: NCBI Description

CanMT-2)

Seq. No. 42403

LIB3170-065-Q1-J1-A4 Seq. ID

Method BLASTN



NCBI GI BLAST score 65 4.0e-28 E value 121 Match length % identity 93

NCBI Description G.max mRNA from stress-induced gene (H4)

42404 Seq. No.

Seq. ID LIB3170-065-Q1-J1-A6

Method BLASTX NCBI GI g2832625 BLAST score 140 E value 9.0e-09 Match length 51

% identity 47

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

42405 Seq. No.

LIB3170-065-Q1-K1-B9 Seq. ID

Method BLASTX NCBI GI g81760 BLAST score 186 9.0e-14E value Match length 101 % identity 44

NCBI Description auxin-induced protein - soybean (fragment)

42406 Seq. No.

LIB3170-065-Q1-K1-C1 Seq. ID

Method BLASTN NCBI GI q169980 BLAST score 51 E value 1.0e-19 Match length 95 % identity 88

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 42407

LIB3170-065-Q1-K1-D9 Seq. ID

BLASTX Method g3746568 NCBI GI BLAST score 174 E value 3.0e-13 Match length 67 % identity 55

(AF061638) branched-chain alpha-keto acid decarboxylase E1 NCBI Description

beta subunit [Arabidopsis thaliana]

Seq. No. 42408

Seq. ID LIB3170-065-Q1-K1-F6

Method BLASTX NCBI GI g1871526 BLAST score 169 E value 1.0e-11 Match length 165 29 % identity

NCBI Description (X81997) leucine-rich-repeat protein [Helianthus annuus]



```
42409
Seq. No.
                  LIB3170-065-Q1-K1-H1
Seq. ID
                  BLASTX
Method
                  g4091080
NCBI GI
BLAST score
                  213
E value
                  6.0e-20
                  131
Match length
                  50
% identity
NCBI Description (AF045571) nucleic acid binding protein [Oryza sativa]
Seq. No.
                  42410
Seq. ID
                  LIB3170-065-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q4091080
BLAST score
                  149
E value
                  1.0e-09
Match length
                  61
                  52
% identity
                 (AF045571) nucleic acid binding protein [Oryza sativa]
NCBI Description
                  42411
Seq. No.
                  LIB3170-066-Q1-J1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18662
BLAST score
                  166
E value
                  2.0e-88
Match length
                  329
% identity
                  87
NCBI Description Glycine max hsp 70 gene
Seq. No.
                  42412
Seq. ID
                  LIB3170-066-Q1-J1-D8
Method
                  BLASTX
NCBI GI
                  g2281449
BLAST score
                  166
E value
                  1.0e-11
                  50
Match length
                   64
% identity
                  (U90214) leucine zipper transcription factor TGA2.1
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                  42413
Seq. ID
                  LIB3170-066-Q1-J1-F2
Method
                  BLASTX
NCBI GI
                  g2462823
BLAST score
                  169
E value
                   6.0e-12
Match length
                  57
                  58
% identity
NCBI Description
                  (AF000657) unknown protein [Arabidopsis thaliana]
                  >gi 2829907 (AC002311) Unknown protein [Arabidopsis
                  thalianal
```

42414

BLASTX

LIB3170-066-Q1-K1-D1

Seq. No.

Seq. ID Method

```
NCBI GI
                  q2440160
BLAST score
                  242
                  2.0e-20
E value
                  124
Match length
                  45
% identity
NCBI Description
                  (Y14836) beta-galactosidase [Phagemid cloning vector
                  pTZ19U]
                  42415
Seq. No.
Seq. ID
                  LIB3170-066-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g1076286
BLAST score
                  212
                  2.0e-17
E value
Match length
                  58
% identity
                  72
                  amidophosphoribosyltransferase - Arabidopsis thaliana
NCBI Description
                  >gi 469193 dbj BAA06023 (D28868)
                  amidophosphoribosyltransferase [Arabidopsis thaliana]
Seq. No.
                  42416
                  LIB3170-066-Q1-K1-G1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g531832
BLAST score
                  49
E value
                  1.0e-18
Match length
                  225
                  80
% identity
NCBI Description Cloning vector pSport2, complete sequence
Seq. No.
                  42417
Seq. ID
                  LIB3170-067-Q1-J1-A1
Method
                  BLASTX
NCBI GI
                  g4388728
                  208
BLAST score
E value
                  3.0e-16
Match length
                  69
                  52
% identity
                  (AC006413) putative grr1-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  42418
Seq. ID
                  LIB3170-067-Q1-J1-A10
Method
                  BLASTX
NCBI GI
                  g1362051
BLAST score
                  595
                  7.0e-62
E value
                  140
Match length
                  81
% identity
                  protein kinase 3 - soybean >gi_310582 (L19361) protein
NCBI Description
                  kinase 3 [Glycine max]
Seq. No.
                  42419
```

Seq. ID LIB3170-067-Q1-J1-B11

Method BLASTN NCBI GI g555615 BLAST score 389



```
E value
                   0.0e+00
Match length
                   413
                   99
% identity
                   Glycine max Mandarin cytokinin induced message (cim1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   42420
Seq. ID
                   LIB3170-067-Q1-J1-D3
Method
                   BLASTN
NCBI GI
                   q2661020
BLAST score
                   143
                   1.0e-74
E value
Match length
                   235
% identity
                   90
NCBI Description Glycine max catalase (cat4) mRNA, complete cds
Seq. No.
                   42421
                   LIB3170-067-Q1-J1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2969887
BLAST score
                   463
                   3.0e-46
E value
Match length
                   124
% identity
                   74
NCBI Description
                   (Y16766) sucrose/H+ symporter [Daucus carota]
                   >gi 2969889 emb CAA76368 (Y16767) sucrose/H+ symporter
                   [Daucus carota]
                   42422
Seq. No.
                   LIB3170-067-Q1-J1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g231585
BLAST score
                   233
E value
                   2.0e-19
Match length
                   142
% identity
                   44
                   ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL
NCBI Description
                   >gi 418790 pir S29792 H+-transporting ATP synthase (EC
                   3.6.1.34) alpha chain - soybean mitochondrion >gi 22739 emb CAA78407 (Z14031) atpA [Glycine max]
Seq. No.
                   42423
Seq. ID
                   LIB3170-067-Q1-J1-F11
Method
                   BLASTN
                   g669093
NCBI GI
BLAST score
                   49
E value
                   9.0e-19
                   65
Match length
                   94
% identity
NCBI Description A.majus chloroplast psaB gene (mutant en:alba-1)
```

Seq. No. 42424

LIB3170-067-Q1-J1-G9 Seq. ID

Method BLASTN NCBI GI g1217993 33 BLAST score E value 4.0e-09



```
Match length
                  61
% identity
                  97
NCBI Description Glycine max dynamin-like protein SDL12A mRNA, complete cds
Seq. No.
                  42425
Seq. ID
                  LIB3170-067-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2264321
BLAST score
                  39
                  2.0e-12
E value
Match length
                  99
                  32
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  42426
Seq. ID
                  LIB3170-067-Q1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3548803
BLAST score
                  267
E value
                  1.0e-23
Match length
                  82
                  70
% identity
                  (AC005313) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4335770 gb AAD17447 (AC006284) putative
                  SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  42427
Seq. ID
                  LIB3170-067-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  g825756
BLAST score
                  169
E value
                  5.0e-12
Match length
                  63
% identity
                  56
                  (U12391) beta-galactosidase alpha peptide [Cloning vector-
NCBI Description
                  pSport2]
Seq. No.
                  42428
                  LIB3170-067-Q1-K1-C3
Seq. ID
Method
                  BLASTX
                  q170920
NCBI GI
BLAST score
                  174
E value
                  2.0e-13
Match length
                  67
% identity
                  66
NCBI Description
                  (M62396) ribosomal protein L41 [Candida maltosa]
Seq. No.
                  42429
                  LIB3170-067-Q1-K1-D10
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI 94510373
BLAST score 210
E value 1.0e-16
Match length 135
% identity 36

NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis



```
thaliana]
                  42430
Seq. No.
Seq. ID
                  LIB3170-067-Q1-K1-G6
                  BLASTX
Method
NCBI GI
                  q531389
BLAST score
                  159
                  9.0e-11
E value
Match length
                  46
% identity
                  65
NCBI Description
                 (U12626) copia-like retrotransposon Hopscotch polyprotein
                  [Zea mays]
                  42431
Seq. No.
Seq. ID
                  LIB3170-067-Q1-K1-G9
Method
                  BLASTX
                  q1174867
NCBI GI
BLAST score
                  291
                  3.0e-26
E value
Match length
                  71
                  76
% identity
NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
                  PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
                  KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275)
                  ubiquinol--cytochrome c reductase [Solanum tuberosum]
                  >gi_1094912_prf__2107179A cytochrome c
                  oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
Seq. No.
                  42432
Seq. ID
                  LIB3170-067-Q1-K1-H6
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  8.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  42433
Seq. ID
                  LIB3170-067-Q1-K1-H8
Method
                  BLASTX
NCBI GI
                  g417154
                  402
BLAST score
E value
                  3.0e-39
Match length
                  129
                  67
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
```

Seq. No. 42434

Seq. ID LIB3170-068-Q1-J1-H6

Method BLASTN
NCBI GI g2052028
BLAST score 81
E value 9.0e-38



Match length 87 % identity

NCBI Description G.max mRNA for glutathione transferase

Seq. No.

42435

Seq. ID

LIB3170-068-Q1-K1-B11

Method NCBI GI BLASTN

BLAST score

q256634 45

E value

3.0e-16

Match length % identity

57 46

NCBI Description

KTil=Kunitz trypsin inhibitor KTil, KTi2=Kunitz trypsin

inhibitor KTi2 [soybeans, Genomic, 3269 nt]

Seq. No.

42436

Seq. ID

LIB3170-068-Q1-K1-G11

Method NCBI GI BLASTX q3122602

BLAST score E value

140

Match length

7.0e-09 73

% identity

37

NCBI Description

PEROXISOMAL TARGETING SIGNAL 2 RECEPTOR (PTS2 RECEPTOR)

(PEROXIN-7) >gi_1890657 (U69171) peroxisomal PTS2 receptor

[Mus musculus]

Seq. No.

42437

Seq. ID

LIB3170-069-01-J1-B10

Method NCBI GI BLASTX g2961389

BLAST score

356

E value

1.0e-33

Match length

92

% identity NCBI Description

68 (AL022141) purple acid phosphatase like protein

[Arabidopsis thaliana] >gi 4006925 emb CAB16853 (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana]

Seq. No.

42438

Seq. ID

LIB3170-069-Q1-J1-C12

Method NCBI GI

BLASTN g1431738

BLAST score

104

E value

3.0e-51

Match length

222 91

% identity NCBI Description

Soybean (Glycine max) low MW heat shock protein gene

(Gmhsp17.5-M)

Seq. No.

42439

Seq. ID

LIB3170-069-Q1-J1-D6

Method

BLASTX

NCBI GI

g2213608

BLAST score

213

E value

7.0e-17

Match length

120



% identity 37
NCBI Description (AC000103) F21J9.2 [Arabidopsis thaliana]

Seq. No. 42440

Seq. ID LIB3170-069-Q1-J1-E4

Method BLASTN
NCBI GI g2342957
BLAST score 100
E value 5.0e-49
Match length 128
% identity 95

NCBI Description Glycine tabacina ribulose 1,5-bisphosphate

carboxylase-oxygenase large subunit (rbcL) gene,

choloroplast gene encoding chloroplast protein, partial cds

Seq. No. 42441

Seq. ID LIB3170-069-Q1-J1-G6

Method BLASTN
NCBI GI 9725331
BLAST score 439
E value 0.0e+00
Match length 447
% identity 100

NCBI Description Glycine max mitochondrion polymorphic marker DNA sequence

Seq. No. 42442

Seq. ID LIB3170-069-Q1-K1-A11

Method BLASTN
NCBI GI g168665
BLAST score 173
E value 8.0e-93
Match length 200
% identity 98

NCBI Description Maize 16-kDa zein-2 mRNA, complete cds

Seq. No. 42443

Seq. ID LIB3170-069-Q1-K1-B9

Method BLASTN
NCBI GI g168700
BLAST score 174
E value 4.0e-93
Match length 204
% identity 96

NCBI Description Z.mays zein mRNA, complete cds

Seq. No. 42444

Seq. ID LIB3170-069-Q1-K1-C9

Method BLASTN
NCBI GI g16072
BLAST score 178
E value 2.0e-95
Match length 213
% identity 97

NCBI Description Acetabularia mediterranea zein gene

Seq. No. 42445

Seq. ID LIB3170-069-Q1-K1-D12

BLAST score

E value

104 1.0e-51



```
BLASTN
Method
                   g22528
NCBI GI
                   104
BLAST score
                   1.0e-51
E value
                   215
Match length
                   88
% identity
NCBI Description Zea mays mRNA encoding a zein (clone A20)
                   42446
Sea. No.
                   LIB3170-069-Q1-K1-F12
Seq. ID
                   BLASTN
Method
                   g168484
NCBI GI
                   86
BLAST score
                   1.0e-40
E value
Match length
                   227
                   92
% identity
NCBI Description Maize endosperm glutelin-2 gene, complete cds
                   42447
Seq. No.
                   LIB3170-069-Q1-K1-H10
Seq. ID
                   BLASTN
Method
                   g16072
NCBI GI
                   170
BLAST score
                    9.0e-91
E value
                    212
Match length
                    96
% identity
NCBI Description Acetabularia mediterranea zein gene
                    42448
Seq. No.
                    LIB3170-069-Q1-K1-H11
Seq. ID
                    BLASTN
Method
                    g22531
NCBI GI
                    92
BLAST score
                    3.0e-44
E value
                    123
Match length
                    94
% identity
                    Zea mays mRNA encoding a zein (clone pZ22.1)
NCBI Description
                    >gi_270688_gb_I03336_Sequence 10 from Patent US 4885357
>gi_270741_gb_I03273_Sequence 2 from Patent US
                    42449
 Seq. No.
                    LIB3170-070-Q1-J1-B2
 Seq. ID
                    BLASTN
 Method
                    q18725
 NCBI GI
                    138
 BLAST score
                    1.0e-71
 E value
                    214
 Match length
                    91
 % identity
                    Soybean (G. max) mRNA for proliferating cell nuclear
 NCBI Description
                    antigen (PCNA), partial
 Seq. No.
                    42450
                    LIB3170-070-Q1-J1-B3
 Seq. ID
                    BLASTN
 Method
                    q984307
 NCBI GI
```

6720



Match length 128 % identity 96

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No.

42451

Seq. ID LIB3170-070-Q1-J1-D2

Method BLASTN
NCBI GI g547507
BLAST score 72
E value 2.0e-32
Match length 172
% identity 85

NCBI Description G.max mRNA for glutamine synthetase

Seq. No.

42452

Seq. ID LIB3170-070-Q1-J1-F3

Method BLASTX
NCBI GI g4115377
BLAST score 147
E value 1.0e-09
Match length 40
% identity 65

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.

42453

Seq. ID LIB3170-070-Q1-J1-F4

Method BLASTX
NCBI GI g2465923
BLAST score 273
E value 4.0e-24
Match length 111
% identity 49

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 42454

Seq. ID LIB3170-070-Q1-J1-H5

Method BLASTX
NCBI GI g882341
BLAST score 164
E value 3.0e-11
Match length 58
% identity 55

NCBI Description (U24702) LRP1 [Arabidopsis thaliana]

Seq. No. 42455

Seq. ID LIB3170-070-Q1-K1-E10

Method BLASTN
NCBI GI g14311
BLAST score 84
E value 1.0e-39
Match length 112
% identity 96



NCBI Description G.max chloroplast gene rps19 and flanking regions

Seq. No. 42456

Seq. ID LIB3170-070-Q1-K2-A4

Method BLASTX
NCBI GI g3608175
BLAST score 274
E value 1.0e-24
Match length 82

% identity 73
NCBI Description (AB008186) proliferating cell nuclear antigen [Pisum

sativum] >gi_3821259 emb_CAA77062_ (Y18135) PCNA protein [Nicotiana tabacum] >gi_4379382 emb_CAA76392_ (Y16796) proliferating cell nuclear antigen [Pisum sativum]

Seq. No. 42457

Seq. ID LIB3170-071-Q1-J1-A3

Method BLASTN
NCBI GI g2924257
BLAST score 50
E value 1.0e-19
Match length 78
% identity 46

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 42458

Seq. ID LIB3170-071-Q1-J1-A8

Method BLASTN
NCBI GI g2924257
BLAST score 213
E value 1.0e-116
Match length 257
% identity 48

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 42459

Seq. ID LIB3170-071-Q1-J1-D1

Method BLASTN
NCBI GI g170087
BLAST score 44
E value 1.0e-15
Match length 241
% identity 84

NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)

Seq. No. 42460

Seq. ID LIB3170-071-Q1-J1-D8

Method BLASTX
NCBI GI g3668091
BLAST score 277
E value 1.0e-24
Match length 93
% identity 11

NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 42461

Seq. ID LIB3170-071-Q1-K1-C11

NCBI Description



```
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  43
E value
                  3.0e-15
                  87
Match length
                  87
% identity
NCBI Description Cloning vector pSport1, complete cds
Seq. No.
                  42462
                  LIB3170-071-Q1-K1-F12
Seq. ID
Method
                  BLASTN
                  g497899
NCBI GI
BLAST score
                  48
E value
                  4.0e-18
Match length
                  64
% identity
                  94
NCBI Description
                  Populus trichocarpa * Populus deltoides (clone
                  sam.Pdx.Pt.2) S-adenosyl methionine synthetase mRNA,
                  complete cds
Seq. No.
                  42463
                  LIB3170-072-Q1-J1-C9
Seq. ID
Method
                  BLASTX
                  g4234955
NCBI GI
BLAST score
                  494
                  8.0e-50
E value
                  186
Match length
% identity
                  56
                  (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
NCBI Description
Seq. No.
                  42464
Seq. ID
                  LIB3170-072-Q1-J1-D12
Method
                  BLASTX
NCBI GI
                  g3122858
BLAST score
                  500
                  1.0e-50
E value
Match length
                  126
                  79
% identity
                  D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR
NCBI Description
                  >gi_2189964_dbj_BAA20405 (AB003280) Phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
                  >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  42465
Seq. ID
                  LIB3170-072-Q1-J1-E3
Method
                  BLASTX
NCBI GI
                  g4325345
BLAST score
                  263
E value
                  1.0e-22
Match length
                  91
% identity
                  18
```

N=1) [Arabidopsis thaliana]

(AF128393) similar to thioredoxin-like proteins (Pfam:

PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,



```
Seq. No.
                  42466
Seq. ID
                  LIB3170-072-Q1-J1-G7
Method
                  BLASTN
NCBI GI
                  g336274
BLAST score
                  53
E value
                  6.0e-21
Match length
                  260
                  56
% identity
NCBI Description Alnus incana chloroplast 23S rRNA, 4.5S rRNA, 5S rRNA,
                  tRNA-Arg, and tRNA-Asn genes
                  42467
Seq. No.
Seq. ID
                  LIB3170-072-Q1-K1-B9
Method
                  BLASTN
NCBI GI
                  q310575
BLAST score
                  161
E value
                  2.0e-85
Match length
                  336
% identity
                  89
NCBI Description Glycine max nodulin-26 mRNA, complete cds
Seq. No.
                  42468
                  LIB3170-072-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467124
BLAST score
                  146
                  3.0e-09
E value
Match length
                  98
% identity
                  37
NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]
                  42469
Seq. No.
Seq. ID
                  LIB3170-072-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g4539373
BLAST score
                  123
E value
                  5.0e-11
Match length
                  88
% identity
                  38
                  (AL049525) putative retrotransposon polyprotein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  42470
                  LIB3170-073-Q1-J1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1663542
BLAST score
                  107
E value
                  5.0e-53
Match length
                  267
                  86
% identity
NCBI Description Glycine max clone RLG4a disease resistance protein homolog
                  gene, partial cds
```

Seq. No. 42471

Seq. ID LIB3170-073-Q1-J1-A3

Method BLASTN NCBI GI g1305548



```
66
BLAST score
                  5.0e-29
E value
                  155
Match length
                  86
% identity
NCBI Description Glycine max asparagine synthetase mRNA, complete cds
                  42472
Seq. No.
                  LIB3170-073-Q1-J1-B9
Seq. ID
                  BLASTX
Method
                  q4432814
NCBI GI
                  247
BLAST score
                  5.0e-21
E value
                  87
Match length
                  56
% identity
NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]
                  42473
Seq. No.
                  LIB3170-073-Q1-J1-D8
Seq. ID
                  BLASTX
Method
                  g1353166
NCBI GI
                  311
BLAST score
                  2.0e-28
E value
                  148
Match length
                   45
% identity
NCBI Description HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III
                  >gi_1055058 (U39850) coded for by C. elegans cDNA cm5h3;
                   weakly similar to PIR:A43289 human CDC4 homolog CDC4L
                   [Caenorhabditis elegans]
                   42474
Seq. No.
                   LIB3170-073-Q1-J1-E10
Seq. ID
                   BLASTX
Method
                   g2244802
NCBI GI
                   151
BLAST score
                   8.0e-10
E value
                   106
Match length
                   35
% identity
                   (Z97336) retrovirus-related polyprotein homolog
NCBI Description
                   [Arabidopsis thaliana]
                   42475
Seq. No.
                   LIB3170-073-Q1-K1-G1
 Seq. ID
                   BLASTX
Method
                   g629693
NCBI GI
BLAST score
                   214
                   1.0e-17
E value
                   62
Match length
 % identity
                   probable integrase - common tobacco (fragment)
NCBI Description
                   >gi_530742_emb_CAA56791_ (X80830) integrase [Nicotiana
```

tabacum]

Seq. ID LIB3170-073-Q1-K1-H4

42476

Method BLASTX
NCBI GI g1370287
BLAST score 205

Seq. No.



```
3.0e-16
E value
Match length
                  66
                  58
% identity
                 (Z73553) core protein [Pisum sativum]
NCBI Description
                  42477
Seq. No.
                  LIB3170-074-Q1-J1-B2
Seq. ID
                  BLASTX
Method
                  q3953470
NCBI GI
                  155
BLAST score
                  2.0e-10
E value
                   47
Match length
                   62
% identity
NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]
                   42478
Seq. No.
                   LIB3170-074-Q1-J1-G6
Seq. ID
                   BLASTX
Method
                   q1788132
NCBI GI
                   142
BLAST score
                   1.0e-08
E value
                   58
Match length
                   47
% identity
                  (AE000277) putative transport protein [Escherichia coli]
NCBI Description
                   42479
Seq. No.
                   LIB3170-074-Q1-J1-H4
Seq. ID
                   BLASTX
Method
                   g1781348
NCBI GI
                   244
BLAST score
                   6.0e-21
E value
                   75
Match length
                   64
% identity
                   (Y10380) homologous to plastidic aldolases [Solanum
NCBI Description
                   tuberosum]
                   42480
Seq. No.
                   LIB3170-075-Q1-K1-G12
Seq. ID
                   BLASTX
Method
                   q1657617
NCBI GI
                   276
BLAST score
                   1.0e-24
E value
                   74
Match length
                   73
 % identity
                   (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236)
NCBI Description
                   putative nuclear DNA-binding protein G2p [Arabidopsis
                   thaliana]
                   42481
 Seq. No.
                   LIB3170-075-Q1-K2-A1
 Seq. ID
 Method
                   BLASTN
                   q529396
 NCBI GI
                   215
 BLAST score
 E value
                   1.0e-117
                   407
 Match length
 % identity
 NCBI Description Human pancreatic amylase (amy2A) mRNA, complete cds.
```



>gi_4502084_ref_NM_000699.1_AMY2A_ Homo sapiens amylase, alpha 2A; pancreatic (AMY2A) mRNA

Seq. No. 42482 Seq. ID LIB3170-075-Q1-K2-A4 Mathod BLASTN

Method BLASTN
NCBI GI g11768
BLAST score 69
E value 2.0e-30
Match length 233
% identity 82

NCBI Description Chloroplast N. tabacum ATPase alpha subunit gene

Seq. No. 42483

Seq. ID LIB3170-075-Q1-K2-B1

Method BLASTN
NCBI GI g164047
BLAST score 154
E value 4.0e-81
Match length 374
% identity 85

NCBI Description Canine lipase mRNA, complete cds

Seq. No. 42484

Seq. ID LIB3170-075-Q1-K2-E2

Method BLASTN
NCBI GI 94322254
BLAST score 36
E value 7.0e-11
Match length 85
% identity 92

NCBI Description Corythophora alta rp120-5'-rps12 intergenic region,

chloroplast sequence

Seq. No. 42485

Seq. ID LIB3170-076-Q1-J1-C12

Method BLASTX
NCBI GI g4376203
BLAST score 214
E value 4.0e-17
Match length 63
% identity 57

NCBI Description (U35226) putative cytochrome P-450 [Nicotiana

plumbaginifolia]

Seq. No. 42486

Seq. ID LIB3170-076-Q1-J1-C6

Method BLASTX
NCBI GI g2961389
BLAST score 363
E value 2.0e-34
Match length 98
% identity 66

NCBI Description (AL022141) purple acid phosphatase like protein

[Arabidopsis thaliana] >gi_4006925_emb_CAB16853_ (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana]



```
Seq. No.
                  42487
Seq. ID
                  LIB3170-076-Q1-J1-D9
                  BLASTX
Method
NCBI GI
                  g2632252
BLAST score
                  265
E value
                  4.0e-23
Match length
                  145
% identity
                  43
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]
Seq. No.
                  42488
                  LIB3170-076-Q1-J1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3319342
BLAST score
                  143
                  2.0e-09
E value
Match length
                  39
                  39
% identity
NCBI Description
                  (AF077407) similar to mitochondrial carrier proteins (Pfam:
                  mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis
                  thaliana]
Seq. No.
                  42489
Seq. ID
                  LIB3170-076-Q1-J1-F10
Method
                  BLASTX
NCBI GI
                  g3342249
BLAST score
                  233
                  2.0e-19
E value
Match length
                  98
                  50
% identity
NCBI Description (AF047719) GA3 [Arabidopsis thaliana] >gi_3342251
                  (AF047720) GA3 [Arabidopsis thaliana]
Seq. No.
                  42490
Seq. ID
                  LIB3170-076-Q1-J1-F9
Method
                  BLASTX
NCBI GI
                  g4325354
BLAST score
                  302
E value
                  4.0e-28
Match length
                  103
                  58
% identity
NCBI Description
                  (AF128395) contains similarity to retrovirus-related
                  polyproteins and to CCHC zinc finger protein (Pfam:
                  PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]
Seq. No.
                  42491
Seq. ID
                  LIB3170-076-Q1-J1-H6
Method
                  BLASTN
NCBI GI
                  g170067
BLAST score
                  49
E value
                  8.0e-19
Match length
                  153
% identity
                  83
NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)
                  gene, complete cds
```

42492

Seq. No.



```
LIB3170-076-Q1-K1-A4
Seq. ID
                  BLASTX
Method
                  g2129840
NCBI GI
                  143
BLAST score
                  4.0e-09
E value
                  49
Match length
                  63
% identity
                  nucleosome assembly protein 1 - soybean >gi_1161252
NCBI Description
                  (L38856) nucleosome assembly protein 1 [Glycine max]
                  42493
Seq. No.
                  LIB3170-076-Q1-K1-F10
Seq. ID
                  BLASTX
Method
                  g3342253
NCBI GI
BLAST score
                   392
                   4.0e-38
E value
                   122
Match length
% identity
                   61
NCBI Description (AF047721) GA3 [Arabidopsis thaliana]
                   42494
Seq. No.
                   LIB3170-076-Q1-K1-H8
Seq. ID
                   BLASTN
Method
                   g170067
NCBI GI
BLAST score
                   80
                   5.0e-37
E value
Match length
                   308
                   84
% identity
NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP3)
                   gene, complete cds
                   42495
Seq. No.
                   LIB3170-077-Q1-J1-G10
Seq. ID
                   BLASTN
Method
                   g456713
NCBI GI
                   116
BLAST score
                   9.0e-59
E value
                   228
Match length
                   88
 % identity
NCBI Description Glycine max gene for ubiquitin, complete cds
                   42496
 Seq. No.
                   LIB3170-077-Q1-J1-H11
 Seq. ID
                   BLASTX
 Method
                   g4454307
 NCBI GI
                   164
 BLAST score
                   3.0e-11
 E value
                   56
 Match length
                   55
 % identity
                   (AJ132763) cyclophilin [Pseudotsuga menziesii]
 NCBI Description
                   42497
 Seq. No.
                   LIB3170-077-Q1-K1-C4
 Seq. ID
                   BLASTN
 Method
                   q609224
 NCBI GI
                   101
 BLAST score
```

1.0e-49

E value



Match length 87 % identity

NCBI Description P.sativum mRNA for SAMS-2 >gi 609558 gb L36681 PEADENSYNB

Pisum sativum S-adenosylmethionine synthase mRNA, complete

Seq. No. 42498

LIB3170-077-Q1-K1-E4 Seq. ID

Method BLASTX NCBI GI g1654140 BLAST score 178 E value 4.0e-13 Match length 53 % identity 72

NCBI Description (U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No. Seq. ID

42499 LIB3170-077-Q1-K1-E7

Method BLASTN NCBI GI g18729 BLAST score 91 1.0e-43 E value Match length 262 % identity 84

NCBI Description Soybean (Glycine max) 18S ribosomal RNA

Seq. No.

42500 LIB3170-077-Q1-K1-E9 Seq. ID

Method BLASTN NCBI GI g1209887

BLAST score 41 7.0e-14 E value Match length 117 % identity 84

NCBI Description Glycine max nonsymbiotic hemoglobin gene, complete cds

Seq. No.

42501

LIB3170-077-Q1-K1-H3 Seq. ID

Method BLASTX NCBI GI g2832709 BLAST score 507 E value 1.0e-51 Match length 114 % identity 83

(AL021713) neoxanthin cleavage enzyme-like protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 42502

Seq. ID LIB3170-078-Q1-J1-E2

Method BLASTN NCBI GI g14311 BLAST score 83 3.0e-39 E value Match length 123 % identity 92

NCBI Description G.max chloroplast gene rps19 and flanking regions

Method

NCBI GI

BLASTN g3063391



```
42503
Seq. No.
                  LIB3170-078-Q1-J1-H12
Seq. ID
                  BLASTX
Method
                  q4467151
NCBI GI
                  203
BLAST score
                  7.0e-16
E value
                  50
Match length
                  74
% identity
                 (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   42504
Seq. No.
                  LIB3170-078-Q1-J1-H3
Seq. ID
                  BLASTX
Method
                   g2342676
NCBI GI
                   157
BLAST score
                   4.0e-11
E value
                   34
Match length
                   82
% identity
                   (AC000106) Strong similarity to Oryza NADPH oxidase
NCBI Description
                   (gb_X93301). [Arabidopsis thaliana]
                   42505
Seq. No.
                   LIB3170-078-Q1-K1-C8
Seq. ID
                   BLASTX
Method
                   g167367
NCBI GI
                   196
BLAST score
                   3.0e-15
E value
                   89
Match length
                   46
% identity
                   (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   42506
Seq. No.
                   LIB3170-078-Q1-K1-E2
Seq. ID
                   BLASTN
Method
                   g12212
NCBI GI
                   66
BLAST score
                   6.0e-29
E value
                   172
Match length
                   87
% identity
                   S.alba chloroplast rp123 and rp12 genes for ribosomal
NCBI Description
                   proteins L23 and L2
                   42507
Seq. No.
                   LIB3170-078-Q1-K1-F10
Seq. ID
                   BLASTX
Method
                   q2443890
NCBI GI
                   172
BLAST score
                   3.0e-12
E value
                   36
Match length
                   89
 % identity
                    (AC002294) similar to NAM (gp_X92205_1321924) and CUC2
 NCBI Description
                    (gp_AB002560_1944132) proteins [Arabidopsis thaliana]
                    42508
 Seq. No.
                   LIB3170-078-Q1-K1-H11
 Seq. ID
```

6731



```
BLAST score
E value
                  7.0e-11
Match length
                  80
% identity
                  86
NCBI Description Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds
                  42509
Seq. No.
                  LIB3170-079-Q1-J1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1346882
BLAST score
                  162
                  3.0e-11
E value
Match length
                  50
% identity
                  64
NCBI Description PHYTOENE SYNTHASE PRECURSOR (MEL5) >gi 2129505 pir S56668
                  geranylgeranyl-diphosphate geranylgeranyltransferase (EC
                  2.5.1.32) precursor - muskmelon >gi 870985 emb CAA85775
                  (Z37543) phytoene synthase [Cucumis melo]
                  42510
Seq. No.
                  LIB3170-079-Q1-J1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914055
                 167
BLAST score
                  2.0e-11
E value
                  88
Match length
% identity
                  41
NCBI Description
                  MUTS PROTEIN HOMOLOG 4 >gi 2463653 (U89293) MSH4 [Homo
                  sapiens] >gi 4505251_ref NP 002431.1 pMSH4 mutS (E. coli)
                  homolog
                  42511
Seq. No.
Seq. ID
                  LIB3170-079-Q1-J1-D3
Method
                  BLASTN
NCBI GI
                  g18764
BLAST score
                  59
E value
                  2.0e-24
                  111
Match length
                  90
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                  42512
Seq. ID
                  LIB3170-079-Q1-J1-G7
                  BLASTN
Method
NCBI GI
                  q18764
BLAST score
                  46
E value
                  1.0e-16
Match length
                  162
% identity
                  82
NCBI Description G.max tefS1 gene for elongation factor EF-la
```

Seq. No. 42513

Seq. ID LIB3170-079-Q1-J1-H2

Method BLASTX NCBI GI g3786006 BLAST score 145 3.0e-09 E value



```
Match length
% identity
                  46
                  (AC005499) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                  LIB3170-079-Q1-K1-A9
Method
                  BLASTN
NCBI GI
                  g531828
BLAST score
                  54
                  1.0e-21
E value
Match length
                  90
% identity
                  90
NCBI Description Cloning vector pSport1, complete cds
                  42515
Seq. No.
                  LIB3170-079-Q1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170089
BLAST score
                  103
                   7.0e-51
E value
                  218
Match length
                  88
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                  42516
Seq. No.
                  LIB3170-079-Q1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4455338
BLAST score
                   155
                   2.0e-10
E value
Match length
                   39
                   67
% identity
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   42517
                   LIB3170-079-Q1-K1-G6
Seq. ID
                   BLASTN
Method
                   q18764
NCBI GI
                   81
BLAST score
                   1.0e-37
E value
                   277
Match length
                   86
% identity
                  G.max tefS1 gene for elongation factor EF-1a
NCBI Description
                   42518
Seq. No.
                   LIB3170-080-Q1-J1-F10
Seq. ID
                   BLASTX
Method
                   g4185513
NCBI GI
BLAST score
                   233
                   2.0e-19
E value
                   63
Match length
                   73
% identity
                   (AF102823) actin depolymerizing factor 5 [Arabidopsis
NCBI Description
                   thaliana] >gi_4185517 (AF102825) actin depolymerizing
```

Seq. No. 42519

factor 5 [Arabidopsis thaliana]



LIB3170-080-Q1-J1-F11 Seq. ID BLASTX Method g2851508 NCBI GI 167 BLAST score 6.0e-16 E value 76 Match length 59 % identity 60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to NCBI Description ribosomal protein L21 (gb L38 $\overline{8}$ 26). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana] 42520 Seq. No. LIB3170-080-Q1-K1-C8 Seq. ID BLASTN Method g343648 NCBI GI 76 BLAST score 1.0e-34 E value 180 Match length % identity 86 Vigna unguiculata chloroplast ribosomal protein (L16 and NCBI Description L14) genes, 3' and 5' end respectively 42521 Seq. No. LIB3170-080-Q1-K1-F12 Seq. ID BLASTX Method g2642158 NCBI GI 270 BLAST score 6.0e-24 E value 111 Match length 52 % identity (AC003000) hypothetical protein [Arabidopsis thaliana] NCBI Description 42522 Seq. No. LIB3170-080-Q1-K1-G3 Seq. ID BLASTX Method g3834302 NCBI GI 442 BLAST score 5.0e-44 E value 117 Match length % identity 79 (AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase NCBI Description from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from this gene. [Arabidopsis tha liana] 42523 Seq. No. LIB3170-080-Q1-K1-G4 Seq. ID BLASTX Method q3834302 NCBI GI 172

BLAST score 2.0e-12 E value 46 Match length 76 % identity NCBI Description

(AC005679) Similar to gb D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from

this gene. [Arabidopsis thaliana]

Seq. ID Method



```
42524
Seq. No.
                  LIB3170-081-Q1-J1-B11
Seq. ID
                  BLASTX
Method
                  g4559342
NCBI GI
                  237
BLAST score
                  8.0e-20
E value
                  63
Match length
% identity
                  (AC007087) putative copper methylamine oxidase [Arabidopsis
NCBI Description
                  thaliana]
                  42525
Seq. No.
                  LIB3170-081-Q1-J1-B4
Seq. ID
Method
                  BLASTX
                  g4006828
NCBI GI
                  226
BLAST score
                  2.0e-18
E value
                  134
Match length
                  32
% identity
NCBI Description (AC005970) putative reverse transcriptase [Arabidopsis
                  thaliana]
                   42526
Seq. No.
                  LIB3170-081-Q1-J1-B5
Seq. ID
                  BLASTX
Method
                   g3935168
NCBI GI
                   163
BLAST score
                   4.0e-11
E value
                   58
Match length
                   48
% identity
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]
                   42527
Seq. No.
                   LIB3170-081-Q1-J1-C11
Seq. ID
                   BLASTX
Method
                   g2388586
NCBI GI
                   444
BLAST score
                   4.0e-44
E value
                   152
Match length
% identity
                   57
                   (AC000098) Similar to Saccharomyces RAD16 (gb_X78993).
NCBI Description
                   [Arabidopsis thaliana]
                   42528
Seq. No.
                   LIB3170-081-Q1-J1-F4
Seq. ID
                   BLASTN
Method
                   g1695795
NCBI GI
BLAST score
                   51
                   1.0e-19
E value
Match length
                   150
                   89
 % identity
NCBI Description Pisum sativum 18S small subunit nuclear ribosomal RNA gene
                   42529
 Seq. No.
```

6735

LIB3170-081-Q1-J1-H3

BLASTX

Method

NCBI GI

BLASTX

q4263831

```
NCBI GI
                  q1223784
BLAST score
                  154
E value
                  3.0e-10
Match length
                  49
% identity
                  57
NCBI Description (X96475) alpha-tubulin [Reticulomyxa filosa]
Seq. No.
                  42530
                  LIB3170-081-Q1-K1-B7
Seq. ID
Method
                  BLASTX
                  g3023713
NCBI GI
BLAST score
                  228
                  7.0e-25
E value
Match length
                  96
% identity
                  67
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372
                  (U09450) enolase [Oryza sativa]
Seq. No.
                  42531
                  LIB3170-081-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2920666
BLAST score
                  205
                  2.0e-16
E value
Match length
                  73
% identity
                  58
                  (AF048978) 2,4-D inducible glutathione S-transferase
NCBI Description
                  [Glycine max]
Seq. No.
                  42532
Seq. ID
                  LIB3170-081-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  q629693
BLAST score
                  164
E value
                  8.0e-12
Match length
                  70
% identity
                  44
                  probable integrase - common tobacco (fragment)
NCBI Description
                  >gi 530742 emb CAA56791 (X80830) integrase [Nicotiana
                  tabacum]
Seq. No.
                  42533
Seq. ID
                  LIB3170-082-Q1-J1-B2
                  BLASTN
Method
NCBI GI
                  q2687430
BLAST score
                  38
E value
                  1.0e-12
Match length
                  42
                  98
% identity
NCBI Description Acorus gramineus large subunit 26S ribosomal RNA gene,
                  partial sequence
Seq. No.
                  42534
Seq. ID
                  LIB3170-082-Q1-J1-B4
```

% identity

41



```
BLAST score
E value
                   8.0e-09
Match length
                  73
                  41
% identity
NCBI Description
                  (AC006067) putative reverse transcriptase [Arabidopsis
                  42535
Seq. No.
                  LIB3170-082-Q1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2920665
BLAST score
                  241
E value
                  1.0e-133
Match length
                  280
% identity
                  97
NCBI Description Glycine max 2,4-D inducible glutathione S-transferase
                  (GSTa) mRNA, complete cds
Seq. No.
                  42536
Seq. ID
                  LIB3170-082-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3297823
BLAST score
                  265
E value
                  1.0e-26
Match length
                  123
% identity
                  46
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                  42537
Seq. ID
                  LIB3170-083-Q1-J1-B12
Method
                  BLASTN
NCBI GI
                  g725331
BLAST score
                  545
                  0.0e + 00
E value
Match length
                  565
% identity
                  99
NCBI Description Glycine max mitochondrion polymorphic marker DNA sequence
Seq. No.
                  42538
Seq. ID
                  LIB3170-083-Q1-J1-B2
Method
                  BLASTN
NCBI GI
                  g1370200
BLAST score
                  140
E value
                  9.0e-73
                  204
Match length
                  92
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC2
Seq. No.
                  42539
Seq. ID
                  LIB3170-083-Q1-J1-B4
Method
                  BLASTX
NCBI GI
                  g1351033
BLAST score
                  167
E value
                  1.0e-11
Match length
                  111
```

NCBI Description STEM 31 KD GLYCOPROTEIN PRECURSOR (VEGETATIVE STORAGE



PROTEIN VSP25) >gi_170088 (M20037) vegetative storage protein [Glycine max]

Seq. No. 42540

Seq. ID LIB3170-083-Q1-J1-C1

Method BLASTN
NCBI GI g3334857
BLAST score 237
E value 1.0e-130
Match length 474

% identity 77 NCBI Description Solanum tuberosum mitochondrial trnC, trnN1, trnY, nad2

genes

Seq. No. 42541

Seq. ID LIB3170-083-Q1-J1-C11

Method BLASTX
NCBI GI g3128177
BLAST score 146
E value 3.0e-09
Match length 59
% identity 51

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 42542

Seq. ID LIB3170-083-Q1-J1-C3

Method BLASTX
NCBI GI g2982459
BLAST score 198
E value 4.0e-15
Match length 76
% identity 53

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3170-083-Q1-J1-C5

42543

Method BLASTX
NCBI GI g3269282
BLAST score 155
E value 3.0e-10
Match length 107
% identity 39

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 42544

Seq. ID LIB3170-083-Q1-J1-C9

Method BLASTX
NCBI GI g4510375
BLAST score 162
E value 7.0e-11
Match length 90
% identity 49

NCBI Description (AC007017) putative homeotic protein BEL1 [Arabidopsis

thaliana]

Seq. No. 42545

Seq. ID LIB3170-083-Q1-J1-E1

6738

BLAST score

E value

332 4.0e-31



```
BLASTX
Method
                  g3650035
NCBI GI
                  285
BLAST score
E value
                  2.0e-25
Match length
                  145
                  42
% identity
                  (AC005396) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                   42546
Seq. No.
                  LIB3170-083-Q1-J1-G4
Seq. ID
                  BLASTN
Method
                  g547507
NCBI GI
                   68
BLAST score
E value
                   4.0e-30
Match length
                   147
                   87
% identity
NCBI Description G.max mRNA for glutamine synthetase
                   42547
Seq. No.
                   LIB3170-084-Q1-J1-B5
Seq. ID
                   BLASTN
Method
                   g849135
NCBI GI
                   99
BLAST score
                   3.0e-48
E value
Match length
                   183
                   97
% identity
                   Vigna radiata vacuolar H+-ATPase subunit A mRNA, complete
NCBI Description
                   42548
Seq. No.
                   LIB3170-084-Q1-J1-G2
Seq. ID
                   BLASTN
Method
                   g2924257
NCBI GI
                   131
BLAST score
                   2.0e-67
E value
                   443
Match length
                   41
% identity
NCBI Description Tobacco chloroplast genome DNA
                   42549
Seq. No.
                   LIB3170-084-Q1-J1-G6
Seq. ID
                   BLASTX
Method
                   g541943
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
                   39
Match length
                   77
% identity
                   metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                   metallothionein-like protein [Glycine max]
Seq. No.
                   42550
                   LIB3170-084-Q1-K1-C2
Seq. ID
                   BLASTX
Method
                   g2129889
NCBI GI
```

6739



```
Match length
                   74
 % identity
 NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
 Seq. No.
                   42551
                   LIB3170-084-Q1-K1-E10
 Seq. ID
                   BLASTN
 Method
                   q169974
 NCBI GI
                   114
 BLAST score
 E value
                   1.0e-57
                   170
 Match length
                   92
 % identity
 NCBI Description Glycine max vspA gene, complete cds
                    42552
 Seq. No.
                   LIB3170-084-Q1-K1-F12
 Seq. ID
                    BLASTX
 Method
                    g1769897
 NCBI GI
                    237
 BLAST score
                    4.0e-20
 E value
 Match length
                    98
 % identity
                    45
 NCBI Description (Y08010) lectin receptor kinase [Arabidopsis thaliana]
                    42553
 Seq. No.
                    LIB3170-084-Q1-K1-G2
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g170089
 BLAST score
                    180
                    1.0e-96
 E value
                    298
 Match length
                    91
 % identity
 NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                    42554
 Seq. No.
                    LIB3170-085-Q1-J1-D4
  Seq. ID
 Method
                    BLASTX
                    g2388710
 NCBI GI
                    283
  BLAST score
                    4.0e-25
  E value
                    93
  Match length
                    49
  % identity
                    (AF017150) betaine aldehyde dehydrogenase [Amaranthus
  NCBI Description
                    hypochondriacus]
                    42555
  Seq. No.
                    LIB3170-085-Q1-J1-D5
  Seq. ID
                    BLASTX
  Method
                    g2618686
  NCBI GI
                    351
  BLAST score
                    4.0e-33
  E value
  Match length
                    89
  % identity
                    72
                    (AC002510) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
```

Seq. No. 42556

Seq. ID LIB3170-085-Q1-J1-E4

Ĵ



Method BLASTN
NCBI GI g2905775
BLAST score 148
E value 7.0e-78
Match length 207
% identity 93
NCBI Description Glycine

NCBI Description Glycine max HMG-1-like protein mRNA, partial cds

Seq. No.

42557

Seq. ID LIB3170-085-Q1-K1-E3 Method BLASTN

NCBI GI g310568
BLAST score 34
E value 1.0e-09
Match length 58
% identity 90

NCBI Description Glycine max homeobox-containing (Sbh1) mRNA, complete cds

Seq. No.

42558

Seq. ID LIB3170-085-Q1-K1-E4

Method BLASTN
NCBI GI g18644
BLAST score 211
E value 1.0e-115
Match length 266
% identity 95

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No.

42559

Seq. ID LIB3170-085-Q1-K1-F12

Method BLASTN
NCBI GI g4039114
BLAST score 144
E value 3.0e-75
Match length 328
% identity 87

NCBI Description Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds

Seq. No.

42560

Seq. ID LIB3170-086-Q1-J1-E2

Method BLASTN
NCBI GI g3142328
BLAST score 301
E value 1.0e-169
Match length 413
% identity 93

NCBI Description Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat,

complete sequence

Seq. No. 42561

Seq. ID LIB3170-086-Q1-J1-F8

Method BLASTX
NCBI GI g632064
BLAST score 168
E value 1.0e-11
Match length 86



```
% identity
                  hypothetical protein - wheat >gi_530779_emb_CAA55731_
NCBI Description
                  (X79130) unnamed protein product [Triticum aestivum]
Seq. No.
                  42562
                  LIB3170-086-Q1-K1-E1
Seq. ID
Method
                  BLASTN
                  q2924257
NCBI GI
                  184
BLAST score
                  4.0e-99
E value
Match length
                  356
                  88
% identity
                  Tobacco chloroplast genome DNA
NCBI Description
                  42563
Seq. No.
Seq. ID
                  LIB3170-086-Q1-K1-G2
Method
                  BLASTN
NCBI GI
                   q3142328
                   308
BLAST score
                   1.0e-173
E value
                   372
Match length
% identity
                   Glycine max partial SIRE-1 sequence ribonuclease H and
NCBI Description
                   envelope-like genes, partial cds, and long terminal repeat,
                   complete sequence
Seq. No.
                   42564
                   LIB3170-087-Q1-J1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3763917
BLAST score
                   141
                   1.0e-08
E value
Match length
                   46
                   54
% identity
                   (AC004450) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4531438 gb AAD22123.1 AC006224_5 (AC006224)
                   hypothetical protein [Arabidopsis thaliana]
                   42565
Seq. No.
                   LIB3170-087-Q1-J1-B8
Seq. ID
Method
                   BLASTX
                   q3135543
NCBI GI
BLAST score
                   269
                   6.0e-24
E value
                   78
Match length
                   67
% identity
                   (AF062393) aquaporin [Oryza sativa]
NCBI Description
                   42566
Seq. No.
                   LIB3170-087-Q1-K1-G10
 Seq. ID
                   BLASTX
Method
                   g1172811
NCBI GI
                   179
BLAST score
```

6742

NCBI Description 60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)

5.0e-15

84

54

E value

Match length

% identity

NCBI Description



>gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic
- rice >gi_575355_emb_CAA57339_ (X81691) putative tumor
suppresser [Oryza sativa]

42567 Seq. No. LIB3170-087-Q1-K1-G12 Seq. ID BLASTN Method g468055 NCBI GI 102 BLAST score 3.0e-50 E value 289 Match length 84 % identity NCBI Description Zea mays B73 QM protein mRNA, complete cds Seq. No. 42568 LIB3170-087-Q1-K1-G9 Seq. ID BLASTN Method g468055 NCBI GI 195 BLAST score 1.0e-105 E value 363 Match length 88 % identity Zea mays B73 QM protein mRNA, complete cds NCBI Description 42569 Seq. No. LIB3170-087-Q1-K1-H9 Seq. ID BLASTX Method g3811007 NCBI GI 237 BLAST score 1.0e-29 E value 114 Match length 62 % identity (AB019327) NADP specific isocitrate dehydrogenase [Daucus NCBI Description carota] 42570 Seq. No. LIB3170-088-Q1-J1-C2 Seq. ID Method BLASTN g2924257 NCBI GI BLAST score 100 4.0e-49 E value 184 Match length 89 % identity NCBI Description Tobacco chloroplast genome DNA 42571 Seq. No. LIB3170-088-Q1-K1-A11 Seq. ID BLASTX Method NCBI GI g549063 292 BLAST score E value 2.0e-26 67 Match length % identity 79

6743

21kd polypeptide [Oryza sativa]

TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)



```
42572
Seq. No.
                  LIB3170-088-Q1-K1-B10
Seq. ID
Method
                  BLASTN
                  q236729
NCBI GI
                  156
BLAST score
                  2.0e-82
E value
                  300
Match length
                  100
% identity
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
                  42573
Seq. No.
                  LIB3170-088-Q1-K1-B11
Seq. ID
Method
                  BLASTX
                  g1345978
NCBI GI
BLAST score
                  531
                   2.0e-54
E value
Match length
                   110
                   82
% identity
                  OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi 457631 (L29214) omega-6 desaturase [Brassica napus]
                   42574
Seq. No.
                   LIB3170-088-Q1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3894193
                   192
BLAST score
                   1.0e-14
E value
                   99
Match length
                   38
% identity
                   (AC005662) putative strictosidine synthase [Arabidopsis
NCBI Description
                   thaliana]
                   42575
Seq. No.
                   LIB3170-088-Q1-K1-B7
Seq. ID
                   BLASTN
Method
                   g710349
NCBI GI
                   53
BLAST score
                   6.0e-21
E value
                   137
Match length
                   85
 % identity
                   Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA,
NCBI Description
                   complete cds
                   42576
Seq. No.
                   LIB3170-088-Q1-K1-C10
 Seq. ID
                   BLASTN
Method
                   g3789951
NCBI GI
                   114
BLAST score
                   2.0e-57
 E value
                   296
Match length
 % identity
                   87
                   Oryza sativa chlorophyll a/b-binding protein presursor
 NCBI Description
                    (Cab27) mRNA, nuclear gene encoding chloroplast protein,
```

Seq. No. 42577

complete cds

BLAST score

E value

268

6.0e-24



```
LIB3170-088-Q1-K1-C12
Seq. ID
                  BLASTN
Method
                  g2285801
NCBI GI
                  33
BLAST score
                  6.0e-09
E value
                  65
Match length
                  88
% identity
                  Spinacia oleracea mRNA for 26S proteasome alpha subunit,
NCBI Description
                  complete cds
                  42578
Seq. No.
                  LIB3170-088-Q1-K1-C6
Seq. ID
                  BLASTX
Method
                  g4218120
NCBI GI
BLAST score
                  176
                  8.0e-13
E value
Match length
                  63
                  57
% identity
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   42579
Seq. No.
                  LIB3170-088-Q1-K1-C8
Seq. ID
                  BLASTN
Method
                   g2924257
NCBI GI
BLAST score
                   37
                   2.0e-11
E value
Match length
                   85
% identity
                   86
NCBI Description Tobacco chloroplast genome DNA
                   42580
Seq. No.
                   LIB3170-088-Q1-K1-D11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3925232
                   299
BLAST score
                   1.0e-167
E value
                   403
Match length
                   95
% identity
NCBI Description Zea mays putative peroxidase P7X mRNA, partial cds
                   42581
Seq. No.
                   LIB3170-088-Q1-K1-D9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1235570
BLAST score
                   125
                   7.0e-64
E value
Match length
                   215
                   92
% identity
NCBI Description P.anserina sul2 gene
Seq. No.
                   42582
                   LIB3170-088-Q1-K1-F11
Seq. ID
                   BLASTX
Method
                   g482311
NCBI GI
```



```
Match length
% identity
                  74
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  42583
Seq. ID
                  LIB3170-088-Q1-K1-F2
Method
                  BLASTN
NCBI GI
                  q12387
```

BLAST score 39 E value 1.0e-12 Match length 51

% identity 94

NCBI Description Vicia faba chloroplast tRNA-Leu, tRNA-Phe, tRNA-His, ORFX,

NADH-deydrogenase genes & partial sequence ORFx & psbA

genes

Seq. No. 42584 Seq. ID LIB3170-088-Q1-K1-F9 Method BLASTN g1498052 NCBI GI BLAST score 390 E value 0.0e+00Match length 394

NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds

Seq. No.

% identity

42585 Seq. ID LIB3170-088-Q1-K1-G12

100

Method BLASTX NCBI GI g3559935 BLAST score 344 2.0e-32 E value Match length 88 % identity 73

NCBI Description (AJ005253) ClpP protease [Mus musculus]

>gi 4454289 emb CAA09966 (AJ012249) ClpP protease [Mus

musculus]

Seq. No. 42586

LIB3170-088-Q1-K1-G9 Seq. ID

Method BLASTX NCBI GI g3549652 BLAST score 326 E value 2.0e-30 Match length 72 % identity 90

NCBI Description (AJ224982) MAP3K epsilon protein kinase [Arabidopsis

thaliana]

42587 Seq. No.

Seq. ID LIB3170-088-Q1-K1-H10

Method BLASTX NCBI GI g2072023 BLAST score 243 E value 1.0e-20



```
Match length
                  71
% identity
                  (U93506) symbiosis-related protein [Laccaria bicolor]
NCBI Description
                  42588
Seq. No.
                  LIB3170-088-Q1-K1-H12
Seq. ID
                  BLASTX
Method
                  q1261917
NCBI GI
                  250
BLAST score
E value
                  2.0e-21
                  97
Match length
% identity
                  49
                  (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
NCBI Description
Seq. No.
                  42589
                  V4L-01-Q1-B1-B3
Seq. ID
Method
                  BLASTX
                  g2760323
NCBI GI
BLAST score
                  287
                   8.0e-26
E value
Match length
                   54
% identity
                   39
                  (AC002130) F1N21.8 [Arabidopsis thaliana]
NCBI Description
                   42590
Seq. No.
                   V4L-01-Q1-B1-C8
Seq. ID
Method
                   BLASTX
                   g4538920
NCBI GI
BLAST score
                   374
                   5.0e-36
E value
Match length
                   83
% identity
                   44
                   (AL049483) nitrogen fixation like protein [Arabidopsis
NCBI Description
                   thaliana]
                   42591
Seq. No.
                   V4L-02-Q1-B1-D1
Seq. ID
                   BLASTN
Method
                   g20672
NCBI GI
BLAST score
                   52
                   2.0e-20
E value
                   154
Match length
                   83
% identity
NCBI Description Pea cap mRNA for carbonic anhydrase (EC 4.2.1.1)
                   42592
Seq. No.
                   V4L-02-Q1-E1-E1
Seq. ID
                   BLASTX
Method
                   g3892057
NCBI GI
BLAST score
                   152
                   4.0e-10
E value
Match length
                   37
                   81
% identity
                   (AC002330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

6747

42593

V4R-01-Q1-B1-A11

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                  q3212848
BLAST score
                  319
                  1.0e-29
E value
                  110
Match length
% identity
                  (AC004005) putative inositol polyphosphate-5-phosphatase
NCBI Description
                   [Arabidopsis thaliana]
                  42594
Seq. No.
                  V4R-01-Q1-B1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q56539
BLAST score
                  91
                  1.0e-43
E value
                  226
Match length
% identity
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi 206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   42595
Seq. No.
                   V4R-01-Q1-B1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2392895
                   372
BLAST score
                   5.0e-36
E value
Match length
                   86
% identity
                  (AF017056) brassinosteroid insensitive 1 [Arabidopsis
NCBI Description
                   thaliana]
                   42596
Seq. No.
Seq. ID
                   V4R-01-Q1-B1-F11
Method
                   BLASTX
NCBI GI
                   q3212848
BLAST score
                   558
E value
                   2.0e-57
                   134
Match length
% identity
                   74
                   (AC004005) putative inositol polyphosphate-5-phosphatase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   42597
                   V4R-01-Q1-B1-F7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2317899
BLAST score
                   102
E value
                   1.0e-50
Match length
                   150
% identity
                   92
NCBI Description Glycine max Sali3-2 mRNA, complete cds
```

42598 Seq. No. V4R-01-Q1-E1-F2 Seq. ID

BLASTN Method

NCBI GI g986968



```
BLAST score
                  2.0e-23
E value
                  161
Match length
                  84
% identity
                  Glycine max TGACG-motif binding protein (STGA1) mRNA,
NCBI Description
                  complete cds
                  42599
Seq. No.
                  V4R-01-Q1-E1-F8
Seq. ID
                  BLASTX
Method
                  g4544412
NCBI GI
                  269
BLAST score
                   9.0e-24
E value
                   66
Match length
% identity
                   73
                   (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   42600
Seq. No.
                   V4R-02-Q1-B1-G8
Seq. ID
                   BLASTN
Method
                   g166421
NCBI GI
                   69
BLAST score
                   2.0e-30
E value
                   219
Match length
                   88
% identity
                   Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
                   42601
Seq. No.
                   V4R-02-Q1-B1-H11
Seq. ID
                   BLASTN
Method
                   g18764
NCBI GI
                   89
BLAST score
                   9.0e-43
E value
                   121
Match length
                   93
% identity
                   G.max tefS1 gene for elongation factor EF-1a
NCBI Description
                   42602
Seq. No.
                   all700863124.hl
Seq. ID
                   BLASTX
Method
                   q4039153
NCBI GI
                   220
BLAST score
                   2.0e-18
E value
                   52
Match length
                   77
% identity
                   (AF104221) low temperature and salt responsive protein
NCBI Description
                   LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302_
                   (AF122005) hydrophobic protein [Arabidopsis thaliana]
                   42603
 Seq. No.
```

all700863168.h1 Seq. ID

BLASTN Method g210811 NCBI GI 102 BLAST score E value 2.0e-50 214 Match length



% identity NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA 42604 Seq. No. all700863182.hl Seq. ID BLASTN Method g2653445 NCBI GI BLAST score 36 5.0e-11 E value 56 Match length 93 % identity NCBI Description Vigna radiata mRNA for proton pyrophosphatase, complete cds 42605 Seq. No. al1700863207.h1 Seq. ID BLASTX Method g3850113 NCBI GI BLAST score 153 2.0e-10 E value 89 Match length 43 % identity NCBI Description (AL033388) hypothetical integral membrane protein [Schizosaccharomyces pombe] 42606 Seq. No. all700863254.h1 Seq. ID BLASTX Method g1370156 NCBI GI 147 BLAST score 6.0e-10 E value 28 Match length 100 % identity NCBI Description (Z73956) RAB11H [Lotus japonicus] 42607 Seq. No. all700863275.hl Seq. ID Method BLASTX q3367570 NCBI GI BLAST score 182 E value 4.0e-26 Match length 85 63 % identity (AL031135) putative protein [Arabidopsis thaliana] NCBI Description 42608 Seq. No. all700863294.h1

Seq. ID

BLASTN Method NCBI GI q479059 254 BLAST score E value 1.0e-141 254 Match length % identity

NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase

42609 Seq. No.

art700605309.h2 Seq. ID

6750



```
BLASTN
Method
NCBI GI
                  q2914688
                  42
BLAST score
E value
                  2.0e-14
Match length
                  62
                  92
% identity
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                   42610
Seq. No.
                  art700605318.h2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4038352
                   196
BLAST score
                   2.0e-15
E value
                   78
Match length
                   49
% identity
                   (AF098951) breast cancer resistance protein [Homo sapiens]
NCBI Description
                   42611
Seq. No.
                   art700605330.h2
Seq. ID
Method
                   BLASTX
                   g3386596
NCBI GI
BLAST score
                   261
                   5.0e-23
E value
Match length
                   62
                   74
% identity
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3702346 (AC005397) unknown protein [Arabidopsis
                   thaliana]
                   42612
Seq. No.
                   art700605414.h2
Seq. ID
Method
                   BLASTX
                   q2407275
NCBI GI
BLAST score
                   142
E value
                   5.0e-09
                   43
Match length
                   63
% identity
                   (AF017360) lipid transfer protein LPT III [Oryza sativa]
NCBI Description
                   42613
Seq. No.
                   ary700764306.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2911066
                   296
BLAST score
                   6.0e-27
E value
                   61
Match length
 % identity
                   (AL021960) adrenodoxin - like protein [Arabidopsis
NCBI Description
                   thaliana]
 Seq. No.
                   42614
                   ary700764319.hl
 Seq. ID
 Method
                   BLASTX
                   g3142300
 NCBI GI
```

6751

211

BLAST score



```
6.0e-17
E value
Match length
                  100
% identity
                  49
NCBI Description
                   (AC002411) Contains similarity to pre-mRNA processing
                  protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb R64908
                  and gb_T88158, gb_N38703 and gb_AA651043 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  42615
Seq. ID
                  ary700764335.h1
                  BLASTX
Method
NCBI GI
                  g3510251
BLAST score
                  271
E value
                  5.0e-24
                  115
Match length
% identity
                  56
NCBI Description
                  (AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.
                  42616
Seq. ID
                  ary700764341.h1
Method
                  BLASTX
                  q3913239
NCBI GI
                  274
BLAST score
E value
                  6.0e-37
Match length
                  102
                  77
% identity
                  PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP
NCBI Description
                  SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like
                  protein [Oryza sativa]
Seq. No.
                  42617
                  ary700764411.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2708484
BLAST score
                  323
E value
                  1.0e-30
Match length
                   67
                   90
% identity
NCBI Description
                  (U79557) IAA24 [Arabidopsis thaliana]
Seq. No.
                  42618
Seq. ID
                  ary700764423.h1
Method
                  BLASTX
NCBI GI
                  g3402719
BLAST score
                  348
E value
                  2.0e-33
```

Match length 69 % identity 86

NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.

42619

ary700764487.h1 Seq. ID

Method BLASTN NCBI GI g1184986 BLAST score 54 E value 8.0e-22 94 Match length



```
% identity
NCBI Description Nicotiana tabacum GTP-binding protein NTGB1 mRNA, partial
                  cds
                  42620
Seq. No.
                  asj700967417.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g166379
                  83
BLAST score
                  5.0e-39
E value
                  135
Match length
                  68
% identity
                  Alfalfa glucose-regulated endoplasmic reticular protein
NCBI Description
                  mRNA, complete cds
                  42621
Seq. No.
                  asj700967429.hl
Seq. ID
                  BLASTX
Method
                  g629693
NCBI GI
                  234
BLAST score
                  5.0e-20
E value
                  76
Match length
                  59
% identity
                  probable integrase - common tobacco (fragment)
NCBI Description
                   >gi 530742_emb_CAA56791_ (X80830) integrase [Nicotiana
                   tabacum]
                   42622
Seq. No.
                  asn701130505.h1
Seq. ID
                  BLASTN
Method
                   q4039114
NCBI GI
                   44
BLAST score
                   9.0e-16
E value
                   112
Match length
% identity
                   85
NCBI Description Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
                   42623
Seq. No.
                   asn701130512.h1
Seq. ID
Method
                   BLASTX
                   a3860331
NCBI GI
                   171
BLAST score
                   1.0e-12
E value
Match length
                   51
                   69
% identity
                   (AJ012692) hypothetical protein [Cicer arietinum]
NCBI Description
                   42624
Seq. No.
Seq. ID
                   asn701130525.h1
                   BLASTN
Method
NCBI GI
                   g22116
BLAST score
                   65
E value
                   3.0e-28
Match length
                   145
                   86
 % identity
NCBI Description Z.mays ZMACK2 mRNA for casein kinase II alpha subunit
```

Method

NCBI GI

BLASTN

g3449329



```
Seq. No.
Seq. ID
                  asn701130535.hl
                  BLASTN
Method
                  q170089
NCBI GI
BLAST score
                   92
                  1.0e-44
E value
                  152
Match length
% identity
                   91
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                   42626
Seq. No.
                   asn701130549.h1
Seq. ID
                   BLASTX
Method
                   g2392769
NCBI GI
BLAST score
                   144
                   2.0e-09
E value
Match length
                   71
% identity
                   48
                  (AC002534) putative histone deacetylase [Arabidopsis
NCBI Description
                   thaliana]
                   42627
Seq. No.
                   asn701130601.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4455278
                   218
BLAST score
                   5.0e-18
E value
                   83
Match length
                   45
% identity
NCBI Description (AL035527) hypothetical protein [Arabidopsis thaliana]
                   42628
Seq. No.
                   asn701130615.h1
Seq. ID
Method
                   BLASTN
                   g1778369
NCBI GI
BLAST score
                   115
                   4.0e-58
E value
Match length
                   167
                   93
% identity
NCBI Description Glycine max asparagine synthetase 2 (AS2) mRNA, complete
                   42629
Seq. No.
                   asn701130751.h1
Seq. ID
Method
                   BLASTX
                   q2827544
NCBI GI
                   182
BLAST score
                   7.0e-14
E value
Match length
                   46
                   76
% identity
                   (AL021635) HSP associated protein like [Arabidopsis
NCBI Description
                   thalianal
                   42630
Seq. No.
                   asn701131035.h1
Seq. ID
```

NCBI GI

E value Match length

BLAST score

g3292827

158 5.0e-11

52



```
BLAST score
E value
                  4.0e-09
Match length
                  131
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  42631
                  asn701131096.hl
Seq. ID
Method
                  BLASTX
                  g4512657
NCBI GI
                  204
BLAST score
E value
                  2.0e-16
Match length
                  79
                  47
% identity
                  (AC006931) putative APG protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4544463_gb_AAD22370.1_AC006580_2 (AC006580) putative
                  APG isolog protein [Arabidopsis thaliana]
                  42632
Seq. No.
                  asn701131131.hl
Seq. ID
                  BLASTX
Method
                  g3043656
NCBI GI
BLAST score
                  142
                  4.0e-09
E value
Match length
                  44
                  59
% identity
                  (AB011138) KIAA0566 protein [Homo sapiens]
NCBI Description
Seq. No.
                  42633
                  asn701131311.h1
Seq. ID
                  BLASTN
Method
                  q1403142
NCBI GI
BLAST score
                  42
                  2.0e-14
E value
Match length
                  50
% identity
                  96
                  C.arietinum mRNA for beta-tubulin
NCBI Description
Seq. No.
                   42634
Seq. ID
                   asn701131389.hl
Method
                  BLASTX
                   g2129758
NCBI GI
                   296
BLAST score
E value
                   3.0e-27
                   61
Match length
% identity
                  ubiquitin conjugating enzyme E2 protein - Arabidopsis
NCBI Description
                   thaliana >gi 992704 (U33757) UBC7 [Arabidopsis thaliana]
Seq. No.
                   42635
Seq. ID
                   asn701131406.h1
Method
                   BLASTX
```

Seq. No.

Seq. ID



```
% identity
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                  42636
Seq. No.
                  asn701131425.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662469
BLAST score
                  267
                  9.0e-24
E value
                   69
Match length
                  77
% identity
                  (AF034217) ribosomal protein S6 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   42637
                  asn701131437.h1
Seq. ID
Method
                  BLASTN
                  g2760316
NCBI GI
                   34
BLAST score
                   9.0e-10
E value
Match length
                   66
                   88
% identity
                  The sequence of BAC F1N21 from Arabidopsis thaliana
NCBI Description
                   chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   42638
                   asn701131459.h1
Seq. ID
                   BLASTX
Method
                   g3980413
NCBI GI
BLAST score
                   112
                   1.0e-12
E value
                   47
Match length
                   46
% identity
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
                   42639
Seq. No.
                   asn701131477.hl
Seq. ID
Method
                   BLASTX
                   g542157
NCBI GI
BLAST score
                   367
E value
                   2.0e-35
Match length
                   83
                   82
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
                   42640
Seq. No.
                   asn701131492.hl
Seq. ID
Method
                   BLASTX
                   g2330739
NCBI GI
BLAST score
                   205
                   9.0e-17
E value
Match length
                   48
                   71
% identity
                   (Z98598) putative transcriptional regulator
NCBI Description
                   [Schizosaccharomyces pombe]
```

6756

asn701131503.hl



```
Method
                  BLASTX
NCBI GI
                  g2582971
BLAST score
                  188
                  3.0e-17
E value
                  85
Match length
                  62
% identity
NCBI Description (D83711) TKRP125 [Nicotiana tabacum]
                  42642
Seq. No.
                  asn701131504.h1
Seq. ID
Method
                  BLASTX
                  g2464865
NCBI GI
BLAST score
                  340
E value
                  3.0e - 32
                  78
Match length
                  74
% identity
                  (Z99707) pectinesterase like protein [Arabidopsis thaliana]
NCBI Description
                  42643
Seq. No.
                  asn701131533.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g3021511
                   100
BLAST score
                   4.0e-49
E value
Match length
                  244
                   86
% identity
NCBI Description N.tabacum mRNA for NADP-dependent isocitrate dehydrogenase
                   42644
Seq. No.
                   asn701131617.hl
Seq. ID
                   BLASTN
Method
                   g2564336
NCBI GI
BLAST score
                   53
E value
                   4.0e-21
Match length
                   193
                   82
% identity
NCBI Description
                   Brassica campestris mRNA for Tat binding protein 1,
                   complete cds
Seq. No.
                   42645
                   asn701131663.hl
Seq. ID
Method
                   BLASTX
                   g1531758
NCBI GI
                   160
BLAST score
E value
                   3.0e-11
                   58
Match length
% identity
                   66
                   (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
Seq. No.
                   42646
                   asn701131665.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2304954
BLAST score
                   243
```

6757

1.0e-134

263

E value

Match length

Seq. ID



```
% identity
NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds
Seq. No.
                  42647
                  asn701131711.hl
Seq. ID
                  BLASTX
Method
                  g3549639
NCBI GI
BLAST score
                  279
                  3.0e-25
E value
Match length
                  71
% identity
                  73
                  (AJ005194) receiver-like protein 3 [Arabidopsis thaliana]
NCBI Description
                   42648
Seq. No.
                   asn701131817.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q556672
BLAST score
                   38
                   2.0e-12
E value
                   74
Match length
                   88
% identity
                  S.cereale (Halo) chloroplast mRNA for heat-shock protein
NCBI Description
                   42649
Seq. No.
                   asn701132039.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1747310
BLAST score
                   377
E value
                   1.0e-36
Match length
                   87
                   85
% identity
                   (D58424) Myb-like DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   42650
Seq. No.
                   asn701132124.h1
Seq. ID
Method
                   BLASTN
                   g2687429
NCBI GI
BLAST score
                   37
                   9.0e-12
E value
                   77
Match length
% identity
                   87
                   Ephedra distachya large subunit 26S ribosomal RNA gene,
NCBI Description
                   partial sequence
                   42651
Seq. No.
                   asn701132155.h1
Seq. ID
                   BLASTX
Method
                   g4454474
NCBI GI
BLAST score
                   163
                   8.0e-12
E value
Match length
                   62
% identity
                   45
                   (AC006234) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   42652
Seq. No.
```

asn701132319.h1

Match length

75

```
BLASTN
Method
                  g2920665
NCBI GI
BLAST score
                  143
                  8.0e-75
E value
Match length
                  227
% identity
                   91
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
                   42653
Seq. No.
                   asn701132328.h1
Seq. ID
                   BLASTX
Method
                   g3885328
NCBI GI
BLAST score
                   198
                   1.0e-15
E value
Match length
                   88
% identity
                   (AC005623) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   42654
Seq. No.
Seq. ID
                   asn701132389.h1
                   BLASTX
Method
                   g3047125
NCBI GI
                   168
BLAST score
                   5.0e-26
E value
Match length
                   85
                   76
% identity
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   42655
Seq. No.
                   asn701132442.h1
Seq. ID
                   BLASTX
Method
                   g4102600
NCBI GI
                   217
BLAST score
                   5.0e-38
E value
                   85
Match length
                   91
% identity
                   (AF013467) ARF6 [Arabidopsis thaliana]
NCBI Description
                   42656
Seq. No.
                   asn701132514.h1
Seq. ID
                   BLASTX
Method
                   q4099317
NCBI GI
                   158
BLAST score
                   6.0e-11
E value
                   85
Match length
                   35
% identity
                   (U86112) NRD convertase [Mus musculus]
NCBI Description
                   42657
 Seq. No.
                   asn701132565.h1
 Seq. ID
                   BLASTX
Method
                   g416688
NCBI GI
                   323
BLAST score
                   3.0e-30
 E value
```



NCBI Description AUXIN-INDUCED PROTEIN X10A >gi_81761_pir__JQ1099

% identity

```
auxin-induced protein 10A - soybean >gi_255579_bbs_113701
                  (S44176) orf X10A [Glycine max=soybeans, cv. Wayne,
                  Peptide, 92 aa] [Glycine max]
                  42658
Seq. No.
                  asn701132594.h1
Seq. ID
                  BLASTX
Method
                  g2228536
NCBI GI
                  247
BLAST score
                  2.0e-21
E value
                  86
Match length
                  56
% identity
NCBI Description (U72352) serine protease [Gallus gallus]
                  42659
Seq. No.
                  asn701132627.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g296408
                  223
BLAST score
                  1.0e-122
E value
                  243
Match length
                  98
% identity
NCBI Description G.max ADR12 mRNA
                  42660
Seq. No.
                  asn701132757.h1
Seq. ID
                  BLASTN
Method
                   g169980
NCBI GI
                   90
BLAST score
                   3.0e-43
E value
                   194
Match length
                   87
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   42661
Seq. No.
                   asn701132772.h1
Seq. ID
Method
                   BLASTX
                   g1076668
NCBI GI
                   260
BLAST score
                   1.0e-30
E value
                   77
Match length
                   88
% identity
                   NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                   >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
Seq. No.
                   42662
                   asn701132773.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3982595
BLAST score
                   55
                   2.0e-22
E value
Match length
                   95
% identity
                   89
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
```



42663 Seq. No. asn701132879.h1 Seq. ID BLASTN Method g19657 NCBI GI 82 BLAST score 2.0e-38 E value 250 Match length 83 % identity M.sativa mRNA for translationally controlled tumor protein NCBI Description (partial) 42664 Seq. No. asn701132914.h1 Seq. ID BLASTX Method g458338 NCBI GI 206 BLAST score 1.0e-16 E value 77 Match length 60 % identity (U06046) 1-aminocylopropane-1-carboxylate oxidase homolog NCBI Description [Vigna radiata] >gi_1093118_prf__2102361A aminocyclopropane carboxylate oxidase [Vigna radiata] Seq. No. 42665 asn701132935.h1 Seq. ID BLASTN Method g2149954 NCBI GI 90 BLAST score 4.0e-43 E value 235 Match length 91 % identity Phaseolus vulgaris putative aquaporin-1 (Mip-1) mRNA, NCBI Description complete cds 42666 Seq. No. asn701133004.h1 Seq. ID BLASTN Method NCBI GI q4336433 BLAST score 51 5.0e-20 E value 151 Match length % identity Lotus japonicus nodule-enhanced protein phosphatase type 2C NCBI Description (NPP2C1) mRNA, complete cds 42667 Seq. No. asn701133056.h1 Seq. ID Method BLASTN NCBI GI q439856 BLAST score 89

NCBI GI g439856 BLAST score 89 E value 1.0e-42 Match length 212 % identity 87

42668

NCBI Description Glycine max Williams 82 lipoxygenase mRNA, complete cds

Seq. No.

BLAST score

E value

334 1.0e-31



```
asn701133141.h1
Seq. ID
Method
                  BLASTX
                  a1084454
NCBI GI
                  188
BLAST score
                  1.0e-14
E value
                  64
Match length
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice
NCBI Description
                  >gi 600765 (L29471) cyclophilin 1 [Oryza sativa]
                  42669
Seq. No.
                  asn701133195.hl
Seq. ID
                  BLASTX
Method
                  g4314356
NCBI GI
                  270
BLAST score
                  4.0e-24
E value
                  81
Match length
                  62
% identity
                  (AC006340) putative anthocyanidin-3-glucoside
NCBI Description
                  rhamnosyltransferase [Arabidopsis thaliana]
                  42670
Seq. No.
                  asn701133295.h1
Seq. ID
                  BLASTX
Method
                  g3687231
NCBI GI
                   320
BLAST score
                   3.0e-30
E value
                   85
Match length
                   77
% identity
                  (AC005169) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   42671
Seq. No.
                   asn701133316.h1
Seq. ID
                   BLASTN
Method
                   g1808591
NCBI GI
                   120
BLAST score
                   5.0e-61
E value
Match length
                   176
                   92
% identity
NCBI Description C.arietinum mRNA for SAM-synthetase
                   42672
Seq. No.
                   asn701133338.h1
Seq. ID
                   BLASTN
Method
                   g3982595
NCBI GI
                   118
BLAST score
                   7.0e-60
E value
                   158
Match length
 % identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   42673
 Seq. No.
                   asn701133370.hl
 Seq. ID
                   BLASTX
 Method
                   g3738308
 NCBI GI
```



```
Match length
% identity
                  70
NCBI Description
                  (AC005309) unknown protein [Arabidopsis thaliana]
                  42674
Seq. No.
                  asn701133387.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1353352
BLAST score
                  173
                  1.0e-12
E value
Match length
                  46
% identity
                  76
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                   42675
Seq. No.
                  asn701133431.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2656031
BLAST score
                   36
                   6.0e-11
E value
Match length
                  75
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
                   42676
Seq. No.
                   asn701133441.h1
Seq. ID
Method
                   BLASTX
                   g3298547
NCBI GI
BLAST score
                   260
                   6.0e-23
E value
                   86
Match length
% identity
                   55
                   (AC004681) putative condensin protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   42677
Seq. ID
                   asn701133575.h2
Method
                   BLASTX
NCBI GI
                   q1752734
BLAST score
                   254
E value
                   1.0e-30
Match length
                   82
% identity
                   69
NCBI Description
                   (D78510) beta-glucan-elicitor receptor [Glycine max]
Seq. No.
                   42678
                   asn701133580.h2
Seq. ID
Method
                   BLASTX
                   q3386598
NCBI GI
BLAST score
                   330
                   4.0e-31
E value
```

85

78

Match length

NCBI Description

% identity

(AC004665) putative cytochrome p450 [Arabidopsis thaliana]



```
42679
Seq. No.
                  asn701133657.h2
Seq. ID
                  BLASTX
Method
                  q4314378
NCBI GI
                  244
BLAST score
                  4.0e-21
E value
                  78
Match length
% identity
                  58
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]
                  42680
Seq. No.
                  asn701133708.hl
Seq. ID
Method
                  BLASTX
                  g3738298
NCBI GI
                  225
BLAST score
                  7.0e-19
E value
                  82
Match length
                   51
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4249394 (AC006072) unknown protein [Arabidopsis
                   thaliana]
                   42681
Seq. No.
                   asn701133872.h1
Seq. ID
                  BLASTX
Method
                   g3021270
NCBI GI
BLAST score
                   262
                   3.0e-23
E value
                   83
Match length
                   58
% identity
NCBI Description (AL022347) serine/threonine kinase -like protein
                   [Arabidopsis thaliana]
                   42682
Seq. No.
                   asn701133878.h1
Seq. ID
                   BLASTN
Method
                   g22073
NCBI GI
BLAST score
                   74
                   1.0e-33
E value
                   112
Match length
% identity
                   92
NCBI Description Mung bean 25S rRNA - 18S rDNA spacer region
                   42683
Seq. No.
                   asn701133880.h1
Seq. ID
Method
                   BLASTN
                   g1778369
NCBI GI
                   131
BLAST score
E value
                   1.0e-67
                   146
Match length
% identity
                   98
                   Glycine max asparagine synthetase 2 (AS2) mRNA, complete
NCBI Description
```

Seq. No. 42684 Seq. ID asn701134201.h1 Method BLASTX

```
436
                  g2642154
NCBI GI
                  206
BLAST score
                  1.0e-16
E value
                  88
Match length
                  48
% identity
                   (AC003000) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3790595 (AF079186) RING-H2 finger protein RHC2a
                   [Arabidopsis thaliana]
                   42685
Seq. No.
                  asn701134207.h1
Seq. ID
                  BLASTX
Method
                   g3033377
NCBI GI
                   275
BLAST score
                   1.0e-24
E value
                   88
Match length
                   57
% identity
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   42686
Seq. No.
                   asn701134229.h1
Seq. ID
                   BLASTN
Method
                   g170073
NCBI GI
                   179
BLAST score
                   3.0e-96
E value
                   240
Match length
                   95
% identity
                   Soybean calmodulin (SCaM-3) mRNA, complete cds
NCBI Description
                   42687
Seq. No.
                   asn701134236.h1
Seq. ID
                   BLASTX
Method
                   g2541876
NCBI GI
                   172
BLAST score
                   1.0e-12
E value
                   87
Match length
                   41
% identity
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
                   42688
Seq. No.
                   asn701134249.h1
Seq. ID
                   BLASTX
Method
                   q4160298
NCBI GI
                   194
BLAST score
                   2.0e-15
E value
                   61
Match length
                   61
 % identity
                   (AJ011892) cyclin D2.1 protein [Nicotiana tabacum]
NCBI Description
 Seq. No.
                   42689
                   asn701134252.h1
```

Seq. ID

BLASTX Method q4006915 NCBI GI BLAST score 157 7.0e-11 E value



Match length 87 % identity 45 NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No. 42690 Seq. ID asn701134269.h1

Method BLASTX
NCBI GI g1169286
BLAST score 142
E value 3.0e-09
Match length 33
% identity 76

NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)

>gi 1085671 pir S49205 betaine-aldehyde dehydrogenase (EC

1.2.1.8) precursor - Atriplex hortensis

>gi_510574_emb_CAA49425_ (X69770) betaine-aldehyde

dehydrogenase [Atriplex hortensis]

Seq. No. 42691

Seq. ID asn701134327.h1

Method BLASTX
NCBI GI g136057
BLAST score 262
E value 4.0e-23
Match length 83
% identity 63

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase Coptis japonica >gi_556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 42692

Seq. ID asn701134408.h1

Method BLASTN
NCBI GI g170089
BLAST score 159
E value 2.0e-84
Match length 159
% identity 100

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 42693

Seq. ID asn701134503.h1

Method BLASTN
NCBI GI g1778369
BLAST score 82
E value 2.0e-38
Match length 257
% identity 83

NCBI Description Glycine max asparagine synthetase 2 (AS2) mRNA, complete

cds

Seq. No. 42694

Seq. ID asn701134609.h2

Method BLASTX
NCBI GI g3122914
BLAST score 191



8.0e-15 E value 88 Match length % identity VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) NCBI Description >gi 1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana] 42695 Seq. No. asn701134686.h2 Seq. ID BLASTX Method g113376 NCBI GI 189 BLAST score 1.0e-14 E value 83 Match length % identity 46 ALCOHOL DEHYDROGENASE 2 >gi_82348_pir__S04039 alcohol NCBI Description dehydrogenase (EC 1.1.1.1) 2 - barley >gi_18884_emb_CAA31230_ (X12733) alcohol dehydrogenase [Hordeum vulgare] 42696 Seq. No. asn701134693.h2 Seq. ID BLASTN Method g2304954 NCBI GI 235 BLAST score 1.0e-129 E value 247 Match length 99 % identity NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds 42697 Seq. No. asn701134709.h2 Seq. ID BLASTN Method g1086988 NCBI GI 75 BLAST score 3.0e - 34E value 244 Match length 86 % identity plasma membrane H(+)-ATPase [Vicia faba, Otafuku, abaxial NCBI Description epidermis, guard cells protoplasts, mRNA, 3319 nt] 42698 Seq. No.

 Seq. No.
 42698

 Seq. ID
 asn701134743.h2

 Method
 BLASTX

 NCBI GI
 g2829894

 BLAST score
 237

 E value
 3.0e-20

E value 3.0 Match length 60 % identity 73

NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No. 42699

Seq. ID asn701134815.h2

Method BLASTX
NCBI GI g3367536
BLAST score 282
E value 2.0e-25



Match length 65 92 % identity (ACO04392) Contains similarity to symbiosis-related like NCBI Description protein F1N20.80 gi_2961343 from A. thaliana BAC gb AL022140. EST gb_T04695 comes from this gene. [Arabidopsis thaliana] 42700 Seq. No. asn701134876.h2 Seq. ID BLASTX Method g2244835 NCBI GI 359 BLAST score 2.0e-34 E value 89 Match length % identity 75 (Z97337) protein kinase homolog [Arabidopsis thaliana] NCBI Description 42701 Seq. No. asn701134909.hl Seq. ID BLASTN Method g296444 NCBI GI BLAST score 182 3.0e-98 E value 182 Match length 100 % identity NCBI Description G.max ADR6 mRNA 42702 Seq. No. asn701135206.hl Seq. ID BLASTX Method g3047104 NCBI GI 154 BLAST score 1.0e-10 E value 68 Match length 49 % identity (AF058919) No definition line found [Arabidopsis thaliana] NCBI Description 42703 Seq. No. asn701135213.h1 Seq. ID BLASTX Method g2282586 NCBI GI 211 BLAST score 3.0e-17 E value 84 Match length

45 % identity

(U82011) methyltransferase [Prunus armeniaca] NCBI Description

42704 Seq. No.

asn701135281.hl Seq. ID

Method BLASTX q3617770 NCBI GI 230 BLAST score E value 2.0e-19 54 Match length % identity 78

(Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana] NCBI Description



```
42705
Seq. No.
Seq. ID
                  asn701135333.h1
Method
                  BLASTN
NCBI GI
                  g2970050
BLAST score
                  34
                  9.0e-10
E value
                  119
Match length
                  89
% identity
NCBI Description Vigna radiata mRNA for ARG10, complete cds
Seq. No.
                  42706
Seq. ID
                  asn701135337.hl
Method
                  BLASTX
NCBI GI
                  g1359905
BLAST score
                  162
                  2.0e-16
E value
                  59
Match length
                  71
% identity
                  (X85138) homologous to glucosyltransferases [Lycopersicon
NCBI Description
                  esculentum]
                  42707
Seq. No.
                  asn701135344.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3982595
BLAST score
                  158
                  9.0e-84
E value
Match length
                  190
                  96
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                  42708
Seq. No.
Seq. ID
                  asn701135354.h1
Method
                  BLASTX
NCBI GI
                  g4056437
BLAST score
                  346
                  5.0e-33
E value
Match length
                  84
% identity
                  79
                  (AC005990) Strong similarity to PFAM PF 00069 Eukaryotic
NCBI Description
                  protein kinase domain. [Arabidopsis thaliana]
                  42709
Seq. No.
Seq. ID
                  asn701135363.h1
                  BLASTX
Method
NCBI GI
                  g4510341
BLAST score
                  173
                  3.0e-16
E value
Match length
                  69
                  36
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
```

Seq. No. 42710

Seq. ID asn701135382.h1

Method BLASTX NCBI GI g3582328 BLAST score 204

```
E value
                   2.0e-16
Match length
                   45
% identity
                   (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   42711
Seq. No.
                   asn701135447.h1
Seq. ID
                   BLASTX
Method
                   g2623304
NCBI GI
                   169
BLAST score
                   2.0e-12
E value
                   60
Match length
                   50
% identity
                  (AC002409) similar to Medicago nodulin N21 [Arabidopsis
NCBI Description
                   thaliana]
                   42712
Seq. No.
                   asn701135475.h1
Seq. ID
Method
                   BLASTX
                   g3873807
NCBI GI
                   156
BLAST score
                   7.0e-11
E value
                   72
Match length
                   46
% identity
                  (Z49907) B0491.1 [Caenorhabditis elegans]
NCBI Description
                   42713
Seq. No.
                   asn701135508.hl
Seq. ID
                   BLASTN
Method
                   q296444
NCBI GI
                   264
BLAST score
                   1.0e-147
E value
                   264
Match length
                   100
% identity
NCBI Description G.max ADR6 mRNA
                   42714
Seq. No.
                   asn701135520.hl
Seq. ID
                   BLASTN
Method
NCBI GI
                   a169920
                   198
BLAST score
                   1.0e-107
E value
                   198
Match length
                   100
% identity
NCBI Description Soybean auxin-regulated protein (Aux28) mRNA, complete cds
                   42715
Seq. No.
                   asn701135564.hl
Seq. ID
Method
                   BLASTX
                   g3894191
NCBI GI
BLAST score
                   141
                   5.0e-09
E value
                   34
Match length
                   71
 % identity
                   (AC005662) unknown protein [Arabidopsis thaliana]
```

42716 Seq. No.

NCBI Description

Match length

57



```
asn701135577.hl
Seq. ID
                  BLASTX
Method
                  q3540208
NCBI GI
                  143
BLAST score
                  3.0e-09
E value
                  81
Match length
                   43
% identity
                  (AC004260) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   42717
Seq. No.
                   asn701135610.hl
Seq. ID
                   BLASTX
Method
                   q3928166
NCBI GI
                   140
BLAST score
                   7.0e-09
E value
                   78
Match length
                   37
% identity
                  (AJ010317) Sand [Fugu rubripes]
NCBI Description
                   42718
Seq. No.
                   asn701135706.hl
Seq. ID
                   BLASTN
Method
                   g4185854
NCBI GI
                   52
BLAST score
                   2.0e-20
E value
                   187
Match length
                   82
% identity
NCBI Description Arabidopsis thaliana mRNA for Ca2+-ATPase, ACA6 gene
                   42719
Seq. No.
                   asn701135732.h1
Seq. ID
                   BLASTX
Method
                   g4006886
NCBI GI
                   160
BLAST score
                   1.0e-21
E value
                   61
Match length
                   87
 % identity
                   (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                   42720
 Seq. No.
                   asn701135746.hl
 Seq. ID
                   BLASTX
 Method
                   q4006924
 NCBI GI
                   219
 BLAST score
                   7.0e-28
 E value
                   75
 Match length
                   79
 % identity
                   (Z99708) beta-galactosidase like protein [Arabidopsis
 NCBI Description
                   thaliana]
 Seq. No.
                    42721
                   asn701135882.h1
 Seq. ID
                   BLASTX
 Method
                    g2062174
 NCBI GI
                    255
 BLAST score
                    2.0e-22
 E value
```



% identity (AC001645) transcription factor (TINY) isolog [Arabidopsis NCBI Description thaliana] 42722 Seq. No. asn701135977.h1 Seq. ID BLASTX Method q3183285 NCBI GI 204 BLAST score 2.0e-16 E value 63 Match length 65 % identity

HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION NCBI Description >gi_1742787_dbj_BAA15475_ (D90813) ORF_ID:o322#7; similar
to [SwissProt Accession Number Q06373] [Escherichia coli]

>gi_1787999 (AE000266) orf, hypothetical protein

[Escherichia coli]

42723 Seq. No. asn701135989.h1 Seq. ID Method BLASTX

g4454483 NCBI GI 198 BLAST score 9.0e-16 E value 57 Match length % identity 72

(AC006234) putative kinase, 5' partial [Arabidopsis NCBI Description

thaliana]

42724 Seq. No.

asn701136072.hl Seq. ID

Method BLASTN q609224 NCBI GI 40 BLAST score 2.0e-13 E value 86 Match length 90 % identity

P.sativum mRNA for SAMS-2 >gi 609558 gb L36681 PEADENSYNB NCBI Description

Pisum sativum S-adenosylmethionine synthase mRNA, complete

42725 Seq. No.

asn701136203.h1 Seq. ID

BLASTX Method g3785971 NCBI GI 235 BLAST score 4.0e-20 E value 90 Match length 53 % identity

(AC005560) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi_4262248_gb_AAD14541_ (AC006200) hypothetical protein

[Arabidopsis thaliana]

42726 Seq. No.

asn701136208.h1 Seq. ID

BLASTX Method g2407800 NCBI GI

E value

Match length



```
BLAST score
                  2.0e-12
E value
                  74
Match length
                  51
% identity
                  (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
                  42727
Seq. No.
                  asn701136258.hl
Seq. ID
                  BLASTN
Method
                  g2827081
NCBI GI
                  149
BLAST score
                   2.0e-78
E value
                   237
Match length
                   91
% identity
                  Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA,
NCBI Description
                   complete cds
                   42728
Seq. No.
                   asn701136290.h1
Seq. ID
                   BLASTX
Method
                   g1888357
NCBI GI
                   359
BLAST score
                   1.0e-34
E value
                   74
Match length
                   81
% identity
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                   >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                   precursor [Arabidopsis thaliana]
                   42729
Seq. No.
                   asn701136319.h1
Seq. ID
                   BLASTN
Method
                   g2852444
NCBI GI
                   32
BLAST score
                   1.0e-08
E value
                   92
Match length
                   84
% identity
                   Salix bakko mRNA for SUI1 homolog, complete cds
NCBI Description
                   42730
 Seq. No.
                   asn701136349.hl
 Seq. ID
                   BLASTN
Method
                   q3309242
 NCBI GI
                   32
 BLAST score
                   1.0e-08
 E value
                   150
 Match length
                   88
 % identity
                   Citrus limon aconitase-iron regulated protein 1 (IRP1)
 NCBI Description
                   mRNA, complete cds
                   42731
 Seq. No.
                 asn701136360.hl
 Seq. ID
                   BLASTX
 Method
                   q3044218
 NCBI GI
                   337
 BLAST score
                   6.0e-32
```



```
% identity
NCBI Description (AF057144) signal peptidase [Arabidopsis thaliana]
                  42732
Seq. No.
Seq. ID
                  asn701136474.h1
Method
                  BLASTN
NCBI GI
                  g1183936
BLAST score
                  64
E value
                  1.0e-27
Match length
                  173
% identity
                  86
NCBI Description P.sativum 5S rRNA gene
                  42733
Seq. No.
Seq. ID
                  asn701136490.h1
Method
                  BLASTX
                  q4262242
NCBI GI
BLAST score
                  331
E value
                  3.0e-31
                  84
Match length
                  77
% identity
                 (AC006200) NADC homolog [Arabidopsis thaliana]
NCBI Description
                  42734
Seq. No.
Seq. ID
                  asn701136581.h1
Method
                  BLASTN
NCBI GI
                  q1370187
                  76
BLAST score
E value
                  6.0e-35
Match length
                  104
                  93
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB7D
                  42735
Seq. No.
Seq. ID
                  asn701136624.h1
Method
                  BLASTX
NCBI GI
                  g1770515
BLAST score
                  257
E value
                  2.0e-22
                  88
Match length
                  55
% identity
NCBI Description
                  (X99459) sigma 3 protein [Homo sapiens] >gi_1923272
                  (U91933) AP-3 complex sigma3B subunit [Mus musculus]
Seq. No.
                  42736
                  asn701136691.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2352492
BLAST score
                  365
```

E value 3.0e-35 Match length 89 % identity 80

(AF005047) transport inhibitor response 1 [Arabidopsis NCBI Description thaliana] >gi_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 42737



asn701136723.hl Seq. ID BLASTX Method g100266 NCBI GI BLAST score 278 5.0e-25 E value Match length 65 78 % identity homeotic protein Hox7 - Peruvian tomato NCBI Description >gi 19486 emb CAA47871 (X67602) homeobox transcription factor Hox7 [Lycopersicon peruvianum] 42738 Seq. No. asn701136758.hl Seq. ID BLASTN Method g3982595 NCBI GI BLAST score 145 5.0e-76 E value 169 Match length 97 % identity NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds 42739 Seq. No. asn701136880.h1 Seq. ID BLASTX Method g1402918 NCBI GI BLAST score 235 5.0e-20 E value Match length 72 % identity 68 (X98320) peroxidase [Arabidopsis thaliana] NCBI Description >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana] 42740 Seq. No. asn701136990.h1 Seq. ID BLASTX Method g4406781 NCBI GI 186 BLAST score 3.0e-14E value Match length 67 % identity (ACO06532) putative Na+/H+ antiporter [Arabidopsis NCBI Description thaliana] 42741 Seq. No. asn701136991.hl Seq. ID BLASTX Method g3378650 NCBI GI 227 BLAST score 2.0e-19 E value Match length 58

78 % identity

(X97606) abscisic acid activated [Medicago sativa] NCBI Description

Seq. No.

42742

asn701137030.h1 Seq. ID

Method BLASTX

BLAST score

E value

149 6.0e-10



```
g1871185
NCBI GI
                  357
BLAST score
                  2.0e-34
E value
                  81
Match length
                  78
% identity
                  (U90439) seven in absentia isolog [Arabidopsis thaliana]
NCBI Description
                  42743
Seq. No.
                  asn701137063.hl
Seq. ID
                  BLASTN
Method
                   g170061
NCBI GI
                   160
BLAST score
                   6.0e-85
E value
                   244
Match length
                   95
% identity
                  Soybean (G.max L.) beta-tubulin (S-beta-2) gene, complete
NCBI Description
                   42744
Seq. No.
                   asn701137240.h1
Seq. ID
                   BLASTN
Method
                   g2459406
NCBI GI
                   48
BLAST score
                   4.0e-18
E value
                   84
Match length
                   89
% identity
                   Arabidopsis thaliana chromosome II BAC F4P9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   42745
Seq. No.
                   asn701137282.h1
Seq. ID
                   BLASTN
Method
                   g256142
NCBI GI
                   49
BLAST score
                   1.0e-18
E value
                   93
Match length
                   89
% identity
                   cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                   Prize, mRNA, 1450 nt]
                   42746
Seq. No.
                   asn701137335.hl
 Seq. ID
                   BLASTN
Method
                   g19657
NCBI GI
                   91
BLAST score
                   9.0e-44
 E value
                   269
Match length
 % identity
                   M.sativa mRNA for translationally controlled tumor protein
 NCBI Description
                    (partial)
                    42747
 Seq. No.
                    asn701137358.hl
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g2924327
```



```
63
Match length
                  54
% identity
                  (Z93766) hypothetical protein [Malus domestica]
NCBI Description
                  42748
Seq. No.
                  asn701137365.hl
Seq. ID
                  BLASTX
Method
                  g1931652
NCBI GI
                  236
BLAST score
                  5.0e-20
E value
                  86
Match length
                  68
% identity
                  (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
NCBI Description
                   [Arabidopsis thaliana]
                  42749
Seq. No.
                  asn701137381.hl
Seq. ID
                  BLASTX
Method
                  q4567286
NCBI GI
                   394
BLAST score
                   1.0e-38
E value
Match length
                   91
                   37
% identity
                  (AC006841) putative coatomer alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
                   42750
Seq. No.
                   asn701137423.hl
Seq. ID
                   BLASTN
Method
                   g3021356
NCBI GI
                   71
BLAST score
                   8.0e-32
E value
                   171
Match length
                   85
% identity
                  Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,
NCBI Description
                   clone GEPI48
                   42751
Seq. No.
                   asn701137450.h1
Seq. ID
                   BLASTX
Method
                   g2281090
NCBI GI
                   194
BLAST score
                   3.0e-15
E value
                   71
Match length
 % identity
                   (AC002333) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   42752
 Seq. No.
                   asn701137465.hl
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3047114
 BLAST score
                   277
                   6.0e-25
 E value
 Match length
                   71
```

(AF058919) No definition line found [Arabidopsis thaliana]

66

% identity

NCBI Description



```
42753
Seq. No.
                  asn701137493.h1
Seq. ID
Method
                  BLASTN
                  g2920665
NCBI GI
                  179
BLAST score
                  3.0e-96
E value
                  215
Match length
                  96
% identity
                  Glycine max 2,4-D inducible glutathione S-transferase
NCBI Description
                   (GSTa) mRNA, complete cds
                   42754
Seq. No.
                   asn701137521.h1
Seq. ID
Method
                  BLASTN
                   g218082
NCBI GI
                   100
BLAST score
                   4.0e-49
E value
                   232
Match length
                  86
% identity
                  Rice mRNA for initiation factor eIF-4D (225 gene), partial
NCBI Description
                   sequence
                   42755
Seq. No.
                   asn701137601.hl
Seq. ID
Method
                   BLASTX
                   g3047085
NCBI GI
BLAST score
                   265
                   2.0e-23
E value
Match length
                   88
                   55
% identity
NCBI Description (AF058914) No definition line found [Arabidopsis thaliana]
                   42756
Seq. No.
                   asn701137642.h1
Seq. ID
Method
                   BLASTN
                   q18764
NCBI GI
BLAST score
                   249
E value
                   1.0e-138
                   257
Match length
                   99
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   42757
Seq. No.
                   asn701137679.h1
Seq. ID
Method
                   BLASTX
                   g2507229
NCBI GI
                   212
BLAST score
E value
                   2.0e-17
Match length
                   79
                   53
% identity
NCBI Description 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
```

(ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED

PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN) >gi_423247_pir__A46579 estrogen receptor-binding

cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074)

cyclophilin [Bos taurus]



```
Seq. No.
                  asn701137681.hl
Seq. ID
                  BLASTX
Method
                  q3386606
NCBI GI
BLAST score
                  216
                  9.0e-18
E value
                  78
Match length
                  53
% identity
                  (AC004665) putative beta-amylase [Arabidopsis thaliana]
NCBI Description
                  42759
Seq. No.
                  asn701137695.h1
Seq. ID
Method
                  BLASTX
                   q4091008
NCBI GI
BLAST score
                   289
                   2.0e-26
E value
                   81
Match length
                   69
% identity
                   (AF040700) methionyl-tRNA synthetase [Oryza sativa]
NCBI Description
                   42760
Seq. No.
                   asn701137709.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539324
BLAST score
                   183
                   7.0e-14
E value
                   91
Match length
                   47
% identity
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                   42761
Seq. No.
                   asn701137723.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2970050
                   112
BLAST score
                   3.0e-56
E value
Match length
                   216
% identity
                  Vigna radiata mRNA for ARG10, complete cds
NCBI Description
                   42762
Seq. No.
                   asn701137731.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g16508
BLAST score
                   62
                   2.0e-26
E value
                   157
Match length
% identity
                   A.thaliana DNA for S-adenosylmethionine synthetase gene
NCBI Description
                   sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana
                   S-adenosylmethionine synthetase gene, complete cds
                   42763
Seq. No.
```

 Seq. No.
 42763

 Seq. ID
 asn701137750.h1

 Method
 BLASTX

 NCBI GI
 g1706323

BLAST score 203



```
2.0e-16
E value
Match length
                  86
                  57
% identity
                  ORNITHINE DECARBOXYLASE (ODC) >gi_2118242_pir__$64704
NCBI Description
                  ornithine decarboxylase (EC 4.1.1.17) - jimsonweed
                  >gi 871008_emb_CAA61121_ (X87847) ornithine decarboxylase
                   [Datura stramonium]
                   42764
Seq. No.
                   asn701137764.h1
Seq. ID
Method
                   BLASTX
                   g2224913
NCBI GI
BLAST score
                   267
                   9.0e-24
E value
                   64
Match length
% identity
                   73
                   (U95967) beta-expansin [Arabidopsis thaliana]
NCBI Description
                   42765
Seq. No.
                   asn701137792.h1
Seq. ID
                   BLASTX
Method
                   q3006183
NCBI GI
                   182
BLAST score
                   9.0e-14
E value
                   76
Match length
                   46
% identity
                   (AL022304) trp-ast repeats containing protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   42766
Seq. No.
                   asn701137833.hl
Seq. ID
Method
                   BLASTX
                   q4455169
NCBI GI
BLAST score
                   164
                   8.0e-12
E value
Match length
                   63
% identity
                   (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   42767
Seq. No.
                   asn701137855.h1
Seq. ID
Method
                   BLASTN
                   g2687432
NCBI GI
                   41
BLAST score
                   6.0e-14
E value
                   41
Match length
                   100
 % identity
                   Plumbago auriculata large subunit 26S ribosomal RNA gene,
 NCBI Description
                   partial sequence
                   42768
 Seq. No.
                   asn701137888.h1
 Seq. ID
                   BLASTN
 Method
                   g1220521
 NCBI GI
                   40
 BLAST score
```

6780

2.0e-13

E value



```
Match length
% identity
                  Glycine max TATA-box binding protein (STBP1) mRNA, complete
NCBI Description
                  42769
Seq. No.
                  asn701137911.hl
Seq. ID
Method
                  BLASTX
                  g2109275
NCBI GI
                  124
BLAST score
                  1.0e-16
E value
                  84
Match length
                  58
% identity
                  (U97106) downy mildew resistance protein RPP5 [Arabidopsis
NCBI Description
                  thaliana]
                   42770
Seq. No.
                   asn701137969.hl
Seq. ID
                  BLASTX
Method
                   g3080421
NCBI GI
                   150
BLAST score
                   1.0e-19
E value
                   70
Match length
                   65
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   42771
Seq. No.
                   asn701138005.h1
Seq. ID
                   BLASTN
Method
                   g170048
NCBI GI
                   37
BLAST score
                   1.0e-11
E value
                   53
Match length
                   92
% identity
                   Glycine max SbPRP1 gene encoding a proline-rich protein,
NCBI Description
                   complete cds
                   42772
Seq. No.
                   asn701138033.hl
Seq. ID
Method
                   BLASTN
                   q2623245
NCBI GI
                   82
BLAST score
                   1.0e-38
E value
                   162
Match length
 % identity
                   Pisum sativum poly(A) polymerase mRNA, nuclear gene
NCBI Description
                   encoding chloroplast protein, complete cds
 Seq. No.
                   42773
                   asn701138104.h1
 Seq. ID
Method
                   BLASTX
```

NCBI GI g2661840 BLAST score 258

1.0e-22 E value Match length 70 % identity 73

NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]

Method

NCBI GI

BLASTN

q3868723



```
Seq. No.
                  42774
Seq. ID
                  asn701138107.hl
Method
                  BLASTX
NCBI GI
                  g114806
BLAST score
                  146
                  1.0e-09
E value
Match length
                  30
% identity
                  83
                  BASIC BLUE PROTEIN (CUSACYANIN) (PLANTACYANIN) (CBP)
NCBI Description
                  >gi_65850_pir__BUKV basic blue protein - cucumber
                  >gi_223531_prf__0811264A protein,blue [Cucumis sativus]
Seq. No.
                  42775
Seq. ID
                  asn701138160.hl
Method
                  BLASTX
NCBI GI
                  q2982303
BLAST score
                  261
E value
                  4.0e-23
Match length
                  77
                  64
% identity
                  (AF051236) hypothetical protein [Picea mariana]
NCBI Description
Seq. No.
                  42776
Seq. ID
                  asn701138186.h1
Method
                  BLASTX
NCBI GI
                  q4220523
BLAST score
                  310
                  9.0e-29
E value
Match length
                  81
% identity
                  64
NCBI Description
                  (AL035356) putative alliin lyase [Arabidopsis thaliana]
                  42777
Seq. No.
Seq. ID
                  asn701138195.h1
Method
                  BLASTX
NCBI GI
                  g2827552
BLAST score
                  226
E value
                  6.0e-19
Match length
                  77
% identity
NCBI Description
                  (AL021635) predicted protein [Arabidopsis thaliana]
Seq. No.
                  42778
                  asn701138358.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220524
BLAST score
                  122
                  1.0è-14
E value
                  83
Match length
% identity
                  43
NCBI Description
                 (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  42779
Seq. ID
                  asn701138423.h1
```

BLAST score

Match length

E value

310 8.0e-29

85



```
BLAST score
E value
                  9.0e-10
                  98
Match length
                  90
% identity
                  Arabidopsis thaliana chromosome V map 60.5 cM, complete
NCBI Description
                  sequence [Arabidopsis thaliana]
                  42780
Seq. No.
                  asn701138432.hl
Seq. ID
                  BLASTX
Method
                  g4455158
NCBI GI
                  265
BLAST score
                  2.0e-23
E value
                  70
Match length
% identity
                   (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
                   42781
Seq. No.
                   asn701138450.h1
Seq. ID
                   BLASTX
Method
                   q4249391
NCBI GI
                   284
BLAST score
                   9.0e-26
E value
                   76
Match length
                   61
% identity
                   (AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase
NCBI Description
                   from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis
                   thalianal
                   42782
Seq. No.
                   asn701138454.h1
Seq. ID
                   BLASTX
Method
                   q4115379
NCBI GI
BLAST score
                   223
                   1.0e-18
E value
                   81
Match length
% identity
                   (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                   thaliana]
                   42783
 Seq. No.
                   asn701138465.h1
 Seq. ID
                   BLASTX
Method
                   g3386622
 NCBI GI
 BLAST score
                   303
                   5.0e-28
 E value
                   72
 Match length
                   79
 % identity
                   (AC004665) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   42784
 Seq. No.
                   asn701138480.hl
 Seq. ID
                   BLASTX
 Method
                   g3482933
 NCBI GI
```



% identity NCBI Description (AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana] Seq. No. 42785 asn701138505.h1 Seq. ID Method BLASTX q4512685 NCBI GI BLAST score 158 E value 6.0e-11 57 Match length % identity 54 (AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana] 42786 Seq. No. asn701138520.h1 Seq. ID Method BLASTX NCBI GI g3688181 BLAST score 255 E value 2.0e-22 Match length 69 % identity 68 (AL031804) putative protein (fragment) [Arabidopsis NCBI Description thaliana] Seq. No. 42787 Seq. ID asn701138560.h1 Method BLASTX NCBI GI g3184283 329 BLAST score E value 5.0e-31 Match length 83 % identity 78 NCBI Description (AC004136) putative TBP-binding protein [Arabidopsis thaliana] Seq. No. 42788 Seq. ID asn701138592.h1 Method BLASTX NCBI GI q2982268 BLAST score 204 2.0e-16 E value 60 Match length 72 % identity NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea mariana] 42789 Seq. No.

Seq. ID asn701138628.h1

Method BLASTX
NCBI GI g4263712
BLAST score 207
E value 1.0e-16
Match length 53
% identity 74



```
(AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                  thaliana]
                  42790
Seq. No.
                  asn701138659.h1
Seq. ID
                  BLASTX
Method
                  g1836028
NCBI GI
                  275
BLAST score
                  1.0e-24
E value
                  70
Match length
                  69
% identity
                  Cel6=cellulase 6 [Lycopersicon esculentum=tomatoes, Mill.,
NCBI Description
                  cv. Castlemart, flower abscission zones, Peptide Partial,
                  163 aa]
                  42791
Seq. No.
                  asn701138674.h1
Seq. ID
                  BLASTX
Method
                  g2660674
NCBI GI
                   193
BLAST score
                   4.0e-15
E value
                   68
Match length
                   56
% identity
                  (AC002342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   42792
Seq. No.
                   asn701138680.h1
Seq. ID
                   BLASTX
Method
                   g3236259
NCBI GI
                   308
BLAST score
                   1.0e-28
E value
                   82
Match length
                   71
% identity
                   (AC004684) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   42793
Seq. No.
                   asn701138723.h1
Seq. ID
                   BLASTX
Method
                   q3850823
NCBI GI
                   169
BLAST score
                   2.0e-12
E value
                   43
Match length
                   74
 % identity
                   (Y18351) U2 snRNP auxiliary factor, large subunit
NCBI Description
                   [Nicotiana plumbaginifolia]
                   42794
 Seq. No.
                   asn701138729.hl
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                   q169980
                   56
 BLAST score
                   6.0e-23
 E value
                   168
 Match length
```

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

85

% identity



```
42795
Seq. No.
Seq. ID
                  asn701138849.h1
Method
                  BLASTX
NCBI GI
                  g282963
BLAST score
                  286
                  7.0e-26
E value
Match length
                  61
                  80
% identity
                  transforming protein (myb) homolog (clone myb.Ph2) - garden
NCBI Description
                  petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia
                  x hybrida]
                  42796
Seq. No.
Seq. ID
                  asn701138855.hl
Method
                  BLASTN
NCBI GI
                  g4455262
BLAST score
                  60
                  3.0e-25
E value
Match length
                  124
                  87
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                   (ESSAII project)
                  42797
Seq. No.
                  asn701138923.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3327389
BLAST score
                  208
                  8.0e-17
E value
Match length
                  74
% identity
                  59
                  (AC004483) putative DNA replication licensing factor, mcm5
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  42798
Seq. ID
                  asn701138964.h1
Method
                  BLASTN
NCBI GI
                  q169980
BLAST score
                  82
                  2.0e-38
E value
Match length
                  230
                  87
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                  42799
Seq. ID
                  asn701139023.hl
Method
                  BLASTX
                  q169459
```

NCBI GI BLAST score 217 7.0e-18 E value Match length 72 % identity 56

NCBI Description (M18538) pop3 peptide [Populus balsamifera subsp.

trichocarpa X Populus deltoides]

Seq. No.

42800

Seq. ID

asn701139024.hl

BLAST score

E value

174 7.0e-13



```
BLASTX
Method
                  g3953471
NCBI GI
                  289
BLAST score
                  2.0e-26
E value
                  76
Match length
                  67
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                  42801
Seq. No.
                  asn701139073.h1
Seq. ID
                  BLASTN
Method
                  g517257
NCBI GI
                  40
BLAST score
                  2.0e-13
E value
Match length
                   52
                   94
% identity
NCBI Description Z.mays MNBla mRNA for DNA-binding protein
                   42802
Seq. No.
                   asn701139117.h1
Seq. ID
                   BLASTX
Method
                   g1652704
NCBI GI
                   141
BLAST score
                   6.0e-09
E value
                   64
Match length
                   42
% identity
                   (D90907) hypothetical protein [Synechocystis sp.]
NCBI Description
                   42803
Seq. No.
                   asn701139178.h1
Seq. ID
                   BLASTX
Method
                   g1350983
NCBI GI
                   270
BLAST score
                   2.0e-24
E value
                   57
Match length
                   91
 % identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                   42804
 Seq. No.
                   asn701139191.hl
 Seq. ID
                   BLASTX
 Method
                   q3367517
 NCBI GI
                   191
 BLAST score
                   7.0e-15
 E value
                   65
 Match length
                   54
 % identity
                   (AC004392) Similar to F4I1.26 putative beta-glucosidase
 NCBI Description
                   gi_3128187 from A. thaliana BAC gb_AC004521. ESTs
                   gb_N97083, gb_F19868 and gb_F15482 come from this gene.
                    [Arabidopsis thaliana]
                    42805
 Seq. No.
                   asn701139209.h1
 Seq. ID
                   BLASTX
 Method
                    g2809263
 NCBI GI
```



Match length 82 % identity 45

NCBI Description (AC002560) F21B7.32 [Arabidopsis thaliana]

Seq. No.

42806

Seq. ID asn701139237.h1

Method BLASTX
NCBI GI g3875246
BLAST score 202
E value 3.0e-16
Match length 77
% identity 28

NCBI Description (Z81490) similar to WD domain, G-beta repeats (2 domains);

cDNA EST EMBL: T00482 comes from this gene; cDNA EST

EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene;

Seq. No. 42807

Seq. ID asn701139347.h1

Method BLASTX
NCBI GI g4508083
BLAST score 148
E value 8.0e-10
Match length 85
% identity 8

NCBI Description (AC005882) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 42808

Seq. ID asn701139348.h1

Method BLASTX
NCBI GI g2827699
BLAST score 252
E value 5.0e-22
Match length 79
% identity 63

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 42809

Seq. ID asn701139365.hl

Method BLASTX
NCBI GI g2827082
BLAST score 217
E value 7.0e-18
Match length 51
% identity 80

NCBI Description (AF020272) malate dehydrogenase [Medicago sativa]

Seq. No. 42810

Seq. ID asn701139406.h1

Method BLASTX
NCBI GI g4128133
BLAST score 141
E value 5.0e-09
Match length 44
% identity 59

NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]



Seq. No. 42811

Seq. ID asn701139414.h1

Method BLASTN
NCBI GI g2304954
BLAST score 257
E value 1.0e-143
Match length 269
% identity 99

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No. 42812

Seq. ID asn701139435.h1

Method BLASTN
NCBI GI g296442
BLAST score 164
E value 2.0e-87
Match length 164
% identity 100

NCBI Description G.max ADR11 mRNA

Seq. No. 42813

Seq. ID asn701139440.hl

Method BLASTX
NCBI GI g1168470
BLAST score 292
E value 1.0e-26
Match length 72
% identity 78

NCBI Description PROTEIN KINASE APKIA >gi_282877_pir__S28615 protein kinase,

tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522)

protein tyrosine-serine-threonine kinase [Arabidopsis

thaliana]

Seq. No. 42814

Seq. ID asn701139475.h1

Method BLASTN 92304954
BLAST score 257
E value 1.0e-143
Match length 257
% identity 100

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No. 42815

Seq. ID asn701139491.h1

Method BLASTN
NCBI GI g1183936
BLAST score 72
E value 2.0e-32
Match length 174
% identity 86

NCBI Description P.sativum 5S rRNA gene

Seq. No. 42816

Seq. ID asn701139505.h1

Method BLASTX



```
NCBI GI
                  g1694621
                  205
BLAST score
                  2.0e-16
E value
                  65
Match length
                  68
% identity
NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
                  42817
Seq. No.
                  asn701139596.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1653245
BLAST score
                  212
E value
                  2.0e-17
Match length
                  72
% identity
NCBI Description (D90912) hypothetical protein [Synechocystis sp.]
                  42818
Seq. No.
                  asn701139603.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171429
                  192
BLAST score
                  5.0e-15
E value
Match length
                  71
% identity
                  35
NCBI Description
                 (U44028) CKC [Arabidopsis thaliana]
                  42819
Seq. No.
Seq. ID
                  asn701139611.h1
Method
                  BLASTX
NCBI GI
                  g537313
BLAST score
                  145
E value
                  2.0e-09
Match length
                  36
% identity
                  78
NCBI Description (L36159) unknown protein [Medicago sativa]
Seq. No.
                  42820
Seq. ID
                  asn701139613.hl
                  BLASTN
Method
                  g1575730
NCBI GI
                  155
BLAST score
E value
                  6.0e-82
Match length
                  155
                  100
% identity
NCBI Description Glycine max 14-3-3 related protein SGF14D mRNA, complete
                  cds
                  42821
Seq. No.
                  asn701139647.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g510545
                  56
BLAST score
E value
                  4.0e-23
Match length
                  144
                  85
% identity
```

NCBI Description P.sativum mRNA for starch branching enzyme I



```
42822
Seq. No.
                  asn701139649.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220535
BLAST score
                  182
                  1.0e-21
E value
Match length
                  66
% identity
                  80
                  (AL035356) clathrin coat assembly like protein [Arabidopsis
NCBI Description
                  thaliana]
                  42823
Seq. No.
                  asn701139694.h1
Seq. ID
Method
                  BLASTX
                  g2443280
NCBI GI
                  167
BLAST score
                  5.0e-12
E value
                  86
Match length
% identity
                  44
                 (AB001432) motor domain of KIF15 [Mus musculus]
NCBI Description
                  42824
Seq. No.
Seq. ID
                  asn701139713.h1
Method
                  BLASTX
                  q3142300
NCBI GI
                  154
BLAST score
                  2.0e-10
E value
Match length
                  62
                  48
% identity
                  (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                  protein PRP39 gb L29224 from S. cerevisiae. ESTs gb_R64908
                  and gb T88158, gb N38703 and gb AA651043 come from this
                  gene. [Arabidopsis thaliana]
                  42825
Seq. No.
Seq. ID
                  asn701139741.h1
Method
                  BLASTX
                  g1174850
NCBI GI
BLAST score
                  267
                  1.0e-23
E value
Match length
                  58
                  86
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)
Seq. No.
                  42826
                  asn701139856.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350783
BLAST score
                  190
                  1.0e-14
E value
```

Match length 100 % identity 4

NCBI Description RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR

>gi_282883_pir__S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660)



receptor-like protein kinase [Arabidopsis thaliana] >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 42827 Seq. ID asn701139877.h1 Method BLASTX NCBI GI q3269291 BLAST score 144 E value 1.0e-09 Match length 41 % identity 66 (AL030978) putative receptor protein kinase [Arabidopsis NCBI Description thaliana] 42828 Seq. No. asn701139885.h1 Seq. ID Method BLASTX NCBI GI g3250676 BLAST score 232 E value 1.0e-19 Match length 91 % identity 51 NCBI Description (AL024486) putative protein [Arabidopsis thaliana] Seq. No. 42829 asn701139962.hl Seq. ID Method BLASTX NCBI GI q3158476 BLAST score 189 E value 5.0e-17 Match length 69 % identity 77 (AF067185) aquaporin 2 [Samanea saman] NCBI Description Seq. No. 42830 Seq. ID asn701139964.h1 Method BLASTN NCBI GI q3287269 BLAST score 43 4.0e-15 E value Match length 67 % identity 91 NCBI Description S.tuberosum mRNA for protein involved in starch metabolism 42831 Seq. No. Seq. ID asn701140012.hl BLASTX Method NCBI GI q3158476 BLAST score 186 E value 3.0e-14 Match length 47 70 % identity NCBI Description (AF067185) aquaporin 2 [Samanea saman]

Seq. No. 42832

Seq. ID asn701140030.h1



```
Method
                  BLASTN
NCBI GI
                  g170073
BLAST score
                  164
                  3.0e-87
E value
                  168
Match length
% identity
                  99
NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds
                  42833
Seq. No.
Seq. ID
                  asn701140040.h1
Method
                  BLASTN
NCBI GI
                  g312571
BLAST score
                  55
E value
                  3.0e-22
Match length
                  59
% identity
                  98
NCBI Description L.angustifolius 26S rRNA (partial)
                  42834
Seq. No.
                  asn701140069.h1
Seq. ID
Method
                  BLASTX
                  g3641837
NCBI GI
                  329
BLAST score
                  5.0e-31
E value
Match length
                  87
                  77
% identity
NCBI Description
                  (AL023094) Nonclathrin coat protein gamma - like protein
                  [Arabidopsis thaliana]
                  42835
Seq. No.
                  asn701140070.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1514643
BLAST score
                  269
E value
                  5.0e-24
Match length
                  86
% identity
                  56
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                  42836
Seq. No.
Seq. ID
                  asn701140071.h1
Method
                  BLASTX
NCBI GI
                  g1839188
                  278
BLAST score
                  4.0e-25
E value
Match length
                  81
% identity
NCBI Description
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
                  42837
Seq. No.
Seq. ID
                  asn701140075.hl
Method
                  BLASTX
NCBI GI
                  g3377517
```

NCBI GI g3377517
BLAST score 140
E value 7.0e-09
Match length 60
% identity 42



NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 42838
Seq. ID 42838 asn701140084.h1

Method BLASTX
NCBI GI g2652938
BLAST score 386
E value 1.0e-37
Match length 88
% identity 52

NCBI Description (Z47554) orf [Zea mays]

Seq. No. 42839

Seq. ID asn701140114.h1

Method BLASTX
NCBI GI g3582345
BLAST score 199
E value 9.0e-16
Match length 62
% identity 56

NCBI Description (AC005496) putative villin protein, 3' partial [Arabidopsis

thaliana]

Seq. No. 42840

Seq. ID asn701140116.h1

Method BLASTX
NCBI GI g3738298
BLAST score 288
E value 3.0e-26
Match length 91
% identity 65

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

>gi 4249394 (AC006072) unknown protein [Arabidopsis

thaliana]

Seq. No. 42841

Seq. ID asn701140149.h1

Method BLASTN
NCBI GI g1556445
BLAST score 102
E value 2.0e-50
Match length 198
% identity 88

NCBI Description Hordeum vulgare alpha tubulin (tubA) mRNA, complete cds

Seq. No. 42842

Seq. ID asn701140195.h1

Method BLASTX
NCBI GI g3482924
BLAST score 214
E value 1.0e-17
Match length 76
% identity 57

NCBI Description (AC003970) Highly similar to cinnamyl alcohol

dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No. 42843



```
asn701140219.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2316102
                  369
BLAST score
                  9.0e-36
E value
                  83
Match length
% identity
                 (AF010168) gibberellin 3 beta-hydroxylase [Pisum sativum]
NCBI Description
                  42844
Seq. No.
Seq. ID
                  asn701140225.h1
Method
                  BLASTX
NCBI GI
                  q4455202
BLAST score
                  219
E value
                  3.0e-18
Match length
                  72
% identity
                  (AL035440) putative APG protein [Arabidopsis thaliana]
NCBI Description
                  42845
Seq. No.
                  asn701140306.h1
Seq. ID
Method
                  BLASTN
                  g296444
NCBI GI
                  252
BLAST score
E value
                  1.0e-140
Match length
                  268
                  99
% identity
NCBI Description G.max ADR6 mRNA
                  42846
Seq. No.
Seq. ID
                  asn701140340.h1
Method
                  BLASTX
NCBI GI
                  g728868
BLAST score
                  168
E value
                  4.0e-12
                  86
Match length
                  38
% identity
                  ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
NCBI Description
                  >gi_99824_pir__S16748 proline-rich protein - rape
                   (fragment) >gi_22597_emb_CAA42924 (X60376) proline-rich
                  protein [Brassica napus]
Seq. No.
                  42847
Seq. ID
                  asn701140364.h1
Method
                  BLASTX
NCBI GI
                  g3510261
BLAST score
                  189
                  1.0e-14
E value
                  56
Match length
% identity
                  66
NCBI Description
                  (AC005310) hypothetical protein [Arabidopsis thaliana]
                  42848
```

Seq. No.

Seq. ID asn701140366.h1

BLASTX Method g537319 NCBI GI BLAST score 234

```
7.0e-20
E value
Match length
                  58
                  76
% identity
                  (L36158) peroxidase [Medicago sativa]
NCBI Description
Seq. No.
                  42849
Seq. ID
                  asn701140382.hl
Method
                  BLASTN
NCBI GI
                  g2995454
BLAST score
                  38
E value
                  2.0e-12
Match length
                  66
% identity
                  89
                  L.luteus mRNA for tRNA-glutamine synthetase
NCBI Description
Seq. No.
                  42850
                  asn701140430.h1
Seq. ID
Method
                  BLASTX
                  q2342727
NCBI GI
BLAST score
                  338
                  6.0e-32
E value
Match length
                  85
% identity
                  66
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  42851
Seq. No.
                  asn701140457.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q961450
                  157
BLAST score
                  8.0e-11
E value
                  62
Match length
                  47
% identity
NCBI Description
                  nucleolin. [Homo sapiens]
                  42852
Seq. No.
Seq. ID
                  asn701140486.h1
Method
                  BLASTX
```

(D63879) KIAA0156 gene product is related to Xenopus

NCBI GI g1074176 BLAST score 173 E value 9.0e-13 74 Match length 43 % identity

heat shock protein (dnaJ) homolog - Haemophilus influenzae NCBI Description (strain Rd KW20) >gi 1574168 (U32803) heat shock protein

(dnaJ) [Haemophilus influenzae Rd]

Seq. No. 42853 Seq. ID asn701140549.h1 Method BLASTX

NCBI GI g3036813 BLAST score 269 6.0e-24E value Match length 87 57 % identity

NCBI Description (AL022373) hypothetical protein [Arabidopsis thaliana]



```
Seq. No. 42854
```

Seq. ID asn701140583.h1

Method BLASTX
NCBI GI g1888357
BLAST score 325
E value 2.0e-30
Match length 85
% identity 67

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >qi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seg. No. 42855

Seq. ID asn701140610.h1

Method BLASTN
NCBI GI g3522932
BLAST score 108
E value 7.0e-54
Match length 212
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC F14M4 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 42856

Seq. ID asn701140631.h1

Method BLASTX
NCBI GI g541943
BLAST score 297
E value 3.0e-27
Match length 67
% identity 75

NCBI Description metallothionein - soybean >gi_228682_prf_ 1808316A

metallothionein-like protein [Glycine max]

Seq. No. 42857

Seq. ID asn701140686.h1

Method BLASTX
NCBI GI g2244849
BLAST score 167
E value 5.0e-12
Match length 81
% identity 41

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 42858

Seq. ID asn701140721.h1

Method BLASTN
NCBI GI g166379
BLAST score 132
E value 3.0e-68
Match length 212
% identity 74

NCBI Description Alfalfa glucose-regulated endoplasmic reticular protein

mRNA, complete cds

Seq. No. 42859

NCBI Description



```
asn701140722.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170089
BLAST score
                  40
E value
                  1.0e-13
Match length
                  54
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
Seq. No.
                  42860
                  asn701140726.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g296444
BLAST score
                  233
E value
                  1.0e-128
Match length
                  253
                  98
% identity
NCBI Description G.max ADR6 mRNA
Seq. No.
                  42861
                  asn701140738.h1
Seq. ID
Method
                  BLASTX
                  g3201627
NCBI GI
BLAST score
                  155
E value
                  7.0e-11
Match length
                  41
                  59
% identity
                  (AC004669) putative SWH1 protein [Arabidopsis thaliana]
NCBI Description
                  42862
Seq. No.
Seq. ID
                  asn701140739.h1
Method
                  BLASTX
NCBI GI
                  q1169017
BLAST score
                  142
E value
                  4.0e-09
Match length
                  58
% identity
                  24
                  COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
NCBI Description
                  >gi 1078361 pir B55123 coatomer complex beta' chain -
                  yeast (Saccharomyces cerevisiae) >gi 595415 (U11237)
                  betaprime COP [Saccharomyces cerevisiae]
                  >gi 1246841_emb CAA63359 (X92670) see also U11237; yeast
                  coatomer subunit [Saccharomyces cerevisiae]
                  >gi 1322710 emb CAA96848 (Z72659) ORF YGL137w
                  [Saccharomyces cerevisiae]
Seq. No.
                  42863
Seq. ID
                  asn701140765.h1
Method
                  BLASTX
NCBI GI
                  g1532175
BLAST score
                  268
                  7.0e-24
E value
Match length
                  55
% identity
                  82
```

[Arabidopsis thaliana]

(U63815) similar to protein disulfide isomerase

Method

NCBI GI BLAST score BLASTX g3114332

162



```
42864
Seq. No.
                  asn701140767.h1
Seq. ID
                  BLASTN
Method
                  g459199
NCBI GI
                  109
BLAST score
                  2.0e-54
E value
                  197
Match length
                  89
% identity
NCBI Description Gossypium hirsutum vacuolar H+-ATPase subunit B mRNA,
                  partial cds
                  42865
Seq. No.
                  asn701140772.h1
Seq. ID
Method
                  BLASTX
                  g571484
NCBI GI
                   290
BLAST score
                   2.0e-26
E value
                   68
Match length
                   81
% identity
                  (U16727) peroxidase precursor [Medicago truncatula]
NCBI Description
                   42866
Seq. No.
                   asn701140905.h1
Seq. ID
                   BLASTN
Method
                   g3941288
NCBI GI
                   133
BLAST score
                   8.0e-69
E value
                   249
Match length
                   89
% identity
NCBI Description Pisum sativum similarity to SCAMP37 (psam2) mRNA, complete
                   cds
                   42867
Seq. No.
                   asn701140979.h1
Seq. ID
Method
                   BLASTN
                   g2598656
NCBI GI
BLAST score
                   139
                   2.0e-72
E value
                   267
Match length
                   88
% identity
NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
                   42868
Seq. No.
                   asn701141080.hl
Seq. ID
Method
                   BLASTN
                   q4127877
NCBI GI
                   135
BLAST score
E value
                   4.0e-70
Match length
                   217
                   97
 % identity
NCBI Description Glycine max mRNA for NDX1 homeobox protein, partial
                   42869
 Seq. No.
                   asn701141106.hl
 Seq. ID
```



E value 2.0e-11
Match length 40
% identity 68
NCBI Description Chain A

Chain A, Beta-Glucosidase A From Bacillus Polymyxa >gi_3114333 pdb_1BGA_B Chain B, Beta-Glucosidase A From Bacillus Polymyxa >gi_3114334_pdb_1BGA_C Chain C,

Beta-Glucosidase A From Bacillus Polymyxa

>gi 3114335_pdb_1BGA_D Chain D, Beta-Glucosidase A From

Bacillus Polymyxa

Seq. No. 42870

Seq. ID asn701141158.h1

Method BLASTX
NCBI GI g3914394
BLAST score 257
E value 1.0e-22
Match length 64
% identity 72

NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_2118335_pir__S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No. 42871

Seq. ID asn701141171.h1

Method BLASTX
NCBI GI g1170619
BLAST score 204
E value 2.0e-16
Match length 84
% identity 45

NCBI Description KINESIN-LIKE PROTEIN A >gi_479594_pir__S34830

kinesin-related protein katA - Arabidopsis thaliana >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi 2911084 emb CAA17546 (AL021960) kinesin-related

protein katA [Arabidopsis thaliana]

Seq. No. 42872

Seq. ID asn701141234.h1

Method BLASTX
NCBI GI g3882151
BLAST score 167
E value 5.0e-12
Match length 82
% identity 37

NCBI Description (AB018258) KIAA0715 protein [Homo sapiens]

Seq. No. 42873

Seq. ID asn701141320.h1

Method BLASTX
NCBI GI g2062167
BLAST score 276
E value 9.0e-25
Match length 72
% identity 68



NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No. 42874

Seq. ID asn701141344.h1

Method BLASTX
NCBI GI g4063743
BLAST score 229
E value 3.0e-19
Match length 83
% identity 59

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No. 42875

Seq. ID asn701141372.h1

Method BLASTN
NCBI GI g296442
BLAST score 45
E value 2.0e-16
Match length 93
% identity 92

NCBI Description G.max ADR11 mRNA

Seq. No. 42876

Seq. ID asn701141405.h1

Method BLASTX
NCBI GI g2760323
BLAST score 343
E value 1.0e-32
Match length 79
% identity 77

NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No. 42877

Seq. ID asn701141414.h1

Method BLASTX
NCBI GI g3861371
BLAST score 141
E value 6.0e-09
Match length 82
% identity 40

NCBI Description (AJ235273) SFHB PROTEIN HOMOLOG (sfhB) [Rickettsia

prowazekii]

Seq. No. 42878

Seq. ID asn701141459.h1

Method BLASTX
NCBI GI g3834316
BLAST score 252
E value 5.0e-22
Match length 78
% identity 69

NCBI Description (AC005679) Similar to gb_X16648 pathogenesis related protein from Hordeum vulgare. EST gb_Z18206 comes from

this gene. [Arabidopsis thaliana]

Seq. No. 42879

E value

1.0e-35



```
asn701141552.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  245
                  3.0e-21
E value
                  86
Match length
% identity
                  59
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                  42880
Seq. No.
Seq. ID
                  asn701141553.h1
Method
                  BLASTX
NCBI GI
                  g1781326
BLAST score
                  170
E value
                  2.0e-12
Match length
                  56
% identity
                  59
NCBI Description (Y10464) peroxidase [Spinacia oleracea]
                  42881
Seq. No.
                  asn701141559.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2827558
BLAST score
                  339
                  3.0e-32
E value
Match length
                  85
                  78
% identity
                  (ALO21635) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   42882
Seq. No.
Seq. ID
                  asn701141594.hl
                  BLASTX
Method
                  g4538939
NCBI GI
                  189
BLAST score
E value
                   2.0e-17
Match length
                   68
% identity
                  (ALO49483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   42883
Seq. No.
                  asn701141630.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g310560
BLAST score
                  259
E value
                   1.0e-144
Match length
                  259
% identity
                   100
NCBI Description Soybean ascorbate peroxidase mRNA, complete cds
Seq. No.
                   42884
Seq. ID
                   asn701141647.hl
Method
                  BLASTX
NCBI GI
                   g927428
BLAST score
                   369
```



```
Match length
% identity
NCBI Description
                  (X86733) fis1 [Linum usitatissimum]
Seq. No.
                  42885
Seq. ID
                  asn701141658.h1
Method
                  BLASTN
NCBI GI
                  q441205
BLAST score
                  65
E value
                  2.0e-28
Match length
                  81
                  95
% identity
NCBI Description Soybean lox1gm4 gene encoding lipxygenase L-4
Seq. No.
                  42886
                  asn701141696.hl
Seq. ID
                  BLASTX
Method
                  g2147966
NCBI GI
BLAST score
                  179
                  2.0e-13
E value
Match length
                  50
                  66
% identity
                  probable 1-acyl-sn-glycerol-3-phosphate acyltransferase -
NCBI Description
                  Limnanthes douglasii >gi_1067138_emb_CAA88620_ (Z48730)
                  1-acyl-sn-glycerol-3-phosphate acyltransferase (putative)
                  [Limnanthes douglasii]
                  42887
Seq. No.
Seq. ID
                  asn701141718.h1
Method
                  BLASTX
NCBI GI
                  g2982434
                  199
BLAST score
E value
                  3.0e-24
Match length
                  74
                  76
% identity
                  (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
                  42888
Seq. No.
Seq. ID
                  asn701141775.h1
Method
                  BLASTN
NCBI GI
                  g296408
BLAST score
                  89
E value
                  1.0e-42
Match length
                  204
                  87
% identity
NCBI Description G.max ADR12 mRNA
                  42889
Seq. No.
                  asn701141804.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g19655
```

Method BLASTN
NCBI GI g19655
BLAST score 47
E value 2.0e-17
Match length 84
% identity 96

NCBI Description M.sativa 26S rRNA



Seq. No. 42890 Seq. ID asn701141967.h1 Method BLASTN NCBI GI g18761 BLAST score 179 3.0e-96 E value 258 Match length 97 % identity

NCBI Description Soybean stem mRNA for 31 kD glycoprotein

Seq. No. 42891

Seq. ID asn701141985.h1

Method BLASTX NCBI GI q4406780 BLAST score 192 E value 4.0e-15 Match length 76 % identity 46

(AC006532) putative multispanning membrane protein NCBI Description

[Arabidopsis thaliana]

42892 Seq. No.

asn701142011.h1 Seq. ID

BLASTX Method NCBI GI g2213594 BLAST score 294 E value 7.0e-27 92 Match length % identity 61

NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

42893 Seq. No.

Seq. ID asn701142029.h1

Method BLASTN NCBI GI g533691 BLAST score 102 3.0e-50 E value 102 Match length 100 % identity

NCBI Description Glycine max Essex protease inhibitor mRNA, complete cds

42894 Seq. No.

Seq. ID asn701142035.h1

BLASTN Method NCBI GI g2290779 BLAST score 72 E value 2.0e-32 Match length 140 % identity 88

NCBI Description Solanum commersonii heat shock cognate protein (SCHSP70)

mRNA, complete cds

Seq. No. 42895

asn701142072,h1 Seq. ID

Method BLASTN g556346 NCBI GI BLAST score 153



```
1.0e-80
E value
                  273
Match length
                  89
% identity
NCBI Description Pea protein kinase (PK5) mRNA, complete cds
                  42896
Seq. No.
                  asn701142119.hl
Seq. ID
                  BLASTN
Method
                  g296444
NCBI GI
BLAST score
                  266
                  1.0e-148
E value
                  278
Match length
                  99
% identity
NCBI Description G.max ADR6 mRNA
                  42897
Seq. No.
                  asn701142178.h1
Seq. ID
                  BLASTN
Method
                  g4191262
NCBI GI
                   34
BLAST score
                   9.0e-10
E value
                   54
Match length
                   91
% identity
NCBI Description Pisum sativum gda-1 gene
                   42898
Seq. No.
                   asn701142328.h1
Seq. ID
                   BLASTX
Method
                   g4567281
NCBI GI
                   234
BLAST score
                   9.0e-20
E value
                   73
Match length
                   60
% identity
                  (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                   42899
 Seq. No.
                   asn701142348.h1
 Seq. ID
                   BLASTN
 Method
                   g2739005
NCBI GI
                   52
 BLAST score
                   1.0e-20
 E value
                   108
 Match length
                   87
 % identity
 NCBI Description Glycine max cytochrome P450 monooxygenase CYP93C1p
                   (CYP93C1) mRNA, complete cds
                   42900
 Seq. No.
                   asn701142362.h1
 Seq. ID
                   BLASTN
 Method
```

g4324966 NCBI GI BLAST score 175

8.0e - 94E value 183 Match length % identity

NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds

42901 Seq. No.



```
asn701142383.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1143445
BLAST score
                  296
E value
                  5.0e-27
Match length
                  97
% identity
                  60
                  (X88797) cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]
NCBI Description
                  42902
Seq. No.
                  asn701142390.hl
Seq. ID
                  BLASTX
Method
                  g1531758
NCBI GI
BLAST score
                  378
                  1.0e-36
E value
                  91
Match length
                  80
% identity
                  (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
NCBI Description
                  unknown protein [Arabidopsis thaliana]
                  42903
Seq. No.
                  asn701142402.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2191136
                  159
BLAST score
                  5.0e-11
E value
                  75
Match length
                   44
% identity
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                  thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                  42904
Seq. No.
Seq. ID
                  asn701142435.h1
                  BLASTN
Method
                  g166421
NCBI GI
BLAST score
                  110
                  4.0e-55
E value
Match length
                  218
% identity
                  Medicago sativa ubiquitin carrier protein mRNA, complete
NCBI Description
                  cds
Seq. No.
                   42905
Seq. ID
                  asn701142474.h1
Method
                  BLASTX
NCBI GI
                  g3128192
BLAST score
                  168
E value
                  3.0e-12
Match length
                  52
% identity
                   62
                  (AC004521) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
```

•

Seq. No. 42906

Seq. ID asn701142481.h1

Method BLASTX



```
NCBI GI
                  g3128192
BLAST score
                  236
                  4.0e-20
E value
                  52
Match length
% identity
                  77
NCBI Description
                  (AC004521) axi 1-like protein [Arabidopsis thaliana]
                  42907
Seq. No.
Seq. ID
                  asn701142523.h1
Method
                  BLASTX
NCBI GI
                  g4510346
BLAST score
                  285
E value
                  8.0e-26
Match length
                  67
% identity
                  85
NCBI Description
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
```

42908 Seq. No. asn701142524.h1 Seq. ID Method BLASTN NCBI GI g2656031 BLAST score 40

2.0e-13 E value Match length 125 % identity 89

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MXC20

Seq. No. 42909

asn701142534.h1 Seq. ID

Method BLASTX NCBI GI g2851394 BLAST score 172 E value 2.0e-22 Match length 84 % identity 68

BETA ENOLASE (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (SKELETAL NCBI Description

MUSCLE ENOLASE)

Seq. No. 42910

Seq. ID asn701142548.h1

Method BLASTX g4512660 NCBI GI BLAST score 280 E value 3.0e-25 Match length 90 % identity 56

(AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description

>qi 4544467 qb AAD22374.1 AC006580 6 (AC006580)

hypothetical protein [Arabidopsis thaliana]

42911 Seq. No.

Seq. ID asn701142561.h1

Method BLASTX NCBI GI g3452263 BLAST score 351 1.0e-33 E value



```
86
Match length
                  76
% identity
                  (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
NCBI Description
                  thaliana]
                  42912
Seq. No.
                  asn701142585.h1
Seq. ID
Method
                  BLASTX
                  g1491776
NCBI GI
                  140
BLAST score
                  7.0e-09
E value
                  66
Match length
                  48
% identity
NCBI Description (M37636) cationic peroxidase [Arachis hypogaea]
                  42913
Seq. No.
                  asn701142617.h1
Seq. ID
                  BLASTN
Method
                  g3158473
NCBI GI
BLAST score
                   36
                   4.0e-11
E value
                   87
Match length
                   85
% identity
NCBI Description Samanea saman aquaporin 1 (Aqp1) mRNA, complete cds
                   42914
Seq. No.
                   asn701142626.h1
Seq. ID
                   BLASTX
Method
                   g4322421
NCBI GI
BLAST score
                   164
                   3.0e-23
E value
                   79
Match length
                   70
% identity
                   (AF085230) cadmium resistance factor 1 [Arabidopsis
NCBI Description
                   thaliana]
                   42915
Seq. No.
                   asn701142734.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q535583
                   85
BLAST score
                   3.0e-40
E value
Match length
                   169
                   88
% identity
NCBI Description Medicago sativa adenosylhomocysteinase mRNA, complete cds
                   42916
Seq. No.
                   asn701142764.hl
Seq. ID
Method
                   BLASTX
                   q3341443
NCBI GI
BLAST score
                   197
```

1.0e-16 E value 73 Match length % identity 55

(AJ223074) acid phosphatase [Glycine max] NCBI Description

Seq. No.

42917



```
asn701142782.hl
Seq. ID
                  BLASTX
Method
                  g2498629
NCBI GI
                  139
BLAST score
                  7.0e-09
E value
                   44
Match length
                   50
% identity
                  TRANSCRIPTIONAL REPRESSOR NF-X1 >gi_2135825_pir__I38869
NCBI Description
                   NFX1 - human >gi_563217 (U15306) NFX1 [Homo sapiens]
                   >gi 4505387_ref_\overline{\text{NP}}_002495.1_pNFX1_ nuclear transcription
                   factor, X-box binding
                   42918
Seq. No.
                   asn701142788.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g556346
BLAST score
                   120
                   4.0e-61
E value
                   208
Match length
% identity
                   89
NCBI Description Pea protein kinase (PK5) mRNA, complete cds
                   42919
Seq. No.
                   asn701142796.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1657381
BLAST score
                   37
E value
                   1.0e-11
Match length
                   57
                   91
% identity
NCBI Description P.sativum mRNA for cholinephosphate cytidylyltransferase
                   42920
Seq. No.
                   asn701142805.h1
Seq. ID
                   BLASTN
Method
                   g255572
NCBI GI
                   46
BLAST score
                   6.0e-17
E value
                   111
Match length
                   85
% identity
                   small auxin up RNA gene cluster: orf 15A [Glycine
NCBI Description
                   max=soybeans, cv. Wayne, Genomic, 637 nt]
                   42921
Seq. No.
                   asn701142852.h1
 Seq. ID
                   BLASTX
Method
                   g4406777
NCBI GI
                   448
BLAST score
                   5.0e-45
E value
                   86
Match length
 % identity
                    (AC006532) putative zinc-finger protein [Arabidopsis
 NCBI Description
                   thaliana]
```

Seq. No.

42922

Seq. ID asn701142884.h1

Method BLASTX



```
NCBI GI g2642450
BLAST score 374
E value 2.0e-36
Match length 85
% identity 79
NCBI Description (AC002391) putative metal ion transporter (Nramp)
[Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]
```

Seq. No. 42923 Seq. ID asn701142885.h1

Method BLASTN
NCBI GI g2304954
BLAST score 244
E value 1.0e-135
Match length 256
% identity 99

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

 Seq. No.
 42924

 Seq. ID
 asn701142886.h1

 Method
 BLASTX

 NCBI GI
 g1001311

 BLAST score
 252

 E value
 5.0e-22

 Match length
 82

Match length 82 % identity 55

NCBI Description (D64006) hypothetical protein [Synechocystis sp.]

Seq. No. 42925

Seq. ID asn701142993.h2

Method BLASTN
NCBI GI g1196896
BLAST score 43
E value 2.0e-15
Match length 70
% identity 92

NCBI Description Glycine max acidic ribosomal protein PO mRNA, complete cds

Seq. No. 42926

Seq. ID asn701143101.h1

Method BLASTN
NCBI GI g1675195
BLAST score 127
E value 3.0e-65
Match length 231
% identity 89

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

Seq. No. 42927

Seq. ID asn701143140.h1

Method BLASTX
NCBI GI g3025189
BLAST score 212
E value 3.0e-17
Match length 88



```
% identity
                  HYPOTHETICAL 67.1 KD PROTEIN SLL1770
NCBI Description
                  >gi 1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis
                  42928
Seq. No.
                  asn701143172.hl
Seq. ID
                  BLASTX
Method
                  q131770
NCBI GI
                  223
BLAST score
                  1.0e-18
E value
                  64
Match length
                  66
% identity
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                  (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                  [Dictyostelium discoideum]
                  42929
Seq. No.
                  asn701143201.h1
Seq. ID
                  BLASTN
Method
                  q169922
NCBI GI
                  86
BLAST score
                   9.0e-41
E value
                   90
Match length
% identity
NCBI Description Soybean beta-1,3-endoglucanase mRNA, complete cds
                   42930
Seq. No.
                   asn701143241.hl
Seq. ID
                   BLASTN
Method
                   q3242700
NCBI GI
                   47
BLAST score
                   2.0e-17
E value
                   131
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC F26B6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   42931
 Seq. No.
Seq. ID
                   asn701143257.hl
Method
                   BLASTX
                   g4220480
NCBI GI
BLAST score
                   212
                   2.0e-17
 E value
                   86
Match length
 % identity
                   13
                  (AC006069) unknown protein [Arabidopsis thaliana]
 NCBI Description
```

Seq. No. Seq. ID

42932

asn701143268.h1

Method BLASTX g4204281 NCBI GI

148 BLAST score 8.0e-10 E value 71 Match length

% identity (AC004146) Hypothetical protein [Arabidopsis thaliana] NCBI Description 42933 Seq. No. asn701143402.h1 Seq. ID BLASTN Method g310575 NCBI GI 94 BLAST score 1.0e-45 E value 218 Match length 86 % identity Glycine max nodulin-26 mRNA, complete cds NCBI Description 42934 Seq. No. awf700836344.h1 Seq. ID BLASTX Method g2352492 NCBI GI 205 BLAST score 1.0e-16 E value 77 Match length 53 % identity (AF005047) transport inhibitor response 1 [Arabidopsis NCBI Description thaliana] >gi 2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

 Seq. No.
 42935

 Seq. ID
 awf700836370.h1

 Method
 BLASTN

 NCBI GI
 g599957

 BLAST score
 62

 E value
 2.0e-26

 Match length
 128

E value 2.0eMatch length 128
% identity 88

NCBI Description P.sativum (miranda) mRNA for chloroplast outer envelope

protein

Seq. No. 42936

Seq. ID awf700836405.hl

Method BLASTX
NCBI GI g3212848
BLAST score 161
E value 9.0e-17
Match length 82
% identity 70

NCBI Description (AC004005) putative inositol polyphosphate-5-phosphatase

[Arabidopsis thaliana]

Seq. No. 42937

Seq. ID awf700836546.h1

Method BLASTN
NCBI GI g479059
BLAST score 242
E value 1.0e-134
Match length 249
% identity 100

NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase



```
Seq. No.
                  42938
Seq. ID
                  awf700836572.h1
Method
                  BLASTN
NCBI GI
                  g479059
                  225
BLAST score
E value
                  1.0e-124
Match length
                  248
                  98
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
Seq. No.
                  42939
                  awf700836577.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22075
BLAST score
                  102
E value
                  2.0e-50
Match length
                  206
% identity
                  91
NCBI Description Vigna unquiculata cDNA for stored cotyledon mRNA
Seq. No.
                  42940
                  awf700836593.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18749
                  40
BLAST score
E value
                  2.0e-13
Match length
                  104
                  85
% identity
NCBI Description G.max mRNA for seed maturation polypeptide
Seq. No.
                  42941
Seq. ID
                  awf700836620.h1
Method
                  BLASTN
NCBI GI
                  g1370284
BLAST score
                  115
E value
                  4.0e-58
Match length
                  195
                  90
% identity
NCBI Description P.sativum mRNA for glutathione reductase
Seq. No.
                  42942
Seq. ID
                  awf700836641.h1
Method
                  BLASTX
NCBI GI
                  g2345100
BLAST score
                  139
E value
                  7.0e-09
Match length
                  60
                  45
% identity
NCBI Description (AF014465) Pad1 homolog [Schistosoma mansoni]
Seq. No.
                  42943
                  awf700836663.h1
Seq. ID
```

Method BLASTN NCBI GI q558544 BLAST score 32 E value 1.0e-08 99 Match length

% identity L.japonicus (Gifu B-129) mRNA for RING finger protein (C NCBI Description terminal) 42944 Seq. No. Seq. ID awf700836713.h1 Method BLASTN NCBI GI q1431744 BLAST score 47 2.0e-17 E value Match length 103 94 % identity NCBI Description Glycine max sucrose binding protein (sbp) mRNA, complete Seq. No. 42945 Seq. ID awf700836727.h1 Method BLASTN NCBI GI g479059 BLAST score 247 E value 1.0e-137 Match length 247 % identity 100 NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase 42946 Seq. No. awf700836729.h1 Seq. ID Method BLASTN q479059 250 1.0e-138 250 100

NCBI GI BLAST score E value Match length % identity

NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase

42947 Seq. No.

Seq. ID awf700836738.h1

BLASTN Method q479059 NCBI GI BLAST score 245 1.0e-135 E value Match length 245 100 % identity

NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase

42948 Seq. No.

Seq. ID awf700836740.h1

Method BLASTN NCBI GI g256426 BLAST score 238 E value 1.0e-131 Match length 246 99 % identity

NCBI Description CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic,

3840 nt]

42949 Seq. No.



```
Seq. ID
                  awf700836749.hl
Method
                  BLASTX
NCBI GI
                  g3600033
BLAST score
                  256
E value
                  2.0e-22
Match length
                  70
% identity
                  67
                  (AF080119) contains similarity to the N terminal domain of
NCBI Description
                  the E1 protein (Pfam: E1 N.hmm, score: 12.36) [Arabidopsis
                  thaliana]
                  42950
Seq. No.
                  awf700836776.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1220178
                  307
BLAST score
                  1.0e-28
E value
                  80
Match length
                  72
% identity
                 (Z69995) dormancy related protein [Trollius ledebourii]
NCBI Description
                  42951
Seq. No.
                  awf700836792.h1
Seq. ID
Method
                  BLASTN
                  g12137
NCBI GI
                  70
BLAST score
                  3.0e-31
E value
Match length
                  220
% identity
                  89
                  Pea chloroplast DNA (4.7 kb) 5' to ATP-synthase a subunit
NCBI Description
                  gene
Seq. No.
                  42952
Seq. ID
                  awf700836793.h1
                  BLASTN
Method
NCBI GI
                  g1778375
BLAST score
                  65
                  3.0e-28
E value
Match length
                  137
                  87
% identity
NCBI Description Pisum sativum PsRT17-1 mRNA, complete cds
Seq. No.
                  42953
Seq. ID
                  awf700836872.h1
Method
                  BLASTX
NCBI GI
                  g3337366
BLAST score
                  221
                  2.0e-18
E value
                  77
Match length
% identity
                  57
NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]
```

Seq. No. 42954

Seq. ID awf700836884.h1 Method BLASTN

Method BLASTN NCBI GI 9479059 BLAST score 237



```
E value 1.0e-131
Match length 237
% identity 100
NCBI Description G max (F
```

NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No. 42955

Seq. ID awf700836935.h1

Method BLASTX
NCBI GI g4455301
BLAST score 354
E value 5.0e-34
Match length 80
% identity 79

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 42956

Seq. ID awf700836945.h1

Method BLASTX
NCBI GI g4105633
BLAST score 274
E value 1.0e-24
Match length 78
% identity 71

NCBI Description (AF048982) putative ethylene receptor [Arabidopsis

thaliana]

Seq. No.

42957

Seq. ID awf700836960.h1

Method BLASTN
NCBI GI g2270991
BLAST score 99
E value 7.0e-49
Match length 99
% identity 100

NCBI Description Glycine max metallothionein-II protein mRNA, complete cds

Seq. No.

42958

Seq. ID awf700836979.h1

Method BLASTN
NCBI GI g170019
BLAST score 219
E value 1.0e-120
Match length 246
% identity 97

NCBI Description Soybean maturation protein (MAT1) gene, complete cds

Seq. No.

42959

Seq. ID awf700837030.h1

Method BLASTX
NCBI GI g464981
BLAST score 339
E value 3.0e-32
Match length 65
% identity 94

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]



```
Seq. No.
                  42960
Seq. ID
                  awf700837087.h1
Method
                  BLASTN
NCBI GI
                  g218264
BLAST score
                  250
E value
                  1.0e-138
                  250
Match length
                  100
% identity
NCBI Description
                  Glycine max mRNA for glycinin A2B1a subunit, complete cds
                  42961
Seq. No.
                  awf700837143.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832366
BLAST score
                  62
                  2.0e-26
E value
Match length
                  194
                  83
% identity
                  Beta vulgaris var. maritima mitochondrial pol and rpo genes
NCBI Description
                  and orf1 and orf2
                  42962
Seq. No.
Seq. ID
                  awf700837152.h1
Method
                  BLASTN
                  q479059
NCBI GI
BLAST score
                  239
E value
                  1.0e-132
Match length
                  247
% identity
                  100
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
Seq. No.
                  42963
                  awf700837164.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4314365
BLAST score
                  202
E value
                  3.0e-16
Match length
                  73
                  58
% identity
NCBI Description
                  (AC006340) putative copia-like retrotransposon Hopscotch
                   [Arabidopsis thaliana]
Seq. No.
                   42964
Seq. ID
                  awf700837183.hl
Method
                  BLASTN
NCBI GI
                  q3985952
BLAST score
                  47
                  2.0e-17
E value
```

Match length 115

% identity 43

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MRC8, complete sequence [Arabidopsis thaliana]

Seq. No. 42965

awf700837245.h1 Seq. ID

Method BLASTN

```
g18764
NCBI GI
                  148
BLAST score
                  8.0e-78
E value
                  192
Match length
                  94
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                  42966
                  awf700837254.h1
Seq. ID
                  BLASTN
Method
                  g1401239
NCBI GI
                  137
BLAST score
                  3.0e-71
E value
                  201
Match length
                  100
% identity
NCBI Description Glycine max 7S seed globulin precursor, mRNA, complete cds
                  42967
Seq. No.
                  awf700837258.h1
Seq. ID
                  BLASTX
Method
                  g4097579
NCBI GI
BLAST score
                  165
                   4.0e-22
E value
Match length
                  76
                   74
% identity
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
                   42968
Seq. No.
                   awf700837327.h1
Seq. ID
                   BLASTX
Method
                   g3122659
NCBI GI
                   156
BLAST score
E value
                   9.0e-11
                   40
Match length
% identity
                   62
                   PEROXIREDOXIN (REHYDRIN HOMOLOG) >gi_1926269_emb_CAA72804_
NCBI Description
                   (Y12089) peroxiredoxin [Arabidopsis Thaliana]
```

42969 Seq. No.

awf700837351.hl Seq. ID

BLASTN Method g3241916 NCBI GI 52 BLAST score 1.0e-20

E value 152 Match length 84 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K15N18, complete sequence [Arabidopsis thaliana]

42970 Seq. No.

awf700837357.h1 Seq. ID

BLASTX Method NCBI GI q4106395 BLAST score 179 3.0e-21 E value 69 Match length 75 % identity



```
NCBI Description (AF073744) raffinose synthase [Cucumis sativus]
```

Seq. No. 42971

Seq. ID awf700837380.h1

Method BLASTN
NCBI GI g169962
BLAST score 60
E value 1.0e-25
Match length 104
% identity 89

NCBI Description Soybean 16 kDa seed maturation protein (gGmpm9) gene exons

1-2, complete cds

Seq. No. 42972

Seq. ID awf700837382.h1

Method BLASTN
NCBI GI g169980
BLAST score 67
E value 2.0e-29
Match length 123
% identity 93

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 42973

Seq. ID awf700837395.h1

Method BLASTX
NCBI GI g2288986
BLAST score 185
E value 3.0e-14
Match length 45
% identity 76

NCBI Description (AC002335) glyoxalase II isolog [Arabidopsis thaliana]

Seq. No. 42974

Seq. ID awf700837441.h1

Method BLASTN
NCBI GI g2828278
BLAST score 40
E value 2.0e-13

Match length 64 % identity 91

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 42975

Seq. ID awf700837448.hl

Method BLASTN
NCBI GI g497416
BLAST score 104
E value 1.0e-51
Match length 167
% identity 92

NCBI Description Glycine max Essex dehydrin-like protein mRNA, complete cds

Seq. No.

Seq. ID awf700837476.hl

42976

Method BLASTN

Match length

% identity

40

41



```
NCBI GI
                  q479059
BLAST score
                  236
                  1.0e-130
E value
                  236
Match length
                  100
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                  42977
Seq. No.
Seq. ID
                  awf700837478.h1
Method
                  BLASTX
NCBI GI
                  g4417267
BLAST score
                  272
E value
                  2.0e-24
                  77
Match length
% identity
                  64
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]
                  42978
Seq. No.
                  awf700837487.h1
Seq. ID
Method
                  BLASTX
                  g3924596
NCBI GI
BLAST score
                  206
                  1.0e-16
E value
Match length
                  44
% identity
                  86
NCBI Description (AF069442) putative phospho-ser/thr phosphatase
                  [Arabidopsis thaliana]
Seq. No.
                  42979
Seq. ID
                  awf700837512.h1
Method
                  BLASTX
NCBI GI
                  g4417279
BLAST score
                  315
                  1.0e-29
E value
                  73
Match length
                  78
% identity
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]
                  42980
Seq. No.
                  awf700837525.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q479059
BLAST score
                  221
E value
                  1.0e-121
Match length
                  225
% identity
                  100
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
Seq. No.
                  42981
Seq. ID
                  awf700837536.h1
Method
                  BLASTX
NCBI GI
                  q3608128
BLAST score
                  154
E value
                  1.0e-10
```

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]



>gi_4263794_gb_AAD15454_ (AC006068) hypothetical protein
[Arabidopsis thaliana]

 Seq. No.
 42982

 Seq. ID
 awf700837547.h1

 Method
 BLASTX

 NCBI GI
 g2500053

 BLAST score
 137

 E value
 1.0e-08

Match length 33 % identity 79

NCBI Description DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS

HOMOLOG) >gi_1314298 (U40604) ORF5; putative Sms protein; similar to Sms proteins from Haemophilus influenzae and

Escherichia coli [Listeria monocytogenes]

Seq. No. 42983

Seq. ID awf700837617.h1

Method BLASTX
NCBI GI g4558566
BLAST score 286
E value 5.0e-26
Match length 84
% identity 63

NCBI Description (AC007138) putative raffinose synthase or seed imbibition

protein [Arabidopsis thaliana]

Seq. No. 42984

Seq. ID awf700837624.h1

Method BLASTN
NCBI GI g2369765
BLAST score 44
E value 9.0e-16
Match length 123

% identity 88

NCBI Description Citrus paradisi mRNA for hypothetical protein

Seq. No. 42985

Seq. ID awf700837637.h1

Method BLASTX
NCBI GI g3746070
BLAST score 175
E value 4.0e-13
Match length 49
% identity 65

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 42986

Seq. ID awf700837652.h1

Method BLASTN
NCBI GI g170019
BLAST score 221
E value 1.0e-121
Match length 245
% identity 98

NCBI Description Soybean maturation protein (MAT1) gene, complete cds



```
42987
Seq. No.
Seq. ID
                  awf700837671.h1
Method
                  BLASTX
NCBI GI
                  g3269287
BLAST score
                  366
                  2.0e-35
E value
Match length
                  80
% identity
                  88
                  (AL030978) GH3 like protein [Arabidopsis thaliana]
NCBI Description
                  42988
Seq. No.
                  awf700837684.h1
Seq. ID
Method
                  BLASTX
                  q4539423
NCBI GI
                  170
BLAST score
                   2.0e-13
E value
Match length
                   57
% identity
                  70
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   42989
Seq. ID
                  awf700837688.h1
Method
                  BLASTX
NCBI GI
                   q1532171
BLAST score
                   181
E value
                   9.0e-14
Match length
                   40
% identity
NCBI Description
                  (U63815) AT.I.24-9 gene product [Arabidopsis thaliana]
                   42990
Seq. No.
Seq. ID
                   awf700837723.h1
Method
                  BLASTX
NCBI GI
                  g3641252
BLAST score
                   185
                   3.0e-14
E value
Match length
                  78
                   45
% identity
NCBI Description
                   (AF053127) leucine-rich receptor-like protein kinase [Malus
                   domestica]
                   42991
Seq. No.
                   awf700837726.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18542
BLAST score
                  132
                  3.0e-68
E value
Match length
                  192
                  100
% identity
NCBI Description Soybean Bg gene for basic 7S globulin
                   42992
Seq. No.
```

Seq. ID awf700837740.h1

Method BLASTX NCBI GI g4220474 BLAST score 177



```
3.0e-13
E value
Match length
                   51
                   73
% identity
                   (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   42993
Seq. ID
                  awf700837783.h1
                  BLASTX
Method
NCBI GI
                  g2262105
BLAST score
                  180
                  1.0e-13
E value
Match length
                   41
                   78
% identity
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                   42994
Seq. ID
                   awf700837809.h1
Method
                  BLASTN
NCBI GI
                   g1930069
BLAST score
                   58
                   4.0e-24
E value
                  166
Match length
                  84
% identity
NCBI Description Oryza sativa proteasome alpha subunit mRNA, complete cds
                   42995
Seq. No.
Seq. ID
                   awf700837816.h1
Method
                  BLASTX
NCBI GI
                   g4580517
BLAST score
                   185
E value
                   3.0e-14
Match length
                   77
% identity
                   51
NCBI Description (AF036302) scarecrow-like 5 [Arabidopsis thaliana]
Seq. No.
                   42996
Seq. ID
                   awf700837821.h1
                  BLASTN
Method
NCBI GI
                   g170007
BLAST score
                   172
                   4.0e-92
E value
Match length
                   216
```

95 % identity

NCBI Description Soybean 18 kD late embryogenesis abundant (Lea) protein mRNA, complete cds

42997 Seq. No.

awf700837835.h1 Seq. ID

Method BLASTX g2739385 NCBI GI BLAST score 201 E value 3.0e-16 Match length 62 % identity 68

NCBI Description (AC002505) putative beta-1,3-glucanase [Arabidopsis

thaliana]



Seq. No. 42998

Seq. ID awf700837858.h1

Method BLASTX
NCBI GI g3914826
BLAST score 139
E value 5.0e-09
Match length 62
% identity 55

NCBI Description DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR

>gi 2330560 emb CAA69972 (Y08722) chloroplast

single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_2330564 emb_CAA69717 (Y08463) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_4115372 (AC005967) chloroplast single subunit

DNA-dependent RNA polymerase [Arabidopsis thaliana]

Seq. No. 42999

Seq. ID awf700837860.h1

Method BLASTN
NCBI GI g18749
BLAST score 158
E value 8.0e-84
Match length 206
% identity 94

NCBI Description G.max mRNA for seed maturation polypeptide

Seq. No. 43000

Seq. ID awf700837864.h1

Method BLASTN
NCBI GI g18749
BLAST score 166
E value 1.0e-88
Match length 218
% identity 94

NCBI Description G.max mRNA for seed maturation polypeptide

Seq. No. 43001

Seq. ID awf700837871.h1

Method BLASTX
NCBI GI g2088651
BLAST score 151
E value 2.0e-10
Match length 37
% identity 76

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No. 43002

Seq. ID awf700837889.h1

Method BLASTN g170023
BLAST score 169
E value 2.0e-90
Match length 181
% identity 98

NCBI Description Glycine max maturation-associated protein (MAT9) mRNA,



complete cds

```
43003
Seq. No.
                  awf700837912.hl
Seq. ID
                  BLASTX
Method
                  g1526422
NCBI GI
                  203
BLAST score
                  2.0e-16
E value
                  67
Match length
                  66
% identity
                  (D64139) LEA protein in group 5 [Arabidopsis thaliana]
NCBI Description
                  43004
Seq. No.
                  awf700837913.hl
Seq. ID
Method
                  BLASTN
                   g18749
NCBI GI
BLAST score
                   167
                   3.0e-89
E value
                   207
Match length
                   95
% identity
NCBI Description G.max mRNA for seed maturation polypeptide
                   43005
Seq. No.
                   awf700837914.h1
Seq. ID
                   BLASTN
Method
                   g18662
NCBI GI
                   166
BLAST score
                   1.0e-88
E value
                   230
Match length
                   93
% identity
NCBI Description Glycine max hsp 70 gene
                   43006
Seq. No.
                   awf700837928.h1
Seq. ID
                   BLASTN
Method
                   g1326160
NCBI GI
                   59
BLAST score
                   1.0e-24
E value
                   150
Match length
                   89
% identity
NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds
                   43007
Seq. No.
                   awf700837942.hl
Seq. ID
                   BLASTX
Method
                   g2662469
NCBI GI
                   169
BLAST score
                   2.0e-12
E value
                   54
Match length
                   65
% identity
                   (AF034217) ribosomal protein S6 [Arabidopsis thaliana]
NCBI Description
                   43008
 Seq. No.
                   awf700837945.hl
 Seq. ID
```

6825

BLASTN

205

g170023

Method NCBI GI

BLAST score



E value 1.0e-112 Match length 229 % identity 97

% identity 97

NCBI Description Glycine max maturation-associated protein (MAT9) mRNA,

complete cds

Seq. No. 43009

Seq. ID awf700837960.h1

Method BLASTX
NCBI GI g2832357
BLAST score 143
E value 2.0e-09
Match length 58
% identity 53

NCBI Description (Y14071) HMG protein [Arabidopsis thaliana] >gi_3068715

(AF049236) unknown [Arabidopsis thaliana]

Seq. No. 43010

Seq. ID awf700837967.h1

Method BLASTN
NCBI GI g18749
BLAST score 188
E value 1.0e-101
Match length 232
% identity 95

NCBI Description G.max mRNA for seed maturation polypeptide

Seq. No. 43011

Seq. ID awf700837972.h1

Method BLASTN
NCBI GI g210811
BLAST score 97
E value 2.0e-47
Match length 217
% identity 86

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 43012

Seq. ID awf700837984.h1

Method BLASTX
NCBI GI g126078
BLAST score 118
E value 5.0e-14
Match length 75
% identity 59

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)

>gi_81554_pir__S04046 embryonic abundant protein gD-34 upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea
protein [Gossypium hirsutum] >gi_167385 (M19389) storage
protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea

D-34 gene [Saguinus oedipus]

Seq. No. 43013

Seq. ID awf700837985.h1

Method BLASTN NCBI GI g479059

Match length

% identity

244



```
BLAST score
                   93
                  5.0e-45
E value
                  109
Match length
                  96
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                  43014
Seq. No.
                  awf700837995.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170021
BLAST score
                  172
E value
                   4.0e-92
Match length
                  208
% identity
                  96
NCBI Description Glycine max maturation-assocated protein (MAT1) mRNA,
                  complete cds
                  43015
Seq. No.
                  awf700838010.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q472849
BLAST score
                  73
E value
                  5.0e~33
Match length
                  141
% identity
                  88
NCBI Description Glycine max Essex desiccation protectant protein Lea14
                  homolog mRNA, complete cds
                   43016
Seq. No.
                   awf700838011.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914002
BLAST score
                  225
                  7.0e-19
E value
Match length
                  83
                  55
% identity
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279
                   (AF033862) Lon protease [Arabidopsis thaliana]
Seq. No.
                  43017
Seq. ID
                  awf700838012.h1
Method
                  BLASTX
NCBI GI
                   g4539005
BLAST score
                  355
E value
                   4.0e-34
                  81
Match length
                  78
% identity
NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                   43018
Seq. ID
                   awf700838062.h1
Method
                  BLASTN
NCBI GI
                   g170019
BLAST score
                  220
E value
                  1.0e-121
```



```
NCBI Description Soybean maturation protein (MAT1) gene, complete cds
                  43019
Seq. No.
                  awf700838086.hl
Seq. ID
                  BLASTX
Method
                  q4106395
NCBI GI
                   258
BLAST score
                   9.0e-23
E value
                   81
Match length
                   58
% identity
NCBI Description (AF073744) raffinose synthase [Cucumis sativus]
                   43020
Seq. No.
                   awf700838125.hl
Seq. ID
                   BLASTX
Method
                   g2909420
NCBI GI
                   195
BLAST score
                   1.0e-15
E value
                   74
Match length
% identity
                   55
                  (AJ224518) LEA protein [Cicer arietinum]
NCBI Description
                   43021
Seq. No.
                   awf700838145.h1 &
Seq. ID
                   BLASTN
Method
                   g4097879
NCBI GI
                   109
BLAST score
                   2.0e-54
E value
                   222
Match length
                   88
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                   gene, complete cds
                   43022
 Seq. No.
                   awf700838156.h1
 Seq. ID
                   BLASTX
 Method
                   g1350720
 NCBI GI
                   181
 BLAST score
                   1.0e-13
 E value
                   35
 Match length
 % identity
                   91
                   60S RIBOSOMAL PROTEIN L32
 NCBI Description
                    43023
 Seq. No.
                    awf700838161.hl
 Seq. ID
                   BLASTX
 Method
                    g2244904
 NCBI GI
                    232
 BLAST score
                    1.0e-19
 E value
                    85
 Match length
 % identity
                    16
                    (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
 NCBI Description
                    [Arabidopsis thaliana]
```

6828

43024

BLASTX

awf700838189.hl

Seq. No.

Seq. ID

Method



```
NCBI GI
                  q1172019
BLAST score
                  304
E value
                  4.0e-28
                  77
Match length
                  73
% identity
                  PEROXISOME BIOSYNTHESIS PROTEIN PAS1 (PEROXIN-1)
NCBI Description
                  >gi 1076972 pir_A55152 PAS1 protein - yeast (Pichia
                  pastoris) >gi_537420_emb_CAA85450_ (Z36987) PAS1 [Pichia
                  pastoris]
                  43025
Seq. No.
Seq. ID
                  awf700838190.h1
Method
                  BLASTX
NCBI GI
                  g2213594
BLAST score
                  362
E value
                  6.0e-35
Match length
                  85
% identity
                  81
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                  43026
                  awf700838220.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g516853
BLAST score
                  79
                  8.0e-37
E value
Match length
                  130
% identity
                  36
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.
                  43027
Seq. ID
                  awf700838229.h1
Method
                  BLASTN
NCBI GI
                  g872115
BLAST score
                  41
                  6.0e-14
E value
Match length
                  131
% identity
                  88
NCBI Description G.max gmsti mRNA
Seq. No.
                  43028
Seq. ID
                  awf700838263.h1
Method
                  BLASTN
NCBI GI
                  g479059
BLAST score
                  248
E value
                  1.0e-137
Match length
                  248
% identity
                  100
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                  43029
Seq. No.
                                                        24
                  awf700838288.h1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2130018
BLAST score 184
E value 4.0e-14
Match length 52



% identity 65
NCBI Description small heat shock protein class I, 17.7K - common sunflower >gi_1235898 (U46545) 17.7 kDa heat shock protein [Helianthus annuus]

Seq. No. 43030

Seq. ID awf700838289.h1

Method BLASTN
NCBI GI g3293200
BLAST score 55
E value 2.0e-22
Match length 171
% identity 86

NCBI Description Pisum sativum GTP-binding protein (IAP34) mRNA, complete

cds

Seq. No. 43031

Seq. ID awf700838292.h1 Method BLASTX

Method BLASTX
NCBI GI g2160167
BEAST score 188
E value 3.0e-29
Match length 79
% identity 80

NCBI Description (AC000132) Identical to A. thaliana Myb-like protein

(gb_D58424). [Arabidopsis thaliana]

Seq. No. 43032

Seq. ID awf700838310.h1

Method BLASTX
NCBI GI g2352492
BLAST score 344
E value 6.0e-33
Match length 74
% identity 88

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi 2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 43033

Seq. ID awf700838338.hl

Method BLASTX
NCBI GI g3600033
BLAST score 311
E value 4.0e-29
Match length 73
% identity 78

NCBI Description (AF080119) contains similarity to the N terminal domain of

the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis

thaliana]

Seq. No. 43034

Seq. ID awf700838384.h1

Method BLASTN
NCBI GI g170023
BLAST score 206
E value 1.0e-112



Match length 100 % identity Glycine max maturation-associated protein (MAT9) mRNA, NCBI Description complete cds 43035 Seq. No. awf700838396.hl Seq. ID BLASTN Method g479059 NCBI GI 83 BLAST score 4.0e-39 E value 171 Match length 87 % identity NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase 43036 Seq. No. awf700838556.hl Seq. ID BLASTN Method g479059 NCBI GI 224 BLAST score 1.0e-123 E value 232 Match length 99 % identity NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase. 43037 Seq. No. awf700838570.h1 Seq. ID BLASTN Method g479059 NCBI GI 231 BLAST score 1.0e-127 E value 231 Match length 100 % identity NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase 43038 Seq. No. awf700838582.h1 Seq. ID BLASTX Method g4455359 NCBI GI BLAST score 142 4.0e-09 E value 51 Match length 55 % identity (AL035524) putative protein [Arabidopsis thaliana] NCBI Description 43039 Seq. No.

awf700838609.h1 Seq. ID

BLASTX Method NCBI GI q3549672 201 BLAST score E value 3.0e-16 46 Match length 87 % identity

(AL031394) putative protein [Arabidopsis thaliana] NCBI Description

43040 Seq. No.

awf700838727.h1 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g2160164
BLAST score
                  173
                  8.0e-13
E value
Match length
                   69
% identity
                  54
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                   43041
Seq. ID
                  awf700838745.hl
Method
                  BLASTN
NCBI GI
                  g479059
BLAST score
                  243
                  1.0e-134
E value
Match length
                  243
% identity
                  100
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                  43042
Seq. No.
                  awf700838773.h1
Seq. ID
Method
                  BLASTN
                  g170019
NCBI GI
BLAST score
                   214
E value
                  1.0e-117
                   238
Match length
                   97
% identity
NCBI Description Soybean maturation protein (MAT1) gene, complete cds
Seq. No.
                   43043
                   awf700838831.h1
Seq. ID
Method
                  BLASTX
                   g1526422
NCBI GI
BLAST score
                   158
E value
                   4.0e-11
Match length
                   52
                   65
% identity
NCBI Description (D64139) LEA protein in group 5 [Arabidopsis thaliana]
                   43044
Seq. No.
Seq. ID
                   awf700838864.hl
Method
                   BLASTX
                   q4467134
NCBI GI
BLAST score
                   189
E value
                   7.0e-15
Match length
                   51
% identity
                   71
                   (AL035540) protein kinase like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   43045
Seq. ID
                   awf700838868.h1
Method
                  BLASTX
NCBI GI
                  g119745
BLAST score
                   141
E value
                   5.0e-09
```

79

42

Match length % identity



NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi 67242_pir__PAWTF fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - wheat >gi_21737_emb_CAA30612_ (X07780) pre-FBPase [Triticum aestivum] >gi_21741_emb_CAA37908_ (X53957) fructose-bisphosphatase [Triticum aestivum] 43046 Seq. No. awf700838884.h1 Seq. ID BLASTX Method g2245113 NCBI GI 232 BLAST score 1.0e-19 E value 72 Match length 71 % identity (Z97343) glycerol-3-phosphate permease homolog [Arabidopsis NCBI Description thaliana] 43047 Seq. No. awf700838895.h1 Seq. ID BLASTN Method g3097320 NCBI GI 211 BLAST score E value 1.0e-115 223 Match length 99 % identity NCBI Description Glycine max gene for Bd 30K, complete cds 43048 Seq. No. awf700838925.hl Seq. ID BLASTX Method q3540219 NCBI GI BLAST score 290 2.0e-26 E value 84 Match length 57 % identity NCBI Description (D87686) KIAA0017 protein [Homo sapiens] 43049 Seq. No. awf700839002.hl Seq. ID BLASTX Method g2737894 NCBI GI 308 BLAST score E value 1.0e-28 84 Match length % identity (U59151) Cbf5p homolog [Homo sapiens] NCBI Description 43050 Seq. No. awf700839073.h1 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g1184123
BLAST score 208
E value 5.0e-17
Match length 74
% identity 42



NCBI Description (U20809) auxin-induced protein [Vigna radiata]

```
43051
Seq. No.
Seq. ID
                  awf700839124.h1
Method
                  BLASTX
                  g2388987
NCBI GI
BLAST score
                  177
E value
                  2.0e-13
Match length
                  56
% identity
                  62
NCBI Description (Z98980) calcium transporting atpase [Schizosaccharomyces
Seq. No.
                  43052
                  awf700839140.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1401239
BLAST score
                  205
E value
                  1.0e-112
Match length
                  213
                  100
% identity
NCBI Description Glycine max 7S seed globulin precursor, mRNA, complete cds
Seq. No.
                  43053
                  awf700839149.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245077
BLAST score
                  234
                  5.0e-20
E value
                  77
Match length
% identity
                  58
NCBI Description (297343) glucanase homolog [Arabidopsis thaliana]
Seq. No.
                  43054
                  awf700839180.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3850070
BLAST score
                  344
E value
                  6.0e-33
Match length
                  77
% identity
                  83
NCBI Description (AL033385) transketolase [Schizosaccharomyces pombe]
                  43055
Seq. No.
Seq. ID
                  awf700839183.h1
                  BLASTX
Method
NCBI GI
                  g1526422
BLAST score
                  237
E value
                  2.0e-20
Match length
                  64
% identity
NCBI Description (D64139) LEA protein in group 5 [Arabidopsis thaliana]
Seq. No.
                  43056
Seq. ID
                  awf700839207.h1
```

BLASTX

g4106395

Method NCBI GI



```
BLAST score
                  2.0e-28
E value
                  81
Match length
% identity
                  67
                  (AF073744) raffinose synthase [Cucumis sativus]
NCBI Description
                  43057
Seq. No.
                  awf700839218.h1
Seq. ID
                  BLASTN
Method
                   g4097879
NCBI GI
                   106
BLAST score
                   1.0e-52
E value
                   210
Match length
                   88
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   43058
Seq. No.
                   awf700839289.h1
Seq. ID
                   BLASTX
Method
                   g4455360
NCBI GI
                   141
BLAST score
                   5.0e-09
E value
                   83
Match length
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   43059
Seq. No.
                   awf700839303.hl
Seq. ID
                   BLASTX
Method
                   g1707657
NCBI GI
                   251
BLAST score
                   7.0e-22
E value
                   82
Match length
% identity
                   50
                   (Z71640) DnaJ homologue [Pisum sativum]
NCBI Description
                   43060
Seq. No.
                   awf700839344.h1
Seq. ID
                   BLASTX
Method
                   q4128197
NCBI GI
                   297
BLAST score
                   2.0e-27
E value
                   83
Match length
                   69
 % identity
                   (U75273) acyl-CoA binding protein [Arabidopsis thaliana]
NCBI Description
                   43061
 Seq. No.
                   awf700839356.hl
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g3256035
BLAST score
                   363
                   5.0e-35
E value
Match length
                   81
 % identity
                   81
                   (Y14274) putative serine/threonine protein kinase [Sorghum
 NCBI Description
```

bicolor]



```
Seq. No.
                   43062
Seq. ID
                  awf700839410.h1
Method
                  BLASTN
NCBI GI
                  q2661020
BLAST score
                  169
                  2.0e-90
E value
Match length
                  217
% identity
                  94
NCBI Description Glycine max catalase (cat4) mRNA, complete cds
                  43063
Seq. No.
                  awf700839438.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539291
BLAST score
                  224
E value
                  6.0e-19
Match length
                  72
% identity
                  64
NCBI Description
                  (AL049480) putative protein [Arabidopsis thaliana]
                  43064
Seq. No.
                  awf700839532.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935177
BLAST score
                  132
E value
                  5.0e-12
Match length
                  65
% identity
                  63
NCBI Description
                  (AC004557) F17L21.20 [Arabidopsis thaliana]
Seq. No.
                  43065
                  awf700839533.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q434060
BLAST score
                  39
                  6.0e-13
E value
Match length
                  175
                  82
% identity
NCBI Description Soybean DNA for basic 7S globulin, complete cds
Seq. No.
                  43066
Seq. ID
                  awf700839537.h1
Method
                  BLASTX
                  q3193234
                  171
                  2.0e-12
```

NCBI GI BLAST score E value Match length 60 % identity 55

(AF068690) peroxisomal targeting signal-1 receptor NCBI Description

[Citrullus lanatus]

Seq. No. 43067

Seq. ID awf700839543.h1

Method BLASTN NCBI GI g479059 BLAST score 52



```
2.0e-20
E value
                   224
 Match length
 % identity
 NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                   43068
 Seq. No.
                    awf700839545.hl
 Seq. ID
                   BLASTX
 Method
                   g2275196
 NCBI GI
                    300
 BLAST score
                    1.0e-27
 E value
                    76
 Match length
                    84
 % identity
                    (AC002337) water stress-induced protein, WSI76 isolog
 NCBI Description
                    [Arabidopsis thaliana]
                    43069
 Seq. No.
                    awf700839554.h1
 Seq. ID
                    BLASTN
 Method
                    g170023
 NCBI GI
                    179
 BLAST score
                    3.0e-96
 E value
                    255
 Match length
                    93
 % identity
                    Glycine max maturation-associated protein (MAT9) mRNA,
 NCBI Description
                    complete cds
                    43070
 Seq. No.
                    awf700839576.h1
 Seq. ID
                    BLASTX
 Method
                    g3790188
 NCBI GI
                    160
 BLAST score
                    2.0e-21
 E value
                    86
 Match length
                    67
 % identity
                    (Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana
 NCBI Description
                    tabacum]
                    43071
 Seq. No.
                    awf700839589.h1
  Seq. ID
                    BLASTN
 Method
                    g14311
  NCBI GI
 BLAST score
                    65
                    3.0e-28
  E value
                    231
 Match length
  % identity
 NCBI Description G.max chloroplast gene rps19 and flanking regions
                    43072
  Seq. No.
                    awf700839595.h1
  Seq. ID
  Method
                    BLASTN
                    q4102691
  NCBI GI
                    49
  BLAST score
  E value
                    5.0e-19
                    109
  Match length
  % identity
                    86
  NCBI Description Glycine max late-embryogenesis abundant protein mRNA,
```

Seq. No.

Seq. ID

Method

43078

BLASTN

awf700839771.h1



complete cds

```
Seq. No.
                  43073
                  awf700839607.hl
Seq. ID
                  BLASTN
Method
                  g479059
NCBI GI
BLAST score
                  103
                  5.0e-51
E value
Match length
                  191
                  94
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                  43074
Seq. No.
                  awf700839666.h1
Seq. ID
                  BLASTN
Method
                  q3097270
NCBI GI
BLAST score
                  96
                  8.0e-47
E value
Match length
                  212
                  86
% identity
NCBI Description Solanum tuberosum, cultivar binje, mRNA for ferrochelatase
                   43075
Seq. No.
                   awf700839671.h1
Seq. ID
Method
                   BLASTX
                   g2642429
NCBI GI
BLAST score
                   220
                   2.0e-18
E value
                   75
Match length
                   19
% identity
                   (AC002391) putative poly(A)-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   43076
Seq. No.
                   awf700839707.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3688173
                   285
BLAST score
                   7.0e-26
E value
Match length
                   70
% identity
                   74
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   43077
Seq. No.
                   awf700839720.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q322867
BLAST score
                   183
E value
                   6.0e-14
Match length
                   80
% identity
                   51
                   translation initiation factor eIF-4F isozyme form subunit
NCBI Description
                   p82 - wheat
```



```
q170019
NCBI GI
BLAST score
                  214
                   1.0e-117
E value
                   246
Match length
                   97
% identity
                  Soybean maturation protein (MAT1) gene, complete cds
NCBI Description
                   43079
Seq. No.
                   awf700839809.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3901009
BLAST score
                   44
E value
                   6.0e-16
Match length
                   76
                   89
% identity
                   Eichhornia crassipes mRNA for metallothionein-like protein,
NCBI Description
                   clone C
                   43080
Seq. No.
                   awf700839829.hl
Seq. ID
                   BLASTN
Method
                   q2270987
NCBI GI
BLAST score
                   82
E value
                   2.0e-38
                   166
Match length
% identity
                   93
                  Glycine max Em protein mRNA, complete cds
NCBI Description
Seq. No.
                   awf700839890.h1
Seq. ID
Method
                   BLASTN
                   g19257
NCBI GI
                   77
BLAST score
E value
                   2.0e-35
                   212
Match length
% identity
                   87
                   Lycopersicon esculentum hsc-2 mRNA for heat shock protein
NCBI Description
                   cognate
                   43082
 Seq. No.
                   awf700839919.h1
 Seq. ID
Method
                   BLASTN
                   g497416
NCBI GI
BLAST score
                   266
                   1.0e-148
E value
                   266
Match length
 % identity
                   87
                   Glycine max Essex dehydrin-like protein mRNA, complete cds
NCBI Description
                   43083
 Seq. No.
                   awf700839961.h1
 Seq. ID
                   BLASTX
Method
                   g2245065
 NCBI GI
 BLAST score
                   186
                   2.0e-14
 E value
                   67
 Match length
```

21

% identity

Method

NCBI GI

BLASTX g1620896



```
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
                   43084
Seq. No.
                   awf700839991.h1
Seq. ID
                   BLASTN
Method
                   g479059
NCBI GI
                   233
BLAST score
                   1.0e-128
E value
                   233
Match length
                   100
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                   43085
Seq. No.
                   awf700840012.hl
Seq. ID
                   BLASTX
Method
                   q2894594
NCBI GI
                   175
BLAST score
                   3.0e-13
E value
Match length
                   52
                   60
% identity
                   (AL021889) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    43086
Seq. No.
                   awf700840048.h1
Seq. ID
                   BLASTN
Method
                    g497416
NCBI GI
                    80
BLAST score
                    3.0e-37
E value
                    100
Match length
                    95
% identity
                   Glycine max Essex dehydrin-like protein mRNA, complete cds
NCBI Description
                    43087
Seq. No.
                    awf700840060.h1
Seq. ID
                    BLASTN
Method
                    g2244991
NCBI GI
BLAST score
                    32
                    1.0e-08
E value
                    60
Match length
                    88
 % identity
                    Arabidopsis thaliana DNA chromosome 4, ESSA I contig
 NCBI Description
                    fragment No
                                                +16<sup>2</sup>
-65<sub>6</sub>
                    43088
 Seq. No.
                    awf700840078.hl
 Seq. ID
                    BLASTN
 Method
                    g479059
 NCBI GI
                    227
 BLAST score
 E value
                    1.0e-125
                    227
 Match length
 % identity
                    100
                   G.max (Fiskeby V) mRNA for cysteine endopeptidase
 NCBI Description
                    43089
 Seq. No.
                    awf700840115.hl
 Seq. ID
```

Match length

% identity



```
BLAST score
                  2.0e-21
E value
                  70
Match length
                  74
% identity
                   (D87956) protein involved in sexual development
NCBI Description
                   [Schizosaccharomyces pombe] >gi_2408048_emb_CAB16251
                   (Z99164) hypothetical protein [Schizosaccharomyces pombe]
                   43090
Seq. No.
                   awf700840140.hl
Seq. ID
                   BLASTN
Method
                   g2924257
NCBI GI
BLAST score
                   60
                   3.0e-25
E value
Match length
                   161
% identity
                   88
                  Tobacco chloroplast genome DNA
NCBI Description
                   43091
Seq. No.
                   awf700840162.hl
Seq. ID
                   BLASTX
Method
                   g2558938
NCBI GI
                   98
BLAST score
                   2.0e-09
E value
                   63
Match length
                   62
% identity
                   (AF024625) arm repeat containing protein [Brassica napus]
NCBI Description
                   43092
Seq. No.
                   awf700840170.hl
Seq. ID
                   BLASTX
Method
                   g4415925
NCBI GI
                   140
BLAST score
                   6.0e-16
E value
                   60
Match length
                   67
% identity
                   (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   43093
 Seq. No.
                   awf700840214.h1
 Seq. ID
                   BLASTN
Method
                   g2661020
NCBI GI
                   186
BLAST score
                   1.0e-100
 E value
                   218
 Match length
 % identity
                   Glycine max catalase (cat4) mRNA, complete cds
 NCBI Description
                    43094
 Seq. No.
                    awf700840234.h1
 Seq. ID
                    BLASTN
 Method
                    q19653
 NCBI GI
                    32
 BLAST score
 E value
                    1.0e-08
```



NCBI Description M.sativa mRNA for protein disulfide isomerase

43095 Seq. No.

awf700840238.hl Seq. ID

BLASTN Method q1431744 NCBI GI 63 BLAST score 4.0e-27

E value 124 Match length 96 % identity

NCBI Description Glycine max sucrose binding protein (sbp) mRNA, complete

43096 Seq. No.

awf700840263.hl Seq. ID

BLASTN Method g1389896 NCBI GI 59 BLAST score 1.0e-24 E value 59 Match length

100 % identity

NCBI Description Glycine max 68 kDa LEA protein mRNA, complete cds

43097 Seq. No.

awf700840266.h1 Seq. ID

BLASTX Method g4469014 NCBI GI 324 BLAST score 2.0e-30 E value 78 Match length 83 % identity

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

43098 Seq. No.

awf700840287.h1 Seq. ID

Method BLASTX NCBI GI q4006873 138 BLAST score 1.0e-08 E value Match length 81 33

% identity (Z99707) hypothetical protein [Arabidopsis thaliana] NCBI Description

43099 Seq. No.

awf700840295.h1 Seq. ID

BLASTX Method g2501460 NCBI GI 141 BLAST score E value 3.0e-09 29 Match length % identity 90

PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP NCBI Description

(UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC

PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE)

>gi 1545952_emb_CAA96580_ (Z72499) herpesvirus associated

ubiquitin-specific protease (HAUSP) [Homo sapiens]



>qi 4507857 ref NP 003461.1 pUSP7 Herpes virus-associated ubiquitin-specific protease

Seq. No. 43100 Seq. ID awf700840341.h1 Method BLASTX g2129854 NCBI GI BLAST score 331 3.0e - 31E value Match length 82 % identity 74

early nodulin 8 precursor - alfalfa >gi 304037 (L18899) NCBI Description

early nodulin [Medicago sativa]

Seq. No. 43101

awf700840396.h1 Seq. ID

Method BLASTX NCBI GI g1871526 BLAST score 244 4.0e-21 E value Match length 82 % identity 11

NCBI Description (X81997) leucine-rich-repeat protein [Helianthus annuus]

Seq. No.

43102

Seq. ID awf700840476.hl

Method BLASTX NCBI GI q2129739 BLAST score 204 2.0e-16 E value Match length 48 % identity 81

NCBI Description

shaggy-like kinase etha - Arabidopsis thaliana >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947)

shaggy-like kinase etha [Arabidopsis thaliana]

Seq. No. 43103

Seq. ID awf700840481.hl

Method BLASTN NCBI GI q210811 BLAST score 105 E value 3.0e-52 Match length 233 % identity

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 43104

awf700840532.h1 Seq. ID

Method BLASTX NCBI GI g2894599 BLAST score 221 E value 2.0e-18 Match length 47 79 % identity

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]



```
43105
Seq. No.
                  awf700840540.h1
Seq. ID
                  BLASTN
Method
                  g169928
NCBI GI
                  32
BLAST score
                  1.0e-08
E value
                  40
Match length
                  95
% identity
                  Glycine max alpha'-type beta conglycinin storage protein
NCBI Description
                  gene, complete cds, clone ch4A
                  43106
Seq. No.
                  awf700840560.h1
Seq. ID
Method
                  BLASTX
                  g1256259
NCBI GI
                  158
BLAST score
                  3.0e-11
E value
                  63
Match length
% identity
                  51
                  (U50900) voltage-dependent anion channel protein [Spinacia
NCBI Description
                  oleracea]
                  43107
Seq. No.
                  awf700840581.h1
Seq. ID
                  BLASTX
Method
                  g138364
NCBI GI
                  190
BLAST score
                   2.0e-15
E value
                   60
Match length
% identity
                   66
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                   bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   43108
Seq. No.
                   awf700840584.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q516853
BLAST score
                   57
                   2.0e-23
E value
                   165
Match length
                   59
% identity
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
                   43109
Seq. No.
                   awf700840586.h1
Seq. ID
Method
                   BLASTN
                   q18764
NCBI GI
BLAST score
                   191
                   1.0e-103
E value
                   235
Match length
```

Seq. No. 43110

% identity

NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. ID

NCBI GI

Method

BLASTX

g4314371



```
awf700840591.hl
Seq. ID
                  BLASTX
Method
                  q3914467
NCBI GI
BLAST score
                  125
                  2.0e-09
E value
                  56
Match length
                  70
% identity
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                  >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana
                  tabacum]
                  43111
Seq. No.
                   awf700840592.h1
Seq. ID
                  BLASTN
Method
                  g170007
NCBI GI
                   112
BLAST score
                   2.0e-56
E value
                   178
Match length
                   93
% identity
                  Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                   mRNA, complete cds
                   43112
Seq. No.
                   awf700840639.h1
Seq. ID
                   BLASTN
Method
                   q4210331
NCBI GI
                   68
BLAST score
                   4.0e-30
E value
                   172
Match length
                   85
% identity
                  Arabidopsis thaliana mRNA for 2-oxoglutarate dehydrogenase
NCBI Description
                   E2 subunit
                   43113
Seq. No.
                   awf700840771.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4468812
                   347
BLAST score
                   3.0e - 33
E value
                   80
Match length
                   79
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                   43114
Seq. No.
                   awf700840804.h1
 Seq. ID
                   BLASTX
Method
                   g2052029
NCBI GI
                   265
BLAST score
                   1.0e-23
E value
                   78
Match length
 % identity
                   64
                  (Y10820) glutathione transferase [Glycine max]
 NCBI Description
                   43115
 Seq. No.
                   awf700840806.hl
```



```
BLAST score
                  1.0e-15
E value
                  76
Match length
                  45
% identity
                  (AC006340) putative G9a protein [Arabidopsis thaliana]
NCBI Description
                  43116
Seq. No.
                  awf700840826.h1
Seq. ID
Method
                  BLASTN
                  g4097879
NCBI GI
                  83
BLAST score
                  5.0e-39
E value
                  175
Match length
                  87
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   43117
Seq. No.
Seq. ID
                   awf700840835.h1
                  BLASTN
Method
NCBI GI
                   g170007
BLAST score
                   187
                   1.0e-101
E value
                   239
Match length
                   95
% identity
                  Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                   mRNA, complete cds
                   43118
Seq. No.
Seq. ID
                   awf700840842.h1
                   BLASTN
Method
NCBI GI
                   g170023
BLAST score
                   57
                   6.0e-24
E value
                   97
Match length
                   90
% identity
                   Glycine max maturation-associated protein (MAT9) mRNA,
NCBI Description
                   complete cds
                   43119
Seq. No.
Seq. ID
                   awf700840853.h1
                   BLASTN
Method
                   g210811
NCBI GI
BLAST score
                   119
E value
                   2.0e-60
                   227
Match length
                   88
% identity
                   Bean pod mottle virus coat protein gene, complete cds,
NCBI Description
                   complete middle component (M) RNA
                   43120
Seq. No.
Seq. ID
                   awf700840857.h1
```

Method BLASTN
NCBI GI g4102691
BLAST score 180
E value 6.0e-97
Match length 232

% identity Glycine max late-embryogenesis abundant protein mRNA, NCBI Description complete cds 43121 Seq. No. awf700840862.h1 Seq. ID BLASTN Method g2832374 NCBI GI BLAST score 32 E value 7.0e-09 Match length 48 92 % identity Arabidopsis thaliana mRNA for AtMYB11 R2R3-MYB NCBI Description transcription factor 43122 Seq. No. awf700840868.h1 Seq. ID Method BLASTX g126078 NCBI GI BLAST score 191 6.0e-15 E value Match length 55 % identity 76 LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34) NCBI Description D-34 gene [Saguinus oedipus] Seq. No. 43123 Seq. ID awf700840885.h1 Method BLASTX

>gi 81554 pir S04046 embryonic abundant protein gD-34 upland cotton >gi 18501 emb CAA31594 (X13206) D-34 Lea protein [Gossypium hirsutum] >gi_167385 (M19389) storage protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea

NCBI GI g120669 320 BLAST score 4.0e-30 E value 77 Match length 79 % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>qi 66014 pir DEJMG qlyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi 19566 emb CAA42905 (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 43124

Seq. ID awf700840916.h1

BLASTX Method q4006886 NCBI GI BLAST score 293 6.0e-27 E value 78 Match length 74 % identity

(Z99708) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 43125

Seq. ID awf700840941.h1

Method BLASTX



```
g1653665
NCBI GI
                  152
BLAST score
                  2.0e-10
E value
                  42
Match length
                  69
% identity
NCBI Description (D90915) peptide chain release factor [Synechocystis sp.]
                  43126
Seq. No.
                  awf700841015.h1
Seq. ID
                  BLASTX
Method
                  q3687237
NCBI GI
                  244
BLAST score
                   4.0e-21
E value
                  79
Match length
                   62
% identity
                   (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   43127
Seq. No.
                   awf700841040.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18693
BLAST score
                   57
                   2.0e-23
E value
                   73
Match length
                   95
% identity
NCBI Description Soybean mRNA for Nodulin-21
                   43128
Seq. No.
                   awf700841130.hl
Seq. ID
                   BLASTN
Method
                   g497416
NCBI GI
                   129
BLAST score
                   2.0e-66
E value
                   237
Match length
                   89
% identity
NCBI Description Glycine max Essex dehydrin-like protein mRNA, complete cds
                   43129
Seq. No.
                   awf700841151.h1
Seq. ID
                   BLASTN
Method
                   g599957
NCBI GI
                   45
BLAST score
                   9.0e-17
E value
                   97
Match length
                   87
% identity
                  P.sativum (miranda) mRNA for chloroplast outer envelope
NCBI Description
                   protein
                   43130
Seq. No.
Seq. ID
                   awf700841164.hl
                   BLASTX
Method
                   g2564066
NCBI GI
                   236
BLAST score
E value
                   3.0e-20
Match length
                   57
```

79

% identity

NCBI Description



```
NCBI Description (D45900) LEDI-3 protein [Lithospermum erythrorhizon]
                  43131
Seq. No.
                  awf700841264.hl
Seq. ID
Method
                  BLASTX
                  g3894158
NCBI GI
BLAST score
                  154
                  1.0e-17
E value
                  77
Match length
                  54
% identity
                  (AC005312) similar to phloem-specific lectin [Arabidopsis
NCBI Description
                  thaliana]
                   43132
Seq. No.
                   awf700841291.hl
Seq. ID
                   BLASTX
Method
                   g3142291
NCBI GI
BLAST score
                   114
E value
                   3.0e-11
Match length
                   74
                   61
% identity
                   (AC002411) Contains similarity to adenylate cyclase
NCBI Description
                   gb_AF012921 from Magnaporthe grisae. EST gb_Z24512 comes
                   from this gene. [Arabidopsis thaliana]
                   43133
Seq. No.
                   awf700841311.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g170007
                   193
BLAST score
E value
                   1.0e-104
                   273
Match length
% identity
                   Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                   mRNA, complete cds
                   43134
Seq. No.
                   awf700841324.h1
Seq. ID
Method
                   BLASTX
                   g282994
NCBI GI
                   173
BLAST score
                   1.0e-12
E value
Match length
                   81
                   48
 % identity
                   Sip1 protein - barley >gi_167100 (M77475) seed imbibition
NCBI Description
                   protein [Hordeum vulgare]
                   43135
 Seq. No.
                   awf700841354.h1
 Seq. ID
                   BLASTX
 Method
                   q2842487
 NCBI GI
                   269
 BLAST score
                   5.0e-24
 E value
                   80
 Match length
 % identity
                    61
```

(AL021749) SOF1 protein-like protein [Arabidopsis thaliana]



```
Seq. No.
                  awf700841357.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18749
                  202
BLAST score
                  1.0e-110
E value
Match length
                  246
% identity
                  96
NCBI Description G.max mRNA for seed maturation polypeptide
                  43137
Seq. No.
                  awf700841359.h1
Seq. ID
Method
                  BLASTX
                  q3738312
NCBI GI
BLAST score
                   261
                   5.0e-23
E value
                   86
Match length
                   63
% identity
                  (AC005309) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   43138
Seq. No.
                   awf700841367.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g584825
BLAST score
                   192
                   6.0e-15
E value
                   38
Match length
                   89
% identity
                   B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot
NCBI Description
                   >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                   carota]
                   43139
Seq. No.
                   awf700841393.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g170007
BLAST score
                   179
                   3.0e-96
E value
Match length
                   199
% identity
                   97
                   Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                   mRNA, complete cds
Seq. No.
                   43140
                   awf700841467.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g479059
BLAST score
                   249
                   1.0e-138
E value
Match length
                   253
% identity
                   100
```

NCBI Description

Seq. No.

Seq. ID awf700841479.h1

43141

Method BLASTN NCBI GI g497416

6850

G.max (Fiskeby V) mRNA for cysteine endopeptidase



```
BLAST score
                   1.0e-139
E value
                   251
Match length
                   76
% identity
NCBI Description Glycine max Essex dehydrin-like protein mRNA, complete cds
                   43142
Seq. No.
                   awf700841491.h1
Seq. ID
                   BLASTX
Method
                   g3451078
NCBI GI
                   137
BLAST score
                   1.0e-08
E value
                   80
Match length
% identity
                   46
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   43143
Seq. No.
                   awf700841557.h1
Seq. ID
                   BLASTX
Method
                   g3292817
NCBI GI
                   279
BLAST score
                   3.0e-25
E value
                   58
Match length
                   84
% identity
                   (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   43144
Seq. No.
                   awf700841571.h1
 Seq. ID
                   BLASTN
Method
                   q2924257
NCBI GI
                   141
BLAST score
                   1.0e-73
 E value
                   226
 Match length
                    45
 % identity
 NCBI Description Tobacco chloroplast genome DNA
                    43145
 Seq. No.
                    awf700841609.h1
 Seq. ID
                    BLASTN
 Method
 NCBI GI
                    q576508
                    34
 BLAST score
                    9.0e-10
 E value
 Match length
                    102
                    83
 % identity
                    Pisum sativum GTP-binding protein (IAP86) mRNA, complete
 NCBI Description
                    43146
 Seq. No.
                    awf700841614.hl
 Seq. ID
                    BLASTX
 Method
                    q1170746
 NCBI GI
                    144
 BLAST score
                    2.0e-09
 E value
                    38
 Match length
```

DESICCATION PROTECTANT PROTEIN LEA14 HOMOLOG >gi_472850

(U08108) putative desiccation protectant protein, homolog

76

% identity

NCBI Description



of Leal4, GenBank Accession Number M88321 [Glycine max]

```
43147
Seq. No.
                    awf700841677.h1
Seq. ID
Method
                    BLASTN
NCBI GI
                    g169986
BLAST score
                    95
E value
                    3.0e-46
Match length
                    119
                    95
% identity
                   Soybean (Glycine max) heat shock protein (Gmhsp17.5-E)
NCBI Description
                    gene, complete cds
Seq. No.
                    43148
                    awf700841689.hl
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2493895
BLAST score
                    202
E value
                    3.0e-16
Match length
                    47
                    85
% identity
                    CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
NCBI Description
                    (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                    >gi_1071911_pir__S46438 cysteine synthase (EC 4.2.99.8) - watermelon >gi_540497_dbj_BAA05965_ (D28777) cysteine
                    synthase [Citrullus lanatus]
Seq. No.
                    43149
                    awf700841709.h1
Seq. ID
Method
                    BLASTX
                    g3150405
NCBI GI
BLAST score
                    214
E value
                    1.0e-17
Match length
                    83
% identity
                    49
                    (AC004165) putative indole-3-acetate
NCBI Description
                    beta-glucosyltransferase [Arabidopsis thaliana]
Seq. No. Seq. ID
                    43150
                    awf700841714.h1
Method
                    BLASTX
                    g2462134
NCBI GI
BLAST score
                    226
E value
                    5.0e-19
                    83
Match length
% identity
                    49
                    (Y13368) reverse transcriptase [Beta vulgaris]
NCBI Description
                    43151
Seq. No.
Seq. ID
                    awf700841728.hl
                    BLASTX
Method
                    g2909420
NCBI GI
BLAST score
                    115
                    1.0e-10
E value
                    55
Match length
                    21
% identity
NCBI Description (AJ224518) LEA protein [Cicer arietinum]
```



43152 Seq. No. awf700841751.hl Seq. ID BLASTN Method g497416 NCBI GI 255 BLAST score 1.0e-141 E value 255 Match length 77 % identity NCBI Description Glycine max Essex dehydrin-like protein mRNA, complete cds 43153 Seq. No. awf700841803.hl Seq. ID Method BLASTN g170023 NCBI GI 241 BLAST score 1.0e-133 E value 248 Match length 100 % identity Glycine max maturation-associated protein (MAT9) mRNA, NCBI Description complete cds 43154 Seq. No. awf700841828.h1 Seq. ID BLASTX Method g2462841 NCBI GI 148 BLAST score 7.0e-10 E value Match length 63 41 % identity (AF000657) similar to selenium-binding protein NCBI Description gp_Z97335_2244760 [Arabidopsis thaliana] 43155 Seq. No. awf700841843.h1 Seq. ID BLASTX Method q126078 NCBI GI BLAST score 159 7.0e-13 E value 56 Match length 70 % identity LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34) NCBI Description >gi_81554_pir__S04046 embryonic abundant protein gD-34 upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea protein [Gossypium hirsutum] >gi_167385 (M19389) storage protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea D-34 gene [Saguinus oedipus] Seq. No. 43156 awf700841855.hl Seq. ID Method BLASTN q2570066 NCBI GI BLAST score 76

 NCBI GI
 g2570066

 BLAST score
 76

 E value
 7.0e-35

 Match length
 222

 % identity
 91

NCBI Description Pisum sativum mRNA for second sucrose synthase



```
Seq. No.
                  43157
                  awf700841930.hl
Seq. ID
Method
                  BLASTX
                  g2244965
NCBI GI
                  268
BLAST score
E value
                   5.0e-24
                   76
Match length
% identity
                  (Z97340) unnamed protein product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  43158
                  awf700841934.hl
Seq. ID
Method
                  BLASTN
                   g2160155
NCBI GI
                   43
BLAST score
                   2.0e-15
E value
Match length
                   75
                   89
% identity
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   awf700841949.hl
                   BLASTN
Method
                   q170019
NCBI GI
                   220
BLAST score
                   1.0e-121
E value
Match length
                   244
                   98
% identity
                  Soybean maturation protein (MAT1) gene, complete cds
NCBI Description
Seq. No.
                   43160
                   awf700841962.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2789660
                   299
BLAST score
                   1.0e-27
E value
Match length
                   79
                   73
% identity
                   (AF040102) p105 [Arabidopsis thaliana]
NCBI Description
                   43161
Seq. No.
                   awf700841967.h1
Seq. ID
                   BLASTN
Method
                   q479059
NCBI GI
BLAST score
                   232
                   1.0e-128
E value
                   240
Match length
                   99
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                   43162
Seq. No.
Seq. ID
                   awf700841987.h1
                   BLASTX
Method
```

g464628

142

NCBI GI BLAST score



E value 3.0e-09

Match length 40

% identity 70

NCBI Description 60S RIBOSOMAL PROTEIN L22 (EPSTEIN-BARR VIRUS SMALL RNA ASSOCIATED PROTEIN) (EBER ASSOCIATED PROTEIN) (EAP) (HEPARIN BINDING PROTEIN HBP15) >gi_542841_pir__JC2120 heparin-binding protein 15 - human >gi_31062_emb_CAA42007_(X59357) Epstein-Barr virus small RNA associated protein [Homo sapiens] >gi_409070_dbj_BAA04545_ (D17652) HBp15/L22 [Homo sapiens] >gi_4506613_ref_NP_000974.1_pRPL22_ribosomal protein L22

 Seq. No.
 43163

 Seq. ID
 awf700842014.h1

 Method
 BLASTN

 NCBI GI
 g3452181

 BLAST score
 255

 E value
 1.0e-141

Match length 255 % identity 100

NCBI Description Glycine soja cv 342-633A clone 2 26S-18S ribosomal RNA

intergenic spacer region

Seq. No. 43164

Seq. ID awf700842017.h1

Method BLASTX
NCBI GI g4191791
BLAST score 331
E value 3.0e-31
Match length 80
% identity 75

NCBI Description (AC005917) putative sf21 {Helianthus annuus} protein

[Arabidopsis thaliana]

Seq. No. 43165

Seq. ID awf700842056.h1

Method BLASTN
NCBI GI g2661020
BLAST score 131
E value 1.0e-67
Match length 187
% identity 93

NCBI Description Glycine max catalase (cat4) mRNA, complete cds

Seq. No. 43166

Seq. ID awf700842087.h1

Method BLASTX
NCBI GI g1707017
BLAST score 258
E value 6.0e-23
Match length 67
% identity 75

NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]

Seq. No. Seq. ID

awf700842115.h1

43167

Method BLASTX



```
NCBI GI
                   q3850588
BLAST score
                   163
                   1.0e-11
E value
                   48
Match length
% identity
                   58
                   (AC005278) Contains similarity to gb AB011110 KIAA0538
NCBI Description
                   protein from Homo sapiens brain and \overline{t}o phospholipid-binding
                   domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   43168
Seq. ID
                   awf700842137.hl
```

Method BLASTN
NCBI GI g22635
BLAST score 122
E value 3.0e-62
Match length 189
% identity 95

NCBI Description P.vulgaris mRNA for 70 kD heat shock protein

Seq. No. 43169

Seq. ID awf700842150.h1 Method BLASTN

NCBI GI g2370311 BLAST score 37 E value 1.0e-11 Match length 97

Match length 9/ % identity 85

NCBI Description Medicago sativa mRNA for DnaJ-like protein

Seq. No.

Seq. ID awf700842167.h1

43170

43171

Method BLASTN
NCBI GI g2270989
BLAST score 39
E value 9.0e-13
Match length 63
% identity 90

NCBI Description Glycine max dehydrin (GmPM12) mRNA, complete cds

Seq. No.

Seq. ID awf700842169.h1

Method BLASTX
NCBI GI g2088647
BLAST score 315
E value 2.0e-29
Match length 75
% identity 83

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

>gi_3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No.

43172

Seq. ID awf700842177.h1

Method BLASTN
NCBI GI g3201571
BLAST score 68



```
4.0e-30
E value
Match length
                  85
                  94
% identity
                  Beta vulgaris mitochondrial rps7 gene for ribosomal protein
NCBI Description
                  S7, complete cds
                   43173
Seq. No.
                   awf700842217.h1
Seq. ID
                  BLASTX
Method
                   g2654210
NCBI GI
BLAST score
                   123
                   2.0e-09
E value
Match length
                   55
                   59
% identity
                   (AF035457) heat shock 70 protein [Spinacia oleracea]
NCBI Description
Seq. No.
                   awf700842232.h1
Seq. ID
                   BLASTN
Method
                   q4406531
NCBI GI
                   104
BLAST score
                   2.0e-51
E value
                   124
Match length
                   96
% identity
                   Vigna radiata NADPH-protochlorophyllide oxidoreductase
NCBI Description
                   mRNA, chloroplast gene encoding chloroplast protein,
                   complete cds
                   43175
Seq. No.
                   awf700842251.hl
Seq. ID
                   BLASTX
Method
                   q3158476
NCBI GI
                   277
BLAST score
                   5.0e-25
E value
                   66
Match length
                   83
% identity
                   (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
 Seq. No.
                   43176
                   awf700842260.hl
 Seq. ID
Method
                   BLASTX
                   g2739168
 NCBI GI
                   245
 BLAST score
                   3:0e-21
 E value
Match length
                   83
                    63
 % identity
                    (AF032386) aldose-1-epimerase-like protein [Nicotiana
 NCBI Description
                    tabacum]
                    43177
 Seq. No.
                    awf700842264.h1
 Seq. ID
                    {\tt BLASTN}
 Method
                    g343344
 NCBI GI
                    234
 BLAST score
```

1.0e-129

255

97

E value

Match length

% identity



NCBI Description Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end), Ile-tRNA, and Ala-tRNA genes

Seq. No. 43178

Seq. ID awf700842279.h1

Method BLASTN
NCBI GI g18749
BLAST score 225
E value 1.0e-124
Match length 248
% identity 98

NCBI Description G.max mRNA for seed maturation polypeptide

Seq. No. 43179

Seq. ID awf700842282.h1

Method BLASTN
NCBI GI 9479059
BLAST score 234
E value 1.0e-129
Match length 246
% identity 99

NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No. 43180

Seq. ID awf700842294.h1

Method BLASTN
NCBI GI g497416
BLAST score 141
E value 1.0e-73
Match length 165
% identity 96

NCBI Description Glycine max Essex dehydrin-like protein mRNA, complete cds

Seq. No. 43181

Seq. ID awf700842295.hl

Method BLASTX
NCBI GI g2804154
BLAST score 106
E value 5.0e-13
Match length 81
% identity 65

NCBI Description (AJ222973) aquaporin [Lupinus albus]

Seq. No. 43182

Seq. ID awf700842296.h1

Method BLASTX
NCBI GI g4262154
BLAST score 365
E value 3.0e-35
Match length 84
% identity 88

NCBI Description (AC005275) putative protein phosphatase regulatory subunit

[Arabidopsis thaliana]

Seq. No. 43183

Seq. ID awf700842312.h1

Method BLASTX



```
q3212250
NCBI GI
                  137
BLAST score
                  1.0e-08
E value
                  59
Match length
                  49
% identity
NCBI Description Tetratricopeptide Repeats Of Protein Phosphatase
                  43184
Seq. No.
                  awf700842332.h1
Seq. ID
                  BLASTX
Method
                  q4455360
NCBI GI
                  185
BLAST score
                   2.0e-14
E value
Match length
                  70
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   43185
Seq. No.
                   awf700842340.h1
Seq. ID
                   BLASTX
Method
                   g2244904
NCBI GI
                   215
BLAST score
                   1.0e-17
E value
                   68
Match length
                   60
% identity
                   (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
NCBI Description
                   [Arabidopsis thaliana]
                   43186
Seq. No.
                   awf700842354.hl
Seq. ID
                   BLASTN
Method
                   q256426
NCBI GI
BLAST score
                   239
E value
                   1.0e-132
                   247
Match length
                   99
% identity
                   CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic,
NCBI Description
                   3840 nt]
                   43187
Seq. No.
                   awf700842367.h1
 Seq. ID
                   BLASTX
Method
                   g419760
NCBI GI
                   219
BLAST score
                   4.0e-18
E value
                   81
Match length
                   26
 % identity
                   P-glycoprotein atpgp1 - Arabidopsis thaliana
 NCBI Description
                   >gi 3849833_emb_CAA43646_ (X61370) P-glycoprotein
                   [Arabidopsis thaliana]
                   43188
 Seq. No.
                   awf700842394.hl
 Seq. ID
                   BLASTN
 Method
                   g3378649
 NCBI GI
```

6859

45

2.0e-16

BLAST score

E value



Match length 113 % identity 85

NCBI Description M.sativa mRNA translated from abscisic activated gene

Seq. No. 43189

Seq. ID awf700842446.h1

Method BLASTN
NCBI GI g2760829
BLAST score 35

E value 2.0e-10 Match length 71 87

NCBI Description Arabidopsis thaliana chromosome II BAC F18A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 43190

Seq. ID awf700842457.h1

Method BLASTN
NCBI GI g497416
BLAST score 251
E value 1.0e-139

Match length 251 % identity 76

NCBI Description Glycine max Essex dehydrin-like protein mRNA, complete cds

Seq. No. 43191

Seq. ID awf700842539.h1

Method BLASTX
NCBI GI g542157
BLAST score 179
E value 2.0e-13
Match length 42
% identity 81

NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 43192

Seq. ID awf700842541.h1

Method BLASTX
NCBI GI g1170746
BLAST score 187
E value 1.0e-26
Match length 78
% identity 83

NCBI Description DESICCATION PROTECTANT PROTEIN LEA14 HOMOLOG >gi_472850 (U08108) putative desiccation protectant protein, homolog

of Leal4, GenBank Accession Number M88321 [Glycine max]

ú

Seq. No. 43193

Seq. ID awf700842550.h1

Method BLASTX
NCBI GI g3176664
BLAST score 238
E value 2.0e-20
Match length 62
% identity 69

NCBI Description (AC004393) Contains similarity to beta scruin gb Z47541 from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955

BLAST score

143



come from this gene. [Arabidopsis thaliana]

```
43194
Seq. No.
                  awf700842639.h1
Seq. ID
                  BLASTX
Method
                   g598073
NCBI GI
BLAST score
                   331
                   2.0e-31
E value
                   77
Match length
                   90
% identity
                   (L36806) GT-1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43195
                   awf700842642.h1
Seq. ID
                   BLASTN
Method
                   q510931
NCBI GI
                   102
BLAST score
E value
                   2.0e-50
                   218
Match length
                   87
% identity
NCBI Description V.faba mRNA for alpha 1,4-glucan phosphorylase type H
                   43196
Seq. No.
                   awf700842735.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2982466
BLAST score
                   201
                   5.0e-16
E value
                   63
Match length
                   54
% identity
                   (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                   43197
Seq. No.
                   awf700842749.h1
Seq. ID
Method
                   BLASTN
                   g1389896
NCBI GI
BLAST score
                   177
                   4.0e-95
E value
                   261
Match length
% identity
                   98
NCBI Description Glycine max 68 kDa LEA protein mRNA, complete cds
                   43198
Seq. No.
                   awf700842793.h1
Seq. ID
Method
                   BLASTN
                   g170019
NCBI GI
BLAST score
                   222
E value
                   1.0e-122
                   246
Match length
                   98
 % identity
NCBI Description Soybean maturation protein (MAT1) gene, complete cds
                   43199
 Seq. No.
                   awf700842817.hl
 Seq. ID
                   BLASTX
 Method
                   g2459437
 NCBI GI
```



```
3.0e-09
E value
                  28
Match length
                  89
% identity
                  (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  43200
                  awf700842872.h1
Seq. ID
Method
                  BLASTN
                  g21012
NCBI GI
BLAST score
                   116
                   9.0e-59
E value
Match length
                   156
% identity
                   94
                  Phaseolus vulgaris mRNA (pR-2) for glutamine synthetase
NCBI Description
                   (GS, EC 6.3.1.2)
Seq. No.
                   43201
Seq. ID
                   awf700842890.h1
Method
                   BLASTX
                   g4455224
NCBI GI
BLAST score
                   171
E value
                   9.0e-13
Match length
                   61
% identity
                   56
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43202
Seq. ID
                   awf700842903.h1
Method
                   BLASTN
NCBI GI
                   g311697
BLAST score
                   160
                   3.0e-85
E value
Match length
                   160
% identity
                   18
NCBI Description G.max Lea protein mRNA, complete CDS
                   43203
Seq. No.
Seq. ID
                   awf700842928.hl
                   {\tt BLASTX}
Method
                   q3287691
NCBI GI
BLAST score
                   153
                   1.0e-10
E value
Match length
                   44
% identity
                   61
                   (AC003979) Contains similarity to RING zinc finger protein
NCBI Description
                   gb_X95455 from Gallus gallus. [Arabidopsis thaliana]
                   43204
Seq. No.
                   awf700842936.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g479059
BLAST score
                   243
E value
                   1.0e-134
                   247
Match length
```

NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase

100

% identity



```
43205
Seq. No.
                  awf700843061.h1
Seq. ID
                  BLASTN
Method
                  g2924653
NCBI GI
                  39
BLAST score
                  5.0e-13
E value
                  47
Match length
                  32
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   43206
                   awf700843063.hl
Seq. ID
Method
                  BLASTN
                   q479059
NCBI GI
                   227
BLAST score
                   1.0e-125
E value
Match length
                   234
                   100
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                   43207
Seq. No.
                   awf700843130.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q232031
BLAST score
                   231
                   1.0e-19
E value
                   63
Match length
% identity
                   65
                   ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224
NCBI Description
                   translation elongation factor eEF-1 beta chain - rice
                   >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza sativa]
Seq. No.
                   43208
                   awf700843153.h1
Seq. ID
Method
                   BLASTN
                   q3859658
NCBI GI
BLAST score
                   37
                   1.0e-11
E value
                   73
Match length
                   88
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1
NCBI Description
                   (ESSAII project)
                   43209
Seq. No.
                   awf700843161.h1
Seq. ID
                   BLASTX
Method
                   g2909420
NCBI GI
                   171
BLAST score
                   9.0e-13
E value
                   48
Match length
                   39
% identity
                  (AJ224518) LEA protein [Cicer arietinum]
```

43210 Seq. No.

NCBI Description

awf700843172.h1 Seq. ID

% identity



```
BLASTN
Method
NCBI GI
                   q1694938
BLAST score
                   88
                   4.0e-42
E value
                   207
Match length
                   93
% identity
NCBI Description Argemone mexicana DNA for 18S ribosomal RNA
                   43211
Seq. No.
                   awf700843183.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455294
BLAST score
                   215
                   5.0e-22
E value
                   70
Match length
                   70
% identity
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   43212
Seq. No.
                   awf700843332.h1
Seq. ID
                   BLASTN
Method
                   g18729
NCBI GI
                   60
BLAST score
                   2.0e-25
E value
                                   4 4 40
Match length
                   67
                   99
% identity
NCBI Description Soybean (Glycine max) 18S ribosomal RNA
                   43213
Seq. No.
                   awf700843343.h1
Seq. ID
                   BLASTX
Method
                   g4105798
NCBI GI
                   241
BLAST score
E value
                   7.0e-21
                   56
Match length
% identity
                   64
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   43214
Seq. No.
                   awf700843352.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1431738
BLAST score
                   221
E value
                    1.0e-121
Match length
                    221
                    100
 % identity
                   Soybean (Glycine max) low MW heat shock protein gene
NCBI Description
                    (Gmhsp17.5-M)
 Seq. No.
                    43215
                    awf700843418.h1
 Seq. ID
                    BLASTX
Method
                    g2055374
NCBI GI
BLAST score
                    136
                    1.0e-08
 E value
                    34
Match length
                    71
```



NCBI Description (U29095) serine-threonine protein kinase [Triticum aestivum]

Seq. No. 43216
Seq. ID awf700843475.h1
Method BLASTX

NCBI GI g3850581 BLAST score 141 E value 4.0e-09 Match length 36 % identity 67

NCBI Description (AC005278) EST gb_N96383 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 43217

Seq. ID bnc700605533.h2

Method BLASTN
NCBI GI g1438878
BLAST score 144
E value 2.0e-75
Match length 285
% identity 98

NCBI Description Glycine max choline kinase GmCK1p mRNA, complete cds

Seq. No. 43218

Seq. ID bnc700605567.h2

Method BLASTX
NCBI GI g2832625
BLAST score 218
E value 5.0e-18
Match length 66
% identity 58

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 43219

Seq. ID bnc700605615.h2

Method BLASTX
NCBI GI g1871193
BLAST score 239
E value 2.0e-20
Match length 80
% identity 57

NCBI Description (U90439) receptor-like protein kinase isolog [Arabidopsis thaliana] >gi 2335090 (AC002339) putative receptor-like

protein kinase [Arabidopsis thaliana]

Seq. No. 43220

Seq. ID bnc700605616.h2

Method BLASTX
NCBI GI g3043428
BLAST score 281
E value 2.0e-25
Match length 61
% identity 84

NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No. 43221



```
bnc700605634.h2
Seq. ID
                  BLASTX
Method
                  g3068705
NCBI GI
                  141
BLAST score
                  5.0e-09
E value
Match length
                  57
% identity
                  51
                   (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   43222
Seq. No.
Seq. ID
                  bnc700605649.h2
Method
                   BLASTX
                   g3128228
NCBI GI
                   312
BLAST score
                   4.0e-29
E value
                   66
Match length
                   91
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
                   43223
Seq. No.
                   bnc700605659.h2
Seq. ID
Method
                   BLASTX
                   q3540181
NCBI GI
                   206
BLAST score
                   1.0e-16
E value
                   59
Match length
% identity
                   71
                   (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   43224
Seq. No.
                   bnc700605660.h2
Seq. ID
                   BLASTX
Method
                   g1370174
NCBI GI
                   305
BLAST score
                   3.0e-28
E value
                   70
Match length
% identity
                   84
                   (Z73936) RAB1Y [Lotus japonicus]
NCBI Description
                   43225
Seq. No.
                   bnc700605677.h2
Seq. ID
                   BLASTN
Method
                   g473216
NCBI GI
                   97
BLAST score
                   2.0e-47
E value
                   249
Match length
                   87
 % identity
                   P.sativum (little marvel) HSC71.0 mRNA
NCBI Description
                   43226
 Seq. No.
                   bnh700764504.h1
 Seq. ID
                   BLASTN
```

Method BLASTN
NCBI GI g1675195
BLAST score 92
E value 2.0e-44



```
Match length 164 % identity 89
```

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

Seq. No. Seq. ID

43227 bnh700764568.h1

Method BLASTN
NCBI GI g506628
BLAST score 159
E value 2.0e-84
Match length 231
% identity 93

NCBI Description Glycine max cv. Dare photosystem II type I chlorophyll

a/b-binding protein (lhcb1*7) gene, complete cds

Seq. No. 43228

Seq. ID bnh700764569.h1

Method BLASTX
NCBI GI g2760839
BLAST score 217
E value 4.0e-18
Match length 73
% identity 66

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 43229

Seq. ID bnh700764570.h1

Method BLASTN
NCBI GI g2791833
BLAST score 105
E value 3.0e-52
Match length 189
% identity 89

NCBI Description Manihot esculenta elongation factor 1-alpha (MeEF1) gene,

complete cds

Seq. No. 43230

Seq. ID bnh700764577.h1

Method BLASTX
NCBI GI g1841464
BLAST score 275
E value 8.0e-25
Match length 67
% identity 39

NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]

Seq. No. 43231

Seq. ID bnh700764660.h1

Method BLASTN
NCBI GI g12974
BLAST score 74
E value 6.0e-34
Match length 86
% identity 97

NCBI Description Soybean mitochondrial COII gene for cytochrome oxidase

subunit II and tRNA-Met (CAT) gene (upstream)



```
Seq. No.
                  43232
                  bnh700764687.h1
Seq. ID
Method
                  BLASTX
                  g3388157
NCBI GI
                  139
BLAST score
                  6.0e-09
E value
                  48
Match length
                  54
% identity
                  (AF079556) poly(ADP-ribose) glycohydrolase [Drosophila
NCBI Description
                  melanogaster]
Seq. No.
                  43233
                  bnu700967504.h1
Seq. ID
                  BLASTN
Method
                  a170089
NCBI GI
                  210
BLAST score
E value
                   1.0e-115
                   234
Match length
                   97
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
Seq. No.
                   43234
                  bnu700967564.h1
Seq. ID
                   BLASTX
Method
                   q2062175
NCBI GI
                   318
BLAST score
E value
                   8.0e-30
Match length
                   81
                   78
% identity
                  (AC001645) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   43235
Seq. No.
                   bnu700967575.h1
Seq. ID
Method
                   BLASTX
                   g3193288
NCBI GI
                   143
BLAST score
                   3.0e-09
E value
Match length
                   42
% identity
                   60
                   (AF069298) similar to bacterial and fungi pectinesterases
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   43236
                   bnu700967579.hl
Seq. ID
                   BLASTX
Method
                   g1710546
NCBI GI
                   163
BLAST score
                   2.0e-22
E value
                   64
Match length
                   89
% identity
                   60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative
NCBI Description
                   ribosomal protein [Daucus carota]
```

Method BLASTX

Seq. No. Seq. ID

43237

bnu700967612.h1



```
q4191791
NCBI GI
                  332
BLAST score
                  2.0e-31
E value
                  78
Match length
                  76
% identity
                   (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                   [Arabidopsis thaliana]
                  43238
Seq. No.
                  bnu700967643.hl
Seq. ID
                  BLASTX
Method
                  g4455155
NCBI GI
BLAST score
                   222
                  2.0e-20
E value
                   69
Match length
                   70
% identity
                   (AL022023) EF-1 alpha - like protein (fragment)
NCBI Description
                   [Arabidopsis thaliana]
                   43239
Seq. No.
                   bnu700967645.h1
Seq. ID
                   BLASTX
Method
                   g1173198
NCBI GI
                   296
BLAST score
                   3.0e-27
E value
                   62
Match length
                   90
% identity
                   40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal
NCBI Description
                   protein S13.e - garden pea >gi 396639_emb_CAA80974_
                   (Z25509) ribosomal protein S13 [Pisum satīvum]
                   43240
Seq. No.
                   bnu700967648.hl
Seq. ID
Method
                   BLASTN
                   q725331
NCBI GI
BLAST score
                   107
                   2.0e-53
E value
                   111
Match length
% identity
NCBI Description Glycine max mitochondrion polymorphic marker DNA sequence
                   43241
Seq. No.
                   bth700843501.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2244820
                   154
BLAST score
                   7.0e-12
E value
                   53
Match length
 % identity
                   37
                   (Z97336) calmodulin [Arabidopsis thaliana]
NCBI Description
                   43242
 Seq. No.
                   bth700843526.h1
 Seq. ID
                   BLASTX
Method
                   g3150407
 NCBI GI
```

306

2.0e-28

BLAST score

E value



```
Match length
                  81
% identity
                  (AC004165) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  43243
Seq. No.
                  bth700843534.h1
Seq. ID
                  BLASTX
Method
                  g3687476
```

NCBI GI 198 BLAST score 1.0e-15 E value 68 Match length 63 % identity

(AL031786) putative atp dependent rna helicase NCBI Description

[Schizosaccharomyces pombe]

43244 Seq. No.

bth700843536.h1 Seq. ID

BLASTN Method g296495 NCBI GI 71 BLAST score 7.0e-32 E value 203 Match length 84 % identity

NCBI Description A.pyhllitidis mRNA for alpha-tubulin

43245 Seq. No.

bth700843552.h1 Seq. ID

BLASTN Method q1277163 NCBI GI 231 BLAST score 1.0e-127 E value 231 Match length 100 % identity

Glycine max cysteine proteinase inhibitor mRNA, partial cds NCBI Description

43246 Seq. No.

bth700843560.h1 Seq. ID

BLASTX Method g1076510 NCBI GI 145 BLAST score 1.0e-09 E value 47 Match length 62 % identity

peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean NCBI Description

>gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus

vulgaris]

43247 Seq. No.

bth700843567.h1 Seq. ID

BLASTN Method NCBI GI g1430886 38 BLAST score 4.0e-12 E value 107 Match length 89 % identity

NCBI Description M.sativa mRNA for 70 kD heat shock protein



```
Seq. No.
                  bth700843595.hl
Seq. ID
                  BLASTX
Method
                  g99711
NCBI GI
                  267
BLAST score
                  6.0e-24
E value
                  71
Match length
                  72
% identity
                  hypothetical protein H1.2flk - Arabidopsis thaliana
NCBI Description
                   (fragment) >gi_16322_emb_CAA44317_ (X62460) H1-2flk
                   [Arabidopsis thaliana]
                   43249
Seq. No.
                  bth700843596.hl
Seq. ID
                   BLASTN
Method
                   a18551
NCBI GI
BLAST score
                   140
E value
                   5.0e-73
                   232
Match length
                   91
% identity
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
Seq. No.
                   43250
                   bth700843662.hl
Seq. ID
                   BLASTX
Method
                   g3953471
NCBI GI
                   231
BLAST score
                   3.0e-30
E value
                   83
Match length
                   82
% identity
                   (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                   43251
Seq. No.
                   bth700843664.hl
Seq. ID
                   BLASTX
Method
                   q2829889
NCBI GI
                   239
BLAST score
                   2.0e-20
E value
Match length
                   48
                   96
% identity
                   (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   43252
Seq. No.
                   bth700843673.hl
Seq. ID
                   BLASTX
Method
                   g1931652
NCBI GI
 BLAST score
                   141
                   4.0e-20
 E value
Match length
                   102
 % identity
                   61
                   (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
 NCBI Description
                    [Arabidopsis thaliana]
```

43253

BLASTN

bth700843701.h1

Seq. No.

Seq. ID

Method



```
g3449322
NCBI GI
                  33
BLAST score
                  3.0e-09
E value
                  157
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC17, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  bth700843732.hl
                  BLASTX
Method
                  g3688173
NCBI GI
                  227
BLAST score
                  4.0e-19
E value
                  73
Match length
% identity
                   (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   43255
Seq. No.
                  bth700843755.h1
Seq. ID
                   BLASTX
Method
                   q1346769
NCBI GI
                   187
BLAST score
                   2.0e-14
E value
                   79
Match length
                   44
% identity
                   PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)
NCBI Description
                   >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase
                   [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase
                   [Homo sapiens] >gi_4506043_ref_NP_002717.1_pPREP_ prolyl
                   endopeptidase
                   43256
Seq. No.
                   bth700843766.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3046848
                   48
BLAST score
                   4.0e-18
E value
                   141
Match length
                   87
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K18C1, complete sequence [Arabidopsis thaliana]
                   43257
Seq. No.
Seq. ID
                   bth700843786.h1
                   BLASTX
Method
                   q3287936
NCBI GI
                   211
BLAST score
                   3.0e-17
E value
                   74
Match length
                   59
 % identity
                   HYPOTHETICAL 38.9 KD PROTEIN SLL0098
NCBI Description
                   >gi_1208474_dbj_BAA10642_ (D64004) hypothetical protein
                   [Synechocystis sp.]
```

Seq. ID bth700843802.h1

Seq. No.

BLAST score

E value

2.0e-39



```
BLASTX
Method
NCBI GI
                   g2290681
                   325
BLAST score
                   1.0e-30
E value
                   79
Match length
                   77
% identity
                   (AF000135) acidic cellulase [Citrus sinensis]
NCBI Description
                   43259
Seq. No.
                   bth700843864.h1
Seq. ID
Method
                   BLASTX
                   g1402912
NCBI GI
BLAST score
                   221
                   2.0e-18
E value
                   61
Match length
                   72
% identity
                   (X98317) peroxidase [Arabidopsis thaliana]
NCBI Description
                   43260
Seq. No.
                   bth700843890.h1
Seq. ID
                   BLASTX
Method
                   q2062169
NCBI GI
BLAST score
                   210
E value
                   1.0e-19
                   76
Match length
                   37
% identity
                   (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                   thaliana]
                   43261
Seq. No.
                   bth700843903.h1
Seq. ID
                   BLASTX
Method
                   q2791900
NCBI GI
BLAST score
                   256
                   2.0e-22
E value
Match length
                   87
% identity
                   64
                   (AJ000057) PP7 [Arabidopsis thaliana]
NCBI Description
                   43262
 Seq. No.
                   bth700843917.h1
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g4220462
 BLAST score
                   138
                   1.0e-08
 E value
                   30
Match length
                   73
 % identity
                   (AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8)
 NCBI Description
                   gene from Arabidopsis thaliana containing Homeobox PF_00046
                   and bZIP PF_00170 domains. [Arabidopsis thaliana]
 Seq. No.
                    43263
                   bth700843928.h1
 Seq. ID
                   BLASTX
 Method
                    g2464915
 NCBI GI
                    393
```



Match length 83 % identity 95

NCBI Description (Z99708) transcription initiation factor like protein

[Arabidopsis thaliana]

Seq. No. 43264

Seq. ID bth700844048.h1

Method BLASTX
NCBI GI g2288999
BLAST score 322
E value 3.0e-30
Match length 81
% identity 68

NCBI Description (AC002335) electron transfer flavoprotein ubiquinone

oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 43265

Seq. ID bth700844075.h1

Method BLASTX
NCBI GI g4567273
BLAST score 216
E value 7.0e-18
Match length 68
% identity 59

NCBI Description (AC006841) putative vacuolar proton ATPase subunit

[Arabidopsis thaliana]

Seq. No. 43266

Seq. ID bth700844123.h1

Method BLASTN
NCBI GI g2465526
BLAST score 68
E value 5.0e-30
Match length 139
% identity 88

NCBI Description Medicago truncatula phosphate transporter (MtPT1) mRNA,

complete cds

43267

Seq. No.

Seq. ID bth700844210.h1

Method BLASTN
NCBI GI g18376
BLAST score 220
E value 1.0e-121
Match length 255
% identity 96

NCBI Description Glycine max PAL1 gene for phenylalanine ammonia lyase (EC

4.3.1.5)

Seq. No. 43268

Seq. ID bth700844244.h1

Method BLASTX
NCBI GI g2288985
BLAST score 176
E value 4.0e-13
Match length 73
% identity 62



NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana] 43269 Seq. No. bth700844313.hl Seq. ID BLASTX Method g2244905 NCBI GI 179 BLAST score 2.0e-13 E value 80 Match length 46 % identity (Z97339) indole-3-acetate beta-glucosyltransferase NCBI Description [Arabidopsis thaliana] Seq. No. 43270 bth700844393.h1 Seq. ID BLASTX Method g1706101 NCBI GI 149 BLAST score 5.0e-10 E value 68 Match length 46 % identity CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD NCBI Description SUBUNIT (CPSF 160 KD SUBUNIT) >gi_1363024_pir__S57335 cleavage and polyadenylation specificity factor 160K chain - bovine >gi_929007_emb_CAA58152_ (X83097) cleavage and polyadenylation specificity factor, 160 kDa subunit [Bos taurus] 43271 Seq. No. bth700844438.hl Seq. ID BLASTN Method q2739003 NCBI GI 58 BLAST score E value 4.0e-24 90 Match length 91 % identity Glycine max cytochrome P450 monooxygenase CYP82C1p NCBI Description (CYP82C1) mRNA, complete cds 43272 Seq. No. bth700844445.h1 Seq. ID BLASTX Method g2088657 NCBI GI 255 BLAST score

2.0e-22 E value 82 Match length 52 % identity

(AF002109) unknown protein [Arabidopsis thaliana] NCBI Description

43273 Seq. No.

bth700844449.hl Seq. ID

BLASTN Method g1778369 NCBI GI 110 BLAST score 4.0e-55 E value 110 Match length 100 % identity

NCBI Description Glycine max asparagine synthetase 2 (AS2) mRNA, complete 43274 Seq. No. bth700844549.h1 Seq. ID Method BLASTX g3980412 NCBI GI BLAST score 347 4.0e-33 E value 85 Match length % identity (AC004561) pumilio-like protein [Arabidopsis thaliana] NCBI Description 43275 Seq. No. bth700844560.h1 Seq. ID Method BLASTN g256142 245 1.0e-135

NCBI GI BLAST score E value 253 Match length % identity

cytosolic glutamine synthetase [Glycine max=soybeans, var NCBI Description

Prize, mRNA, 1450 nt]

43276 Seq. No.

bth700844565.h1 Seq. ID

BLASTN Method q2677823 NCBI GI BLAST score 39 1.0e-12 E value 111 Match length % identity

Prunus armeniaca abscisic stress ripening protein homolog NCBI Description

mRNA, complete cds

43277 Seq. No.

Seq. ID bth700844578.h1

Method BLASTX NCBI GI q4432821 BLAST score 137 1.0e-08 E value Match length 55 49 % identity

(AC006593) putative transmembrane protein [Arabidopsis NCBI Description

thaliana]

43278 Seq. No.

Seq. ID bth700844589.h1

Method BLASTN NCBI GI q170048 BLAST score 149 2.0e-78 E value Match length 217 % identity 30

Glycine max SbPRP1 gene encoding a proline-rich protein, NCBI Description

complete cds



```
Seq. No.
Seq. ID
                  bth700844618.h1
                  BLASTX
Method
                  g2293360
NCBI GI
                  146
BLAST score
                  5.0e-10
E value
                   46
Match length
                   72
% identity
NCBI Description (D87670) polyphenol oxidase [Malus domestica]
                   43280
Seq. No.
                  bth700844665.h1
Seq. ID
                   BLASTX
Method
                   g4049399
NCBI GI
                   164
BLAST score
                   6.0e-12
E value
                   71
Match length
                   45
% identity
NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]
                   43281
Seq. No.
                   bth700844673.h1
Seq. ID
                   BLASTX
Method
                   g3152607
NCBI GI
BLAST score
                   179
                   1.0e-13
E value
                   69
Match length
                   43
% identity
NCBI Description (AC004482) putative receptor kinase [Arabidopsis thaliana]
                   43282
Seq. No.
                   bth700844754.h1
Seq. ID
                   BLASTX
Method
                   g2459419
NCBI GI
                   159
BLAST score
                   3.0e-11
E value
                   72
Match length
                   42
% identity
                   (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   43283
Seq. No.
                   bth700844823.h1
Seq. ID
                   BLASTN
Method
                   g2832611
NCBI GI
BLAST score
                   58
E value
                   4.0e-24
                   138
Match length
 % identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
 NCBI Description
                    (ESSAII project)
                   43284
 Seq. No.
                   bth700844979.h1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4115377
```

5.0e-10

BLAST score

E value

NCBI Description



```
Match length
                  47
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                  43285
Seq. No.
                  bth700844982.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g532754
                  174
BLAST score
                  5.0e-13
E value
                  53
Match length
% identity
                  53
                  (U13256) RNase NE [Nicotiana alata]
NCBI Description
                  43286
Seq. No.
                  bth700845018.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913793
BLAST score
                  142
                   4.0e-09
E value
                   42
Match length
                   60
% identity
                  GLUTATHIONE PEROXIDASE 2 >gi_2569989_emb_CAA75009_ (Y14707)
NCBI Description
                   glutathione peroxidase [Helianthus annuus]
                   43287
Seq. No.
                   bth700845029.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2252831
                   173
BLAST score
                   9.0e-23
E value
                   79
Match length
                   70
% identity
                   (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                   43288
Seq. No.
                   bth700845070.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2462833
                   209
BLAST score
E value
                   4.0e-17
Match length
                   75
                   47
% identity
                   (AF000657) highly similar to froha and frohb, potential
NCBI Description
                   frohc [Arabidopsis thaliana]
Seq. No.
                   43289
                   bth700845082.h1
Seq. ID
                   BLASTX
Method
                   q4262160
NCBI GI
                   241
BLAST score
                   8.0e-21
E value
                   77
Match length
                   57
 % identity
```

6878

[Arabidopsis thaliana]

(AC005275) putative chloroplast protein import component



```
43290
     Seq. No.
                       bth700845090.h1
     Seq. ID
     Method
                       BLASTN
                       q4103958
     NCBI GI
                       105
     BLAST score
     E value
                       3.0e-52
     Match length
                       144
                       94
     % identity
     NCBI Description Phaseolus vulgaris calmodulin (CaM) mRNA, PvCaM-2 allele,
                       complete cds
                       43291
     Seq. No.
                       bth700845110.h1
     Seq. ID
     Method
                       BLASTX
                       q4490706
     NCBI GI
                       220
     BLAST score
                       3.0e-18
     E value
Match length
                       82
                       66
     % identity
     NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
                       43292
     Seq. No.
                       bth700845168.h1
     Seq. ID
                       BLASTX
     Method
     NCBI GI
                       g4454010
                       265
     BLAST score
                       1.0e-23
     E value
                        82
     Match length
                        61
     % identity
     NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
                        43293
     Seq. No.
                        bth700845223.h1
     Seq. ID
     Method
                        BLASTN
                        g577294
     NCBI GI
     BLAST score
                        240
     E value
                        1.0e-132
                        240
     Match length
                        100
     % identity
     NCBI Description Human mRNA for KIAA0088 gene, partial cds
                        43294
     Seq. No.
                        bth700845234.h1
     Seq. ID
                        BLASTX
     Method
     NCBI GI
                        g2262105
                        343
     BLAST score
                        9.0e-33
     E value
                        80
     Match length
      % identity
                        78
     NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
                        43295
      Seq. No.
                        bth700845308.h1
      Seq. ID
                        BLASTX
     Method
                        g2244759
      NCBI GI
                        318
      BLAST score
```

1.0e-29

E value



```
Match length
% identity
                   74
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
NCBI Description
                   43296
Seq. No.
                  bth700845320.h1
Seq. ID
Method
                   BLASTX
                   g3915826
NCBI GI
                   302
BLAST score
                   7.0e-28
E value
                   71
Match length
                   77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   43297
Seq. No.
                   bth700845328.hl
Seq. ID
                   BLASTX
Method
                   g3608137
NCBI GI
BLAST score
                   148
                   8.0e-10
E value
                   55
Match length
                   51
% identity
                  (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43298
                   bth700845470.h1
Seq. ID
                   BLASTN
Method
                   g1408470
NCBI GI
                   64
BLAST score
                   1.0e-27
E value
                   120
Match length
                   88
% identity
                   Arabidopsis thaliana actin depolymerizing factor 1 (AtADF1)
NCBI Description
                   mRNA, complete cds
                   43299
Seq. No.
                   bth700845593.hl
Seq. ID
                   BLASTN
Method
                   q170065
NCBI GI
                   88
BLAST score
                   5.0e-42
E value
                   189
Match length
                   97
% identity
                   Soybean (G.max) proline-rich cell wall protein (SbPRP2)
NCBI Description
                   gene, complete cds
                   43300
 Seq. No.
                   bth700845630.h1
 Seq. ID
                   BLASTX
 Method
                   g3927836
 NCBI GI
 BLAST score
                   306
                   2.0e-28
 E value
                   79
 Match length
                   77
 % identity
```

Seq. No. 43301

NCBI Description

(AC005727) unknown protein [Arabidopsis thaliana]



```
bth700845703.h1
Seq. ID
Method
                  BLASTX
                  a3065835
NCBI GI
                  289
BLAST score
                  2.0e-31
E value
                  86
Match length
% identity
                  (AF058800) putative methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  43302
Seq. No.
                  bth700845715.h1
Seq. ID
Method
                  BLASTN
                  q1236948
NCBI GI
                  227
BLAST score
                  1.0e-125
E value
                  259
Match length
                  97
% identity
NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds
                   43303
Seq. No.
                  bth700845726.h1
Seq. ID
                  BLASTN
Method
                   g1066498
NCBI GI
BLAST score
                   98
                   6.0e-48
E value
                   218
Match length
                   85
% identity
                  Medicago sativa (clone GG16-1) NADH-dependent glutamate
NCBI Description
                   synthase gene, complete cds
Seq. No.
                   43304
                   bth700845730.h1
Seq. ID
                   BLASTX
Method
                   g4406781
NCBI GI
BLAST score
                   286
                   5.0e-26
E value
Match length
                   86
                   73
% identity
                   (AC006532) putative Na+/H+ antiporter [Arabidopsis
NCBI Description
                   thaliana]
                   43305
Seq. No.
                   bth700845827.h1
Seq. ID
Method
                   BLASTX
                   q3036807
NCBI GI
                   276
BLAST score
                   7.0e-25
E value
                   80
Match length
% identity
                   66
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

bth700845833.h1 Seq. ID

43306

BLASTX Method NCBI GI g1304227 BLAST score 218



```
5.0e-18
E value
                  89
Match length
% identity
                  48
                  (D63781) Epoxide hydrolase [Glycine max]
NCBI Description
                  >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase
                  [Glycine max]
                  43307
Seq. No.
                  bth700845949.hl
Seq. ID
Method
                  BLASTX
                  g4049353
NCBI GI
BLAST score
                  240
                   1.0e-20
E value
                   81
Match length
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
                   43308
Seq. No.
                  bth700845990.h1
Seq. ID
                   BLASTX
Method
                   q3355487
NCBI GI
BLAST score
                   233
                   8.0e-20
E value
                   70
Match length
% identity
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]
                   43309
Seq. No.
                   bth700846056.h1
Seq. ID
Method
                   BLASTX
                   g3075399
NCBI GI
BLAST score
                   255
                   2.0e-22
E value
                   83
Match length
                   57
% identity
NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]
                   43310
Seq. No.
                   bth700846063.h1
Seq. ID
                   BLASTN
Method
                   g256142
NCBI GI
                   242
BLAST score
                   1.0e-134
E value
                   246
Match length
                   100
 % identity
                   cytosolic glutamine synthetase [Glycine max=soybeans, var
 NCBI Description
                   Prize, mRNA, 1450 nt]
                   43311
 Seq. No.
                   bth700846085.hl
 Seq. ID
                   BLASTN
 Method
                   g886099
 NCBI GI
                   49
 BLAST score
                   1.0e-18
 E value
                   65
 Match length
 % identity
 NCBI Description Glycine max putative water channel protein (Pip1) mRNA,
```

Method

NCBI GI



complete cds

```
43312
Seq. No.
                  bth700846123.h1
Seq. ID
Method
                  BLASTN
                  g2317899
NCBI GI
BLAST score
                  235
                  1.0e-129
E value
                  247
Match length
% identity
                  99
NCBI Description Glycine max Sali3-2 mRNA, complete cds
Seq. No.
                  43313
Seq. ID
                  bth700846144.h1
                  BLASTX
Method
                  q3335373
NCBI GI
                  152
BLAST score
                  2.0e-10
E value
Match length
                  60
                  50
% identity
                  (AC003028) putative GTL1 protein [Arabidopsis thaliana]
NCBI Description
                  43314
Seq. No.
                  bth700846190.h1
Seq. ID
                  BLASTX
Method
                  q2317908
NCBI GI
                   294
BLAST score
E value
                   6.0e-27
Match length
                   83
                   66
% identity
                  (U89959) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   43315
Seq. No.
                   bth700846237.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q404688
BLAST score
                   265
                   2.0e-23
E value
                   87
Match length
% identity
                   62
NCBI Description (L19074) cytochrome P450 [Catharanthus roseus]
                   43316
Seq. No.
Seq. ID
                   bth700846243.h1
Method
                   BLASTN
NCBI GI
                   g493019
BLAST score
                   209
E value
                   1.0e-114
                   213
Match length
                   100
% identity
                   Glycine max delta-aminolevulinic acid dehydratase (Alad)
NCBI Description
                   mRNA, complete cds
                   43317
Seq. No.
                   bth700846269.h1
Seq. ID
                   BLASTX
```

6883

g1723182



```
BLAST score
                  4.0e-23
E value
                  83
Match length
% identity
                  67
NCBI Description SUGAR CARRIER PROTEIN A >gi_169736 (L08197) sugar carrier
                  protein [Ricinus communis]
                  43318
Seq. No.
                  bth700846283.h1
Seq. ID
                  BLASTX
Method
                  g4455299
NCBI GI
                  241
BLAST score
                   6.0e-21
E value
                   66
Match length
% identity
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
                   43319
Seq. No.
                  bth700846320.h1
Seq. ID
                   BLASTX
Method
                   g2443348
NCBI GI
BLAST score
                   308
                   1.0e-28
E value
                   86
Match length
                   66
% identity
NCBI Description (AB001379) cytochrome P450 [Glycyrrhiza echinata]
                   43320
Seq. No.
                   bth700846330.h1
Seq. ID
                   BLASTN
Method
                   g256142
NCBI GI
BLAST score
                   242
                   1.0e-134
E value
                   254
Match length
                   99
% identity
                   cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                   Prize, mRNA, 1450 nt]
                   43321
Seq. No.
                   bth700846336.h1
 Seq. ID
                   BLASTX
Method
                   g4455276
NCBI GI
                   317
BLAST score
                   1.0e-29
E value
                   74
Match length
                   84
 % identity
                   (AL035527) peptide transporter-like protein [Arabidopsis
 NCBI Description
                   thaliana]
                   43322
 Seq. No.
                   bth700846411.h1
 Seq. ID
                   BLASTX
 Method
                   a2262172
 NCBI GI
                    223
 BLAST score
                    1.0e-18
 E value
                    83
 Match length
```

% identity

Seq. No.

Seq. ID



```
(ACO02329) predicted protein of unknown function
NCBI Description
                  [Arabidopsis thaliana]
                  43323
Seq. No.
                  bth700846421.hl
Seq. ID
                  BLASTX
Method
                  g2213594
NCBI GI
                  350
BLAST score
                  1.0e-33
E value
                  81
Match length
                  72
% identity
                  (AC000348) T7N9.14 [Arabidopsis thaliana]
NCBI Description
                  43324
Seq. No.
                  bth700846492.h1
Seq. ID
                  BLASTX
Method
                  g2062176
NCBI GI
BLAST score
                  243
                  5.0e-21
E value
Match length
                   80
% identity
                   71
                  (AC001645) Myb-related transcription activator (MybSt1)
NCBI Description
                   isolog [Arabidopsis thaliana]
                   43325
Seq. No.
                  bth700846493.h1
Seq. ID
                  BLASTX
Method
                   g2739383
NCBI GI
                   160
BLAST score
                   3.0e-11
E value
                   79
Match length
                   48
% identity
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
                   43326
Seq. No.
                   bth700846556.h1
Seq. ID
Method
                   BLASTN
                   q1408470
NCBI GI
BLAST score
                   44
E value
                   9.0e-16
                   119
Match length
% identity
                   Arabidopsis thaliana actin depolymerizing factor 1 (AtADF1)
NCBI Description
                   mRNA, complete cds
                   43327
Seq. No.
                   bth700846585.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4262226
                   153
BLAST score
                   2.0e-10
E value
Match length
                   46
                   70
% identity
                   (AC006200) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   43328
```

6885

bth700846591.hl

% identity

58



```
BLASTX
Method
NCBI GI
                   q4455159
BLAST score
                   283
                   1.0e-25
E value
                   68
Match length
% identity
                   72
                  (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43329
Seq. ID
                  bth700846625.h1
Method
                  BLASTX
NCBI GI
                   g2213629
BLAST score
                   168
                   3.0e-25
E value
Match length
                   82
                   78
% identity
NCBI Description
                  (AC000103) F21J9.21 [Arabidopsis thaliana]
                   43330
Seq. No.
                  bth700846715.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4455350
BLAST score
                   141
                   1.0e-16
E value
Match length
                   85
% identity
                   58
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43331
Seq. ID
                   bth700846730.h1
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   129
E value
                   2.0e-66
Match length
                   260
                   88
% identity
NCBI Description Tobacco chloroplast genome DNA
Seq. No.
                   43332
Seq. ID
                   bth700846742.h1
                   BLASTN
Method
NCBI GI
                   g2351070
BLAST score
                   42
                   2.0e-14
E value
Match length
                   106
% identity
                   85
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                   43333
                  bth700846755.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3212868
BLAST score
                   188
                   2.0e-14
E value
Match length
                   62
```

Seq. No.

Seq. ID

Method

43339

BLASTX

bth700847055.h1



```
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  43334
Seq. ID
                  bth700846850.h1
                  BLASTN
Method
NCBI GI
                  g169348
BLAST score
                  127
                  3.0e-65
E value
Match length
                  218
% identity
                  31
NCBI Description
                  P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3'
Seq. No.
                  43335
Seq. ID
                  bth700846947.h1
Method
                  BLASTX
NCBI GI
                  g2245077
BLAST score
                  368
                  1.0e-35
E value
Match length
                  86
                  79
% identity
NCBI Description
                  (Z97343) glucanase homolog [Arabidopsis thaliana]
Seq. No.
                  43336
Seq. ID
                  bth700846971.h1
Method
                  BLASTX
NCBI GI
                  q1514643
BLAST score
                  159
                  3.0e-11
E value
Match length
                  45
                  73
% identity
NCBI Description
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
                  43337
Seq. No.
Seq. ID
                  bth700847027.h1
Method
                  BLASTX
                  g3158476
NCBI GI
BLAST score
                  273
E value
                  2.0e-24
Match length
                  64
% identity
                  84
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  43338
Seq. ID
                  bth700847035.h1
Method
                  BLASTX
NCBI GI
                  g4106690
BLAST score
                  242
                  7.0e-21
E value
Match length
                  66
% identity
                  67
NCBI Description
                  (AL035065) putative urea active transporter
                  [Schizosaccharomyces pombe]
```



NCBI GI g2190551 BLAST score 336 7.0e-32 E value Match length 81 84 % identity

(ACO01229) Similar to C. elegans hypothetical protein NCBI Description

K07C5.6 (gb_Z71181). ESTs gb H36844,gb AA394956 come from

this gene. [Arabidopsis thaliana]

43340 Seq. No.

Seq. ID bth700847068.h1

Method BLASTX g3236259 NCBI GI BLAST score 244 4.0e-21 E value Match length 74 % identity 61

(AC004684) putative alcohol dehydrogenase [Arabidopsis NCBI Description

thaliana]

Seq. No. 43341

Seq. ID bth700847070.h1

Method BLASTN g18766 NCBI GI BLAST score 114 2.0e-57 E value Match length 223 % identity 87

NCBI Description Soybean Tgm5 transposable element

Seq. No. 43342

Seq. ID bth700847087.h1

Method BLASTN NCBI GI g510514 BLAST score 188 1.0e-101 E value 192 Match length

99 % identity NCBI Description G.max KTi-S mRNA

Seq. No. Seq. ID bth700847154.h1

43343

Method BLASTX NCBI GI g3132473 BLAST score 144 E value 2.0e-09 Match length 37 % identity 73

NCBI Description (AC003096) similar to rapb transcription factor

[Arabidopsis thaliana]

Seq. No. 43344

Seq. ID bth700847162.h1

Method BLASTN NCBI GI q463251 BLAST score 52 E value 2.0e-20



Match length 80 % identity 91

NCBI Description M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5

Seq. No.

Seq. ID bth700847163.h1

Method BLASTN
NCBI GI g4115338
BLAST score 145
E value 5.0e-76
Match length 205

Match length 205 % identity 21

NCBI Description Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds

Seq. No. 43346

Seq. ID bth700847168.h1

Method BLASTX
NCBI GI 94467121
BLAST score 353
E value 7.0e-34
Match length 82
% identity 82

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 43347

Seq. ID bth700847169.h1

Method BLASTX
NCBI GI g3075400
BLAST score 249
E value 9.0e-22
Match length 76
% identity 67

NCBI Description (AC004484) putative thromboxane-A synthase [Arabidopsis

thaliana] >gi 3413720 (AC004747) putative thromboxin-A

synthase [Arabidopsis thaliana]

Seq. No. 43348

Seq. ID bth700847179.h1

Method BLASTN
NCBI GI g1305548
BLAST score 72
E value 1.0e-32
Match length 183
% identity 98

NCBI Description Glycine max asparagine synthetase mRNA, complete cds

Seq. No. 43349

Seq. ID bth700847210.h1

Method BLASTX
NCBI GI g3252805
BLAST score 189
E value 1.0e-14
Match length 67
% identity 51

NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

>gi_3650027 (AC005396) hypothetical protein [Arabidopsis

thaliana]



```
43350
Seq. No.
Seq. ID
                  bth700847221.h1
Method
                  BLASTX
                  g4469025
NCBI GI
BLAST score
                  179
                  2.0e-13
E value
Match length
                  54
                  57
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                  43351
                  bth700847270.h1
Seq. ID
Method
                  BLASTX
                  q3805844
NCBI GI
BLAST score
                  157
E value
                  7.0e-11
Match length
                   48
                   62
% identity
                  (AL031986) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43352
Seq. ID
                  bth700847286.h1
Method
                  BLASTN
NCBI GI
                  q169090
BLAST score
                  90
                   3.0e-43
E value
Match length
                   166
% identity
                   89
                  Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA,
NCBI Description
                  complete cds
Seq. No.
                   43353
Seq. ID
                  bth700847288.h1
Method
                  BLASTN
NCBI GI
                   q1155053
BLAST score
                  58
E value
                   4.0e-24
                   143
Match length
                   90
% identity
                  Phaseolus vulgaris regulator of MAT2 (ROM2) mRNA, complete
NCBI Description
                   cds
                   43354
Seq. No.
Seq. ID
                  bth700847309.h1
Method
                  BLASTX
                   g2894568
NCBI GI
BLAST score
                   268
                   7.0e-24
E value
                   83
Match length
                   63
% identity
                  (AL021890) putative protein [Arabidopsis thaliana]
NCBI Description
                   43355
```

Seq. No.

Seq. ID bth700847345.h1

Method BLASTN NCBI GI g18642



BLAST score 69
E value 1.0e-30
Match length 181
% identity 86
NCBI Description G.max mRNA from stress-induced gene (H4)

Seq. No. 43356

Seq. ID bth700847357.h1

Method BLASTX
NCBI GI g1762142
BLAST score 191
E value 7.0e-15
Match length 85
% identity 48

NCBI Description (U48434) putative cytochrome P450 [Solanum chacoense]

Seq. No. 43357

Seq. ID bth700847374.h1

Method BLASTX
NCBI GI g4455179
BLAST score 194
E value 3.0e-15
Match length 82
% identity 48

NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 43358

Seq. ID bth700847407.h1

Method BLASTX
NCBI GI g2245136
BLAST score 219
E value 2.0e-18
Match length 52
% identity 87

NCBI Description (Z97344) trehalose-6-phosphate synthase homolog

[Arabidopsis thaliana]

Seq. No. 43359

Seq. ID bth700847451.h1

Method BLASTX
NCBI GI g4539301
BLAST score 227
E value 3.0e-19
Match length 51
% identity 80

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 43360

Seq. ID bth700847453.h1

Method BLASTN
NCBI GI g4558461
BLAST score 49
E value 6.0e-19
Match length 89
% identity 89

NCBI Description Medicago sativa subsp. X varia cell cycle switch protein

NCBI GI



(ccs52) mRNA, complete cds

```
Seq. No.
                     43361
                     bth700847477.h1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g3122059
  BLAST score
                     180
                     9.0e-14
E value
                     49
  Match length
                     69
  % identity
                     ELONGATION FACTOR 2 (EF-2) >gi 706975 (U21667) elongation
  NCBI Description
                     factor-2 [Cryptosporidium parvum]
                     43362
  Seq. No.
                     bth700847489.h1
   Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g4415908
  BLAST score
                     164
  E value
                     7.0e-12
  Match length
                     46
                     72
   % identity
  NCBI Description
                     (AC006282) unknown protein [Arabidopsis thaliana]
   Seq. No.
                     43363
                     bth700847525.h1
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     q2367431
   BLAST score
                     147
  E value
                     9.0e-10
                     77
  Match length
                     42
   % identity
                     (AF000403) putative cytochrome P450 [Lotus japonicus]
   NCBI Description
                     43364
   Seq. No.
   Seq. ID
                     bth700847584.h1
   Method
                     BLASTX
                     g3402684
   NCBI GI
   BLAST score
                     310
                     7.0e-29
   E value
   Match length
                     79
                     75
   % identity
                     (AC004697) hypothetical protein [Arabidopsis thaliana]
   NCBI Description
   Seq. No.
                     43365
                     bth700847586.h1
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g2062172
   BLAST score
                     215
                     6.0e-18
   E value
   Match length
                     79
                     54
   % identity
                     (AC001645) unknown protein [Arabidopsis thaliana]
   NCBI Description
   Seq. No.
                     43366
   Seq. ID
                     bth700847620.h1
                     BLASTN
   Method
```

6892

g1052779



```
BLAST score
                   9.0e-56
E value
                  211
Match length
% identity
                   88
NCBI Description P.vulgaris beta-1,3-glucanase gene
Seq. No.
                   43367
                  bth700847647.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1049407
BLAST score
                   253
E value
                   3.0e-22
Match length
                   76
                   61
% identity
                   (U39655) Similar to long-chain-fatty-acid coA ligase.
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                   43368
                   bth700847664.h1
Seq. ID
Method
                   BLASTX
                   q4220479
NCBI GI
                   326
BLAST score
E value
                   8.0e-31
Match length
                   76
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   43369
Seq. No.
                   bth700847674.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4210948
BLAST score
                   219
E value
                   3.0e-18
Match length
                   43
                   95
% identity
                  (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
                   43370
Seq. No.
                   bth700847684.h1
Seq. ID
Method
                   BLASTX
                   g4309734
NCBI GI
                   354
BLAST score
                   4.0e-34
E value
Match length
                   75
% identity
                   93
                   (AC006439) putative 26S proteosome regulatory subunit 8
NCBI Description
                   [Arabidopsis thaliana]
                   43371
Seq. No.
                   bth700847717.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q313143
BLAST score
                   49
                   1.0e-18
E value
                   105
Match length
                   87
% identity
```

NCBI Description A.medicago MSK-1 mRNA for protein kinase



thaliana]

% identity

NCBI Description

```
43372
Seq. No.
Seq. ID
                  bth700847748.h1
                  BLASTX
Method
NCBI GI
                  g2618705
BLAST score
                  337
                  6.0e-32
E value
Match length
                  85
                  76
% identity
                   (AC002510) putative ABC transporter, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
                  43373
Seq. No.
                  bth700847756.h1
Seq. ID
Method
                  BLASTN
                  g4103958
NCBI GI
BLAST score
                  130
E value
                  5.0e-67
Match length
                  182
% identity
                   93
                  Phaseolus vulgaris calmodulin (CaM) mRNA, PvCaM-2 allele,
NCBI Description
                  complete cds
Seq. No.
                   43374
                  bth700847759.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352681
BLAST score
                   204
                   2.0e-16
E value
Match length
                   65
% identity
                   62
                  PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457
NCBI Description
                   phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
                   thaliana >gi 633028 dbj BAA07287 (D38109) protein
                  phosphatase 2C [Arabidopsis thaliana]
                   43375
Seq. No.
Seq. ID
                  bth700847769.h1
Method
                   BLASTX
                   g2245108
NCBI GI
BLAST score
                   139
                   9.0e-09
E value
Match length
                   43
                   63
% identity
                  (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
NCBI Description
                   43376
Seq. No.
Seq. ID
                   bth700847809.h1
Method
                   BLASTX
NCBI GI
                   g4115379
BLAST score
                   118
                   1.0e-13
E value
Match length
                   73
```

(AC005967) putative carbonyl reductase [Arabidopsis



```
Seq. No.
                  bth700847810.h1
Seq. ID
Method
                  BLASTX
                  g4455329
NCBI GI
BLAST score
                  141
E value
                  1.0e-14
                  79
Match length
% identity
                  54
                   (AL035525) lysine-ketoglutarate reductase/saccharopine
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  43378
                  bth700847832.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170048
BLAST score
                  135
E value
                  5.0e-70
Match length
                  203
% identity
                  Glycine max SbPRP1 gene encoding a proline-rich protein,
NCBI Description
                  complete cds
Seq. No.
                  43379
Seq. ID
                  bth700847839.h1
Method
                  BLASTX
NCBI GI
                  g2352492
BLAST score
                  148
E value
                   4.0e-17
                  77
Match length
% identity
                   62
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                  thaliana] >gi_2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
Seq. No.
                   43380
Seq. ID
                  bth700847848.h1
                  BLASTN
Method
NCBI GI
                  q1518539
BLAST score
                   121
                   9.0e-62
E value
                  140
Match length
                   97
% identity
                  Glycine max UDP-glucose dehydrogenase mRNA, complete cds
NCBI Description
                   43381
Seq. No.
                  bth700847882.h1
Seq. ID
                  BLASTN
Method
                   g2677827
NCBI GI
                   54
BLAST score
                  1.0e-21
E value
                  153
Match length
                   84
% identity
NCBI Description Prunus armeniaca cysteine protease mRNA, complete cds
```

43382

BLASTX

bth700847922.h1

Seq. No. Seq. ID

Method

% identity

43



```
NCBI GI
                   q3643604
BLAST score
                   214
E value
                   1.0e-17
Match length
                   83
% identity
                   48
NCBI Description
                   (AC005395) receptor-like protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   43383
Seq. ID
                   bth700847947.h1
Method
                   BLASTX
NCBI GI
                   q4314363
BLAST score
                   282
E value
                   1.0e-25
Match length
                   86
% identity
                   59
NCBI Description
                   (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   43384
Seq. ID
                   bth700847960.h1
Method
                   BLASTX
NCBI GI
                   g2160150
BLAST score
                   255
E value
                   2.0e-22
Match length
                   82
% identity
                   61
NCBI Description
                   (AC000375) EST gb_T43829 comes from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   43385
Seq. ID
                   bth700848034.h1
Method
                   BLASTX
NCBI GI
                   g3136057
BLAST score
                   135
E value
                   9.0e-12
Match length
                   85
% identity
                   46
NCBI Description
                  (AL023592) actin-like protein [Schizosaccharomyces pombe]
Seq. No.
                   43386
Seq. ID
                  bth700848096.h1
Method
                   BLASTX
NCBI GI
                   g4508079
BLAST score
                   146
E value
                   2.0e-20
Match length
                   79
% identity
                   66
NCBI Description
                 (AC005882) 66284 [Arabidopsis thaliana]
Seq. No.
                  43387
Seq. ID
                  bth700848108.h1
Method
                  BLASTX
NCBI GI
                  g3068714
BLAST score
                  373
E value
                  3.0e-36
Match length
                  85
```



NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 43388

Seq. ID bth700848116.h1

Method BLASTX
NCBI GI g1304227
BLAST score 233
E value 9.0e-20
Match length 84
% identity 51

NCBI Description (D63781) Epoxide hydrolase [Glycine max]

>gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase

[Glycine max]

Seq. No. 43389

Seq. ID bth700848170.h1

Method BLASTN
NCBI GI 94432829
BLAST score 34
E value 9.0e-10
Match length 134
% identity 87

NCBI Description Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 43390

Seq. ID bth700848185.h1

Method BLASTX
NCBI GI g2961352
BLAST score 159
E value 4.0e-11
Match length 84
% identity 42

NCBI Description (AL022140) putative protein [Arabidopsis thaliana]

Seq. No. 43391

Seq. ID bth700848301.h1

Method BLASTX
NCBI GI g4056482
BLAST score 319
E value 8.0e-30
Match length 75
% identity 46

NCBI Description (AC005896) putative ABC transporter [Arabidopsis thaliana]

Seq. No. 43392

Seq. ID bth700848338.h1

Method BLASTX
NCBI GI g4008008
BLAST score 237
E value 3.0e-20
Match length 88
% identity 52

NCBI Description (AF084035) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 43393



bth700848408.h1 Seq. ID Method BLASTX q2414584 NCBI GI 153 BLAST score 2.0e-10 E value Match length 83 36 % identity (Z99292) dna repair protein [Schizosaccharomyces pombe] NCBI Description 43394 Seq. No. bth700848446.h1 Seq. ID Method BLASTX NCBI GI g3334409 BLAST score 155 1.0e-10 E value 37 Match length 81 % identity VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) NCBI Description >gi 2129765 pir S71261 V-type proton-ATPase - Arabidopsis tha $\overline{1}$ iana $>g\overline{1}_{11}\overline{43}394_{emb}CAA63086_ (X92117)$ V-type proton-ATPase [Arabidopsis thaliana] 43395 Seq. No. bth700848447.h1 Seq. ID Method BLASTX g4006915 NCBI GI 143 BLAST score 3.0e-09 E value 66 Match length 50 % identity (Z99708) hypothetical protein [Arabidopsis thaliana] NCBI Description 43396 Seq. No. bth700848484.h1 Seq. ID Method BLASTX g3158476 NCBI GI BLAST score 273 2.0e-24 E value Match length 64 84 % identity (AF067185) aquaporin 2 [Samanea saman] NCBI Description 43397 Seq. No. bth700848508.h1 Seq. ID Method BLASTX g2959781 NCBI GI 214 BLAST score 1.0e-17 E value Match length 82 60 % identity (AJ223508) Zwille protein [Arabidopsis thaliana] NCBI Description 43398

Seq. No.

bth700848522.h1 Seq. ID

Method BLASTX NCBI GI g3859944 BLAST score 365



E value 2.0e-35 Match length 85 % identity 84 (AF084570) FKBP12 interacting protein [Arabidopsis NCBI Description thaliana] Seq. No. 43399 bth700848576.h1 Seq. ID Method BLASTX NCBI GI q4539351 BLAST score 206 E value 9.0e-17 Match length 82 46 % identity (AL035539) putative protein [Arabidopsis thaliana] NCBI Description 43400 Seq. No. Seq. ID bth700848579.h1 BLASTX Method q3582332 NCBI GI BLAST score 162 3.0e-21 E value Match length 71 % identity 73 (AC005496) unknown protein [Arabidopsis thaliana] NCBI Description 43401 Seq. No. bth700848591.h1 Seq. ID Method BLASTX q1361983 NCBI GI BLAST score 152 3.0e-10 E value 37 Match length % identity 86 ARP protein - Arabidopsis thaliana >gi 886434 emb CAA89858_ NCBI Description (Z49776) ARP protein [Arabidopsis thaliana] Seq. No. 43402 Seq. ID bth700848648.h1 Method BLASTX NCBI GI q3695399 BLAST score 175 E value 5.0e-13 Match length 83 % identity 45 (AF096372) contains similarity to Arabidopsis thaliana NCBI Description retrotransposon Athila (GB:X81801) [Arabidopsis thaliana] Seq. No. 43403 Seq. ID bth700848655.h1 Method BLASTN g829118 NCBI GI BLAST score 105 4.0e-52 E value Match length 205

6899

88

NCBI Description P.vulgaris gene for cyclophilin

% identity

NCBI GI



```
Seq. No.
                  43404
                  bth700848679.h1
Seq. ID
Method
                  BLASTX
                  g4530126
NCBI GI
BLAST score
                  168
E value
                   3.0e-12
Match length
                   59
                   51
% identity
                   (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
Seq. No.
                   43405
                  bth700848721.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2911052
BLAST score
                   348
E value
                   3.0e-33
Match length
                   71
                   92
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43406
                  bth700848748.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4490706
BLAST score
                   173
E value
                   9.0e-13
Match length
                   55
                   64
% identity
                  (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43407
                   bth700848795.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1514643
BLAST score
                   352
                   9.0e-34
E value
Match length
                   85
% identity
                   74
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                   43408
Seq. No.
                   bth700848805.h1
Seq. ID
Method
                   BLASTX
                   g3335376
NCBI GI
                   264
BLAST score
E value
                   2.0e-23
                   50
Match length
% identity
                   90
                   (AC003028) putative ammonium transporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   43409
                   bth700848830.h1
Seq. ID
                   BLASTX
Method
```

6900

g2809246



```
BLAST score
                  384
                  2.0e-37
E value
Match length
                  84
% identity
                  87
NCBI Description
                  (AC002560) F2401.15 [Arabidopsis thaliana]
Seq. No.
                  43410
                  bth700848908.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406781
BLAST score
                  165
E value
                   6.0e-12
Match length
                  78
                  49
% identity
                   (AC006532) putative Na+/H+ antiporter [Arabidopsis
NCBI Description
```

thaliana]

Seq. No. 43411 bth700848963.h1 Seq. ID Method BLASTN NCBI GI g256142 BLAST score 117 E value 2.0e-59

Match length 241 % identity 88

cytosolic glutamine synthetase [Glycine max=soybeans, var NCBI Description

Prize, mRNA, 1450 nt]

Seq. No. 43412

Seq. ID bth700848971.h1

Method BLASTN NCBI GI q170048 BLAST score 158 E value 8.0e-84 Match length 232 % identity

NCBI Description Glycine max SbPRP1 gene encoding a proline-rich protein,

complete cds

43413 Seq. No.

Seq. ID bth700848981.h1

Method BLASTX NCBI GI g629597 BLAST score 176 3.0e-13E value Match length 45 % identity 76

proline-rich protein - rape >gi_545029_bbs_142669 (S68113) NCBI Description

proline-rich SAC51 [Brassica napus=oilseed rape, pods,

Peptide, 147 aa] [Brassica napus]

Seq. No. 43414

Seq. ID bth700848990.h1

BLASTN Method NCBI GI g1786114 BLAST score 96 E value 8.0e-47



```
Match length
                   159
                   93
% identity
                  Vigna unguiculata phosphoinositide-specific phospholipase C
NCBI Description
                  mRNA, complete cds
                   43415
Seq. No.
                  bth700849018.h1
Seq. ID
                   BLASTX
                                                         . <del>1</del> 7.
Method
                   g2911060
NCBI GI
                   149
BLAST score
                   6.0e-10
E value
                   77
Match length
                   39
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein
                   [Arabidopsis thaliana]
                   43416
Seq. No.
                   bth700849020.h1
Seq. ID
                   BLASTN
Method
                   g310560
NCBI GI
                   47
BLAST score
                   2.0e-17
E value
Match length
                   47
                   100
% identity
                   Soybean ascorbate peroxidase mRNA, complete cds
NCBI Description
                   43417
Seq. No.
                   bth700849029.h1
Seq. ID
                   BLASTX
Method
                   q4204281
NCBI GI
                   148
BLAST score
                   4.0e-10
E value
Match length
                   83
                   34
% identity
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   43418
Seq. No.
                   bth700849043.h1
Seq. ID
                   BLASTN
Method
                   q3204107
NCBI GI
                   44
BLAST score
                   1.0e-15
E value
                   116
Match length
                   85
 % identity
                   Cicer arietinum mRNA for putative cytidine or
NCBI Description
                   deoxycytidylate deaminase, partial
                   43419
 Seq. No.
                   bth700849051.h1
 Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3522933
BLAST score 266
E value 1.0e-23
Match length 92
% identity 59

NCBI Description (AC004411) putative anion exchange protein 3 [Arabidopsis

Seq. No.

Seq. ID Method

43425

BLASTN

bth700849156.h1



thaliana]

```
43420
Seq. No.
Seq. ID
                  bth700849063.h1
Method
                  BLASTX
                  g3150407
NCBI GI
BLAST score
                  183
                  6.0e-14
E value
                  66
Match length
                  56
% identity
                  (AC004165) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  43421
Seq. No.
                  bth700849068.h1
Seq. ID
                  BLASTX
Method
                  g2497539
NCBI GI
                  292
BLAST score
                  1.0e-26
E value
                  85
Match length
                  59
% identity
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi 169703
NCBI Description
                  (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
                  43422
Seq. No.
                  bth700849115.h1
Seq. ID
                  BLASTN
Method
                  g3452136
NCBI GI
                  178
BLAST score
                  1.0e-95
E value
Match length
                  194
                  99
% identity
                  Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                  partial
Seq. No.
                  43423
Seq. ID
                  bth700849123.h1
Method
                  BLASTX
                  g2626753
NCBI GI
                  315
BLAST score
E value
                  2.0e-29
                  83
Match length
                  76
% identity
NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana]
                   43424
Seq. No.
                  bth700849145.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2829868
BLAST score
                   166
                   6.0e-12
E value
Match length
                   69
                   52
% identity
                  (AC002396) Unknown protein [Arabidopsis thaliana]
NCBI Description
```



```
NCBI GI
                   q3212102
BLAST score
                   53
                   4.0e-21
E value
                   156
Match length
% identity
                  Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   43426
Seq. No.
                   bth700849193.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169954
BLAST score
                   80
                   3.0e-37
E value
                   236
Match length
                   90
% identity
                  Glycine max iron superoxide dismutase (FeSOD) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   43427
                   bth700849201.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g347452
BLAST score
                   99
                   1.0e-48
E value
Match length
                   252
                   14
% identity
                   Soybean hydroxyproline-rich glycoprotein (sbHRGP3) mRNA,
NCBI Description
                   partial cds
                   43428
Seq. No.
                   bth700849204.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1370284
BLAST score
                   51
E value
                   7.0e-20
Match length
                   145
                   88
% identity
NCBI Description P.sativum mRNA for glutathione reductase
Seq. No.
                   43429
                   bth700849214.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4324966
                   125
BLAST score
                   5.0e-64
E value
Match length
                   157
% identity
                   95
                  Glycine max ADP-ribosylation factor mRNA, partial cds
NCBI Description
Seq. No.
                   43430
Seq. ID
                   bth700849228.h1
                   BLASTX
Method
                   g3193327
NCBI GI
                   302
BLAST score
```

6904

7.0e-28

87

E value

Match length



```
% identity
                  (AF069299) No definition line found [Arabidopsis thaliana]
NCBI Description
                  43431
Seq. No.
                  bth700849234.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4389416
                  162
BLAST score
                  3.0e-86
E value
                  238
Match length
% identity ·
                  92
NCBI Description Glycine max nitrate reductase (nr2) gene, partial cds
                  43432
Seq. No.
                  bth700849240.h1
Seq. ID
Method
                  BLASTX
                  g2853077
NCBI GI
BLAST score
                  164
                  1.0e-11
E value
Match length
                  54
                  56
% identity
                  (ALO21768) resistence protein - like [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  43433
                  bth700849250.h1
Seq. ID
                  BLASTX
Method
                  q1708191
NCBI GI
                  165
BLAST score
E value
                  6.0e-12
Match length
                  71
                  52
% identity
                  HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose
NCBI Description
                  carrier protein [Ricinus communis]
                   43434
Seq. No.
Seq. ID
                  bth700849261.h1
Method
                  BLASTX
NCBI GI
                  q3319990
BLAST score
                   143
                   3.0e-09
E value
Match length
                   69
                   56
% identity
                  (Y17267) ubiquitin-conjugating enzyme [Mus musculus]
NCBI Description
Seq. No.
                   43435
                  bth700849273.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3874761
BLAST score
                   155
E value
                   1.0e-10
Match length
                   50
% identity
                   56
                   (Z71185) Similarity to yeast hypothetical protein Swiss
NCBI Description
                   Prot accession number P28606. [Caenorhabditis elegans]
```

6905

43436

bth700849279.h1

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                  q3335376
                  293
BLAST score
E value
                  8.0e-27
                  80
Match length
                  74
% identity
                  (AC003028) putative ammonium transporter [Arabidopsis
NCBI Description
                  43437
Seq. No.
                  bth700849344.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3834303
BLAST score
                  130
                  8.0e-17
E value
                  70
Match length
                   68
% identity
                  (AC005679) F9K20.3 [Arabidopsis thaliana]
NCBI Description
                   43438
Seq. No.
                  bth700849359.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g571484
BLAST score
                   339
                   3.0e-32
E value
                   80
Match length
                   79
% identity
NCBI Description (U16727) peroxidase precursor [Medicago truncatula]
                   43439
Seq. No.
                   bth700849362.h1
Seq. ID
                   BLASTX
Method
                   q2224911
NCBI GI
BLAST score
                   140
                   5.0e-14
E value
Match length
                   73
% identity
                  (U93048) somatic embryogenesis receptor-like kinase [Daucus
NCBI Description
                   carota]
                   43440
 Seq. No.
                   bth700849376.h1
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g2507426
 BLAST score
                   106
                   2.0e-10
 E value
 Match length
                   69
                   61
 % identity
 NCBI Description ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR
                   (ALANINE--TRNA LIGASE) (ALARS) >gi_1673365_emb_CAA80380_
                    (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis
                   thaliana]
```

Seq. No. 43441

Seq. ID bth700849389.h1

Method BLASTN NCBI GI g511937



```
BLAST score
                  1.0e-98
E value
                  190
Match length
                  99
% identity
NCBI Description Soybean mRNA for cysteine proteinase, complete cds
                  43442
Seq. No.
                  bth700849436.h1
Seq. ID
                  BLASTX
Method
                  g2191136
NCBI GI
                  186
BLAST score
                   3.0e-14
E value
                  76
Match length
                   46
% identity
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                   43443
Seq. No.
                   bth700849473.h1
Seq. ID
                   BLASTN
Method
                   g2465528
NCBI GI
                   61
BLAST score
                   7.0e-26
E value
                   109
Match length
                   89
% identity
                  Medicago truncatula phosphate transporter (MtPT2) mRNA,
NCBI Description
                   complete cds
                   43444
Seq. No.
                   bth700849526.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2342690
BLAST score
                   289
E value
                   2.0e-26
Match length
                   83
                   71
 % identity
                   (ACO00106) Similar to Homo copine I (gb U83246).
NCBI Description
                   [Arabidopsis thaliana]
                   43445
 Seq. No.
                   bth700849594.h1
 Seq. ID
                   BLASTX
 Method
                   g2739004
 NCBI GI
                   299
 BLAST score
                   1.0e-27
 E value
 Match length
                   81
                   73
 % identity
 NCBI Description (AF022461) CYP82C1p [Glycine max]
```

Seq. No.

43446

Seq. ID

bth700849627.h1

BLASTX Method g3914359 NCBI GI 277 BLAST score 5.0e-25 E value



Match length 89 % identity PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) NCBI Description (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1928979 (U92656) phospholipase D [Vigna unguiculata] 43447 Seq. No. bth700849666.h1 Seq. ID BLASTX Method g2829894 NCBI GI 275 BLAST score E value 9.0e-25 80 Match length 72 % identity (AC002311) Unknown protein [Arabidopsis thaliana] NCBI Description 43448 Seq. No. bth700849676.h1 Seq. ID BLASTN Method g2688829 NCBI GI 64 BLAST score 1.0e-27 E value Match length 176 % identity 84 Prunus armeniaca putative sugar transporter mRNA, complete NCBI Description 43449 Seq. No. bth700849680.h1 Seq. ID BLASTX Method g1173027 NCBI GI 107 BLAST score 1.0e-09 E value 54 Match length 72 % identity 60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal NCBI Description protein L31 [Nicotiana glutinosa] 43450 Seq. No. bth700849735.h1 Seq. ID BLASTN Method g3046856 NCBI GI 32 BLAST score 1.0e-08 E value 74 Match length 92 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MXI22, complete sequence [Arabidopsis thaliana] 43451 Seq. No.

Seq. ID bth700849784.h1

BLASTN Method q516853 NCBI GI 117 BLAST score 3.0e-59 E value Match length 249 29 % identity



NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No. 43452 Seq. ID bth700849790.hl

Method BLASTX
NCBI GI g3193292
BLAST score 311.
E value 4.0e-33
Match length 81
% identity 79

NCBI Description (AF069298) similar to ATPases associated with various

cellular activites (Pfam: AAA.hmm, score: 230.91)

[Arabidopsis thaliana]

Seq. No. 43453

Seq. ID bth700849803.h1

Method BLASTX
NCBI GI g1708191
BLAST score 217
E value 6.0e-18
Match length 64
% identity 62

NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose

carrier protein [Ricinus communīs]

Seq. No. 43454

Seq. ID bth700849819.h1

Method BLASTN
NCBI GI g349436
BLAST score 32
E value 1.0e-08
Match length 40
% identity 95

NCBI Description Carrot EP1 mRNA, complete cds

Seq. No. 43455

Seq. ID bth700849826.hl

Method BLASTX
NCBI GI g1657617
BLAST score 179
E value 2.0e-13
Match length 68
% identity 78

NCBI Description (U72503) G2p [Arabidopsis thaliana] >gi 3068707 (AF049236)

putative nuclear DNA-binding protein G2p [Arabidopsis

thaliana]

Seq. No. 43456

Seq. ID bth700849846.hl

Method BLASTN
NCBI GI g18764
BLAST score 76
E value 7.0e-35
Match length 118
% identity 99

NCBI Description G.max tefS1 gene for elongation factor EF-1a



```
Seq. No.
                   43457
                  bth700849874.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g531389
BLAST score
                  255
                  2.0e-22
E value
Match length
                  74
% identity
                  62
NCBI Description (U12626) copia-like retrotransposon Hopscotch polyprotein
                   [Zea mays]
                  43458
Seq. No.
Seq. ID
                  bth700849882.h1
Method
                  BLASTX
NCBI GI
                  a2832677
BLAST score
                  244
E value
                  4.0e-21
Match length
                  78
% identity
NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  43459
Seq. ID
                  cf1700863516.h1
Method
                  BLASTX
NCBI GI
                  g2827699
                  384
BLAST score
E value
                  2.0e-37
                  83
Match length
% identity
                  81
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
                  43460
Seq. No.
                  cf1700863593.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006878
BLAST score
                  164
E value
                  7.0e-12
Match length
                  53
% identity
                   62
NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
Seq. No.
                   43461
                  cf1700863594.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618683
BLAST score
                  88
E value
                   5.0e-42
Match length
                  200
% identity
                  86
NCBI Description Arabidopsis thaliana chromosome II BAC T32G6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   43462
```

Seq. ID ckk700605742.h2

BLASTN Method NCBI GI g170023 BLAST score 285



```
1.0e-159
E value
                  292
Match length
                  100
% identity
                  Glycine max maturation-associated protein (MAT9) mRNA,
NCBI Description
                  complete cds
                  43463
Seq. No.
                  ckk700605743.h2
Seq. ID
                  BLASTN
Method
                  g22635
NCBI GI
                  37
BLAST score
                  5.0e-12
E value
                  69
Match length
                  88
% identity
NCBI Description P.vulgaris mRNA for 70 kD heat shock protein
                  43464
Seq. No.
                  ckk700605779.h2
Seq. ID
                  BLASTN
Method
                  g3334755
NCBI GI
                  83
BLAST score
                  6.0e-39
E value
                  206
Match length
                  86
% identity
                  Medicago sativa mRNA for putative arginine/serine-rich
NCBI Description
                  splicing factor
                   43465
Seq. No.
                   ckk700605855.h2
Seq. ID
                   BLASTX
Method
                   g1346769
NCBI GI
                   227
BLAST score
                   6.0e-37
E value
                   96
Match length
                   73
% identity
                   PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)
NCBI Description
                   >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase
                   [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase
                   [Homo sapiens] >gi_4506043_ref_NP_002717.1_pPREP_ prolyl
                   endopeptidase
                   43466
Seq. No.
                   ckk700605865.h2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2980764
 BLAST score
                   161
                   3.0e-11
 E value
                   56
 Match length
 % identity
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
                   43467
 Seq. No.
```

Seq. ID ckk700605886.h2

Method BLASTN
NCBI GI g1498314
BLAST score 77
E value 2.0e-35



Match length 288 % identity 82

NCBI Description Pisum sativum import intermediate associated protein 100

mRNA, nuclear gene encoding chloroplast protein, complete

cds

Seq. No. 43468

Seq. ID ckk700605893.h2

Method BLASTN
NCBI GI g1401239
BLAST score 71
Final No. 200-32

E value 9.0e-32 Match length 110 % identity 96

NCBI Description Glycine max 7S seed globulin precursor, mRNA, complete cds

Seq. No. 43469

Seq. ID cks700764759.h1

Method BLASTN
NCBI GI g22172
BLAST score 209
E value 1.0e-114
Match length 305
% identity 93

NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 43470

Seq. ID cks700764770.h1

Method BLASTX
NCBI GI g1524370
BLAST score 110
E value 8.0e-09
Match length 68
% identity 49

NCBI Description (X92491) TOM20 [Solanum tuberosum]

Seq. No. 43471

Seq. ID cks700764787.h1

Method BLASTX
NCBI GI g2271477
BLAST score 193
E value 3.0e-15
Match length 55
% identity 71

NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No. 43472

Seq. ID cks700764807.h1

Method BLASTN
NCBI GI g169928
BLAST score 184
E value 2.0e-99
Match length 196
% identity 98

NCBI Description Glycine max alpha'-type beta conglycinin storage protein

gene, complete cds, clone ch4A

Seq. No.

Seq. ID

43478

crh700849916.hl



```
Seq. No.
                  43473
                  cks700764861.h1
Seq. ID
Method
                  BLASTN
                  g4102189
NCBI GI
BLAST score
                  35
                  1.0e-10
E value
Match length
                  75
% identity
                  87
NCBI Description Glycine max 35 kDa seed maturation protein (pGmPM18) mRNA,
                  complete cds
Seq. No.
                  43474
Seq. ID
                  cle700967780.h1
Method
                  BLASTX
NCBI GI
                  q3176709
BLAST score
                  145
E value
                  2.0e-09
Match length
                  82
                  40
% identity
NCBI Description
                  (AC002392) putative anthranilate
                  N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                  thaliana]
Seq. No.
                  43475
Seq. ID
                  cle700967818.hl
Method
                  BLASTN
NCBI GI
                  g2281638
                  38
BLAST score
                  4.0e-12
E value
                  82
Match length
                  87
% identity
NCBI Description Arabidopsis thaliana AP2 domain containing protein RAP2.7
                  mRNA, partial cds
                  43476
Seq. No.
Seq. ID
                  cle700967833.hl
Method -
                  BLASTN
NCBI GI
                  g1778371
BLAST score
                  94
E value
                  1.0e-45
Match length
                  144
                  99
% identity
NCBI Description Glycine max asparagine synthetase 1 (AS1) mRNA, complete
                  43477
Seq. No.
                  crh700849912.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q479059
BLAST score
                  71
                  3.0e - 32
E value
Match length
                  99
% identity
                  93
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
```



Method BLASTN NCBI GI q18542 BLAST score 154 E value 2.0e-81 Match length 234 % identity 99 NCBI Description Soybean Bg gene for basic 7S globulin 43479 crh700849923.h1

Seq. No. Seq. ID

Method BLASTN NCBI GI g1401239 BLAST score 126 E value 7.0e-65 173 Match length 93 % identity

NCBI Description Glycine max 7S seed globulin precursor, mRNA, complete cds

Seq. No. 43480

Seq. ID crh700850035.h1

Method BLASTX NCBI GI q3176687 BLAST score 184 E value 4.0e-22 72 Match length 61 % identity

NCBI Description (AC003671) Strong similarity to trehalose-6-phosphate

synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No. 43481

Seq. ID crh700850052.h1

Method BLASTX NCBI GI q4510386 BLAST score 173 E value 5.0e-16 Match length 67 % identity 67

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 43482

Seq. ID crh700850066.h1

Method BLASTN NCBI GI q479059 BLAST score 139 E value 2.0e-72 Match length 196 98 % identity

NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No. 43483

Seq. ID crh700850119.h1

Method BLASTX NCBI GI q4455225 BLAST score 158 E value 4.0e-11



```
Match length
                   76
% identity
                   (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   43484
Seq. No.
                   crh700850138.hl
Seq. ID
                  BLASTN
Method
                   g256426
NCBI GI
BLAST score
                   241
E value
                   1.0e-133
Match length
                   245
% identity
                   100
                  CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic,
NCBI Description
                   3840 nt]
                   43485
Seq. No.
                   crh700850156.h1
Seq. ID
Method
                   BLASTX
                   g3021267
NCBI GI
                   164
BLAST score
                   9.0e-12
E value
                   70
Match length
                   47
% identity
                   (AL022347) serine/threonine kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   43486
Seq. No.
Seq. ID
                   crh700850275.h1
Method
                   BLASTX
                   g2244835
NCBI GI
BLAST score
                   231
                   1.0e-19
E value
Match length
                   71
% identity
                   66
                  (Z97337) protein kinase homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43487
                   crh700850280.h1
Seq. ID
                   BLASTX
Method
                   g2914703
NCBI GI
                   186
BLAST score
                   3.0e-14
E value
                   60
Match length
% identity
                   58
                   (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43488
                   crh700850313.h1
Seq. ID
                   BLASTN
Method
                   g2661022
NCBI GI
                   199
BLAST score
                   1.0e-108
E value
                   199
Match length
                   100
 % identity
NCBI Description Glycine max catalase (cat5) mRNA, partial cds
```

6915

43489

Seq. No.



```
crh700850365.hl
Seq. ID
                  BLASTX
Method
                  g3297814
NCBI GI
                  142
BLAST score
                  2.0e-09
E value
                   40
Match length
                   60
% identity
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
                   43490
Seq. No.
                   crh700850395.hl
Seq. ID
                  BLASTN
Method
                   q508575
NCBI GI
                   172
BLAST score
                   4.0e-92
E value
                   248
Match length
% identity
                   92
NCBI Description Oryza sativa beta-tubulin mRNA
                   43491
Seq. No.
                   crh700850469.h1
Seq. ID
Method
                   BLASTX
                   q3687224
NCBI GI
                   339
BLAST score
                   3.0e-32
E value
                   84
Match length
                   75
% identity
                   (AC005169) putative N-acetyl-gamma-glutamyl-phosphate
NCBI Description
                   reductase [Arabidopsis thaliana]
                   43492
Seq. No.
Seq. ID
                   crh700850484.hl
Method
                   BLASTX
                   g82045
NCBI GI
BLAST score
                   162
                   2.0e-11
E value
                   68
Match length
                   54
% identity
                   embryonic protein ecp31 - carrot >gi 18337 emb CAA43046
NCBI Description
                   (X60593) embryonic cell protein [Daucus carota]
                   43493
Seq. No.
                   crh700850543.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4324966
                   75
BLAST score
                   2.0e-34
E value
Match length
                   83
% identity
NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds
                   43494
Seq. No.
Seq. ID
                   crh700850552.h1
```

Method BLASTX
NCBI GI g485110
BLAST score 315
E value 2.0e-29



Match length 81
% identity 74
NCBI Description (U00050) similarity across entire gene to DNA-directed RNA
polymerase [Caenorhabditis elegans]

Seq. No. 43495 Seq. ID crh700850575.h1

Method BLASTX
NCBI GI g3402719
BLAST score 183
E value 1.0e-16
Match length 71
% identity 63

% identity 63 NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No. 43496

Seq. ID crh700850590.h1

Method BLASTN
NCBI GI g18662
BLAST score 92
E value 8.0e-45
Match length 100
% identity 98

NCBI Description Glycine max hsp 70 gene

Seq. No. 43497

Seq. ID crh700850601.h1

Method BLASTN
NCBI GI g2687433
BLAST score 51
E value 3.0e-20
Match length 130
% identity 86

NCBI Description Tragopogon dubius large subunit 26S ribosomal RNA gene,

partial sequence

Seq. No. 43498

Seq. ID crh700850621.hl

Method BLASTN
NCBI GI g479059
BLAST score 33
E value 2.0e-09
Match length 73
% identity 86

NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase

Seq. No. 43499

Seq. ID crh700850631.hl

Method BLASTX
NCBI GI g3335378
BLAST score 309
E value 9.0e-29
Match length 80
% identity 70

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]



```
Seq. No.
                   43500
                   crh700850693.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4490317
                   214
BLAST score
                   9.0e-18
E value
Match length
                   61
                   66
% identity
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43501
                   crh700850705.h1
Seq. ID
Method
                   BLASTX
                   q1916290
NCBI GI
                   210
BLAST score
                   3.0e-17
E value
                   74
Match length
% identity
                   61
                   (U89876) ALY [Mus musculus]
NCBI Description
                   43502
Seq. No.
                   crh700850725.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4454471
                   290
BLAST score
                   1.0e-26
E value
                   77
Match length
                   69
% identity
                   (AC006234) putative G protein coupled receptor [Arabidopsis
NCBI Description
                   thaliana]
                   43503
Seq. No.
                   crh700850745.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3618316
BLAST score
                   217
E value
                   5.0e-18
                   47
Match length
                   45
% identity
                   (AB001886) zinc finger protein [Oryza sativa]
NCBI Description
                   43504
Seq. No.
                   crh700850771.hl
Seq. ID
Method
                   BLASTX
                   g4490937
NCBI GI
                   143
BLAST score
E value
                   2.0e-09
Match length
                   67
% identity
                    42
                    (AJ132261) hypothetical helicase K12H4.8-like protein [Homo
NCBI Description
                   sapiens]
                    43505
 Seq. No.
```

crh700850872.h1 Seq. ID

BLASTX Method g3892054 NCBI GI 160 BLAST score



```
2.0e-11
E value
                  77
Match length
% identity
                  48
                   (AC002330) putative glycosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  43506
Seq. No.
                  crh700850911.h1
Seq. ID
Method
                  BLASTN
                  g473216
NCBI GI
                  98
BLAST score
                  5.0e-48
E value
Match length
                  170
                  89
% identity
                  P.sativum (little marvel) HSC71.0 mRNA
NCBI Description
                   43507
Seq. No.
Seq. ID
                   crh700850912.h1
Method
                  BLASTX
NCBI GI
                   g2851508
BLAST score
                   199
                   7.0e-16
E value
Match length
                   67
% identity
                   58
                   60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
NCBI Description
                   ribosomal protein L21 (gb_L38826). ESTs
                   gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis
                   thaliana] >gi 3482935 (AC003970) Putative ribosomal protein
                   L21 [Arabidopsis thaliana]
                   43508
Seq. No.
                   crh700850956.hl
Seq. ID
Method
                   BLASTN
                   q434060
NCBI GI
BLAST score
                   42
                   1.0e-14
E value
                   114
Match length
                   85
% identity
                  Soybean DNA for basic 7S globulin, complete cds
NCBI Description
                   43509
Seq. No.
                   crh700850986.h1
Seq. ID
                   {\tt BLASTX}
Method
                   g3367576
NCBI GI
BLAST score
                   245
                   3.0e-21
E value
                   79
Match length
                   61
% identity
                  (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
NCBI Description
                   43510
Seq. No.
Seq. ID
                   crh700851136.h1
```

Method BLASTX
NCBI GI g481131
BLAST score 154
E value 2.0e-10
Match length 33



% identity 85

NCBI Description sucrose transport protein SUC2 - Arabidopsis thaliana

>gi_407092_emb_CAA53150_ (X75382) sucrose-proton symporter
[Arabidopsis thaliana]

Seq. No. 43511
Seq. ID crh700851283.h1
Method BLASTN
NCBI GI g3097320

NCBI GI g3097320
BLAST score 113
E value 6.0e-57
Match length 222
% identity 86

NCBI Description Glycine max gene for Bd 30K, complete cds

Seq. ID crh700851311.h1
Method BLASTX
NCBI GI g2829871
BLAST score 144
E value 2.0e-09

43512

Match length 47 % identity 62

Seq. No.

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 43513

Seq. ID crh700851313.h1

Method BLASTX
NCBI GI g1495366
BLAST score 130
E value 6.0e-12
Match length 76
% identity 44

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 43514

Seq. ID crh700851315.h1

Method BLASTN
NCBI GI g169928
BLAST score 251
E value 1.0e-139
Match length 276
% identity 98

NCBI Description Glycine max alpha'-type beta conglycinin storage protein

gene, complete cds, clone ch4A

Seq. No. 43515

Seq. ID crh700851331.h1

Method BLASTX
NCBI GI g1703292
BLAST score 158
E value 1.0e-15
Match length 65
% identity 75

NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER >gi_551219_emb_CAA53473_

(X75879) amt1 [Arabidopsis thaliana]

BLAST score

E value

326 1.0e-30



```
Seq. No.
                   crh700851401.h1
Seq. ID
                  BLASTX
Method
                   g1526422
NCBI GI
                   228
BLAST score
                   4.0e-19
E value
Match length
                   63
                   73
% identity
                   (D64139) LEA protein in group 5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   crh700851427.h1
Seq. ID
Method
                   BLASTN
                   q2959780
NCBI GI
                   43
BLAST score
                   2.0e-15
E value
                   82
Match length
                   88
% identity
                   Arabidopsis thaliana mRNA for Zwille protein
NCBI Description
                   43518
Seq. No.
                   crh700851452.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4417267
BLAST score
                   258
                   1.0e-22
E value
                   83
Match length
                   60
% identity
                   (AC007019) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43519
                   crh700851455.hl
Seq. ID
Method
                   BLASTN
                   g479059
NCBI GI
                   245
BLAST score
                   1.0e-135
E value
                   253
Match length
                   99
% identity
                   G.max (Fiskeby V) mRNA for cysteine endopeptidase
NCBI Description
                   43520
 Seq. No.
                   crh700851505.h1
 Seq. ID
                   BLASTN
Method
                   g414976
 NCBI GI
                   68
BLAST score
                    4.0e-30
E value
Match length
                   156
                    91
 % identity
                   Glycine max Shi-shi 51 kDa seed maturation protein
 NCBI Description
                    (pGmPM10) mRNA, complete cds
                    43521
 Seq. No.
                    crh700851515.hl
 Seq. ID
                    BLASTX
 Method
                    g1171978
 NCBI GI
```



```
Match length
                  75
% identity
                  POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
NCBI Description
                  (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                  [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
Seq. No.
                  43522
                  crh700851559.hl
Seq. ID
Method
                  BLASTN
```

q170023 NCBI GI BLAST score 122 E value 2.0e-62 194 Match length 91 % identity

Glycine max maturation-associated protein (MAT9) mRNA, NCBI Description

complete cds

43523 Seq. No. crh700851567.hl Seq. ID Method BLASTX NCBI GI g2829911 BLAST score 220

E value 3.0e-18 75 Match length 65 % identity

(AC002291) Unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. Seq. ID crh700851584.h1

Method BLASTX g2656017 NCBI GI BLAST score 143 3.0e-09 E value Match length 37

62 % identity

(Z99292) vacuolar atp synthase subunit a NCBI Description

[Schizosaccharomyces pombe]

43525 Seq. No.

crh700851632.h1 Seq. ID

BLASTN Method g4102691 NCBI GI 93 BLAST score 5.0e-45 E value 93 Match length % identity 100

Glycine max late-embryogenesis abundant protein mRNA, NCBI Description

complete cds

43526 Seq. No.

Seq. ID crh700851662.h1

BLASTX Method NCBI GI g1914685 295 BLAST score 4.0e-27 E value 64 Match length



```
% identity
NCBI Description (Y12014) RAD23 protein, isoform II [Daucus carota]
                  43527
Seq. No.
                  crh700851825.hl
Seq. ID
Method
                  BLASTN
                  g780371
NCBI GI
                  52
BLAST score
                  2.0e-20
E value
Match length
                  116
% identity
                  86
NCBI Description Oryza sativa enolase mRNA, complete cds
Seq. No.
                  43528
                  crh700851884.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2687434
BLAST score
                  34
                  4.0e-10
E value
Match length
                  102
                  84
% identity
                  Eucryphia lucida large subunit 26S ribosomal RNA gene,
NCBI Description
                  partial sequence
Seq. No.
                  43529
                  crh700851991.hl
Seq. ID
Method
                  BLASTX
                  g267055
NCBI GI
BLAST score
                  371
                   4.0e-36
E value
                   77
Match length
                   91
% identity
                  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                   >gi 66572_pir__YUMU sucrose synthase (EC 2.4.1.13) -
                   Arabidopsis thaliana >gi_16526_emb_CAA43303 (X60987)
                   sucrose synthase [Arabidopsis thaliana]
                   43530
Seq. No.
Seq. ID
                   crh700852028.h1
                   BLASTN
Method
                   g169928
NCBI GI
                   150
BLAST score
                   5.0e-79
E value
                   226
Match length
                   92
% identity
                  Glycine max alpha'-type beta conglycinin storage protein
NCBI Description
                   gene, complete cds, clone ch4A
                   43531
Seq. No.
Seq. ID
                   crh700852044.h1
                   BLASTX
Method
                   g126078
NCBI GI
BLAST score
                   194
                   3.0e-15
E value
                   55
Match length
```

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)

75

% identity



>gi_81554_pir__S04046 embryonic abundant protein gD-34 upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea
protein [Gossypium hirsutum] >gi_167385 (M19389) storage
protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea
D-34 gene [Saguinus oedipus]

Seq. No. 43532 crh700852060.h1 Seq. ID Method BLASTX g1771162 NCBI GI BLAST score 219 E value 3.0e-18 Match length 66 67 % identity

NCBI Description (X98930) SBT2 [Lycopersicon esculentum]

>gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 43533

Seq. ID crh700852110.h1

Method BLASTX
NCBI GI g3402685
BLAST score 353
E value 7.0e-34
Match length 82
% identity 76

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 43534

Seq. ID crh700852128.h1

Method BLASTX
NCBI GI g126078
BLAST score 203
E value 3.0e-16
Match length 55
% identity 42

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)

>gi_81554_pir__S04046 embryonic abundant protein gD-34 upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea
protein [Gossypium hirsutum] >gi_167385 (M19389) storage
protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea

D-34 gene [Saguinus oedipus]

Seq. No. 43535

Seq. ID crh700852150.h1

Method BLASTN
NCBI GI g256428
BLAST score 233
E value 1.0e-128
Match length 245
% identity 99

NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and

Forrest, mRNA, 1259 nt]

Seq. No. 43536

Seq. ID crh700852178.h1

Method BLASTX

```
q1711382
NCBI GI
BLAST score
                  1.0e-08
E value
                  64
Match length
                  58
% identity
                  SET PROTEIN >gi_940889 (U30470) SET [Drosophila
NCBI Description
                  melanogaster]
                  43537
Seq. No.
                  crh700852191.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18542
BLAST score
                   141
                   1.0e-73
E value
                   210
Match length
                   100
% identity
NCBI Description Soybean Bg gene for basic 7S globulin
                   43538
Seq. No.
                   crh700852192.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g170023
BLAST score
                   198
E value
                   1.0e-107
Match length
                   217
                   98
% identity
NCBI Description Glycine max maturation-associated protein (MAT9) mRNA,
                   complete cds
                   43539
Seq. No.
                   crh700852283.h1
Seq. ID
                   BLASTN
Method
                   g20880
NCBI GI
BLAST score
                   35
                   2.0e-10
E value
Match length
                   51
% identity
                   92
NCBI Description Pea mRNA for plastid ribosomal protein CL9
 Seq. No.
                   43540
                   crh700852308.h1
 Seq. ID
Method
                   BLASTX
                   g2129608
NCBI GI
BLAST score
                   114
                   7.0e-13
E value
Match length
                   63
                   65
 % identity
                   GTP-binding protein, 68K - Arabidopsis thaliana >gi_807577
 NCBI Description
                    (L38614) GTP-binding protein [Arabidopsis thaliana]
                   43541
 Seq. No.
                   crh700852309.h1
 Seq. ID
                   BLASTN
 Method
                   g4567237
 NCBI GI
                   39
 BLAST score
```

9.0e-13

79

E value

Match length



% identity NCBI Description Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence Seq. No. 43542 Seq. ID crh700852387.hl Method BLASTN NCBI GI g1401239 BLAST score 57 E value 2.0e-23 Match length 115 % identity 92 NCBI Description Glycine max 7S seed globulin precursor, mRNA, complete cds Seq. No. 43543 Seq. ID crh700852388.h1 Method BLASTN NCBI GI g479059 BLAST score 196 E value 1.0e-106 Match length 247 % identity 96 NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase Seq. No. 43544 crh700852392.h1 Seq. ID Method BLASTN NCBI GI g256426 BLAST score 233 E value 1.0e-128 Match length 244 % identity 99 NCBI Description CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic, 3840 nt] Seq. No. 43545 Seq. ID crh700852411.h1 Method BLASTN NCBI GI g13384 91 9.0e-44 108 % identity 97 NCBI Description Pea mitochondrial coxI gene for cytochrome oxidase subunit

BLAST score E value Match length

Seq. No. 43546

Seq. ID crh700852418.h1

Method BLASTN NCBI GI g170007 BLAST score 128 E value 7.0e-66 Match length 168 % identity 95

NCBI Description Soybean 18 kD late embryogenesis abundant (Lea) protein

mRNA, complete cds

BLAST score



```
43547
Seq. No.
                  crh700852435.h1
Seq. ID
                  {\tt BLASTX}
Method
                  g3859534
NCBI GI
                   317
BLAST score
                   1.0e-29
E value
                   62
Match length
                   92
% identity
                   (AF095452) asparagine synthetase [Arabidopsis thaliana]
NCBI Description
                   43548
Seq. No.
                   crh700852436.h1
Seq. ID
                   BLASTN
Method
                   g1762954
NCBI GI
                   120
BLAST score
                   4.0e-61
E value
                   172
Match length
% identity
                   92
                   Glycine max late embryogenesis-abundant protein mRNA,
NCBI Description
                   complete cds
Seq. No.
                   43549
                   crh700852454.h1
Seq. ID
                   BLASTN
Method
                   g3021337
NCBI GI
BLAST score
                   63
E value
                   4.0e-27
Match length
                   99
                   91
% identity
                   Cicer arietinum mRNA for cytosolic
NCBI Description
                   fructose-1,6-bisphosphate aldolase
                   43550
Seq. No.
                   crh700852455.h1
Seq. ID
                   BLASTN
Method
                   g1401239
NCBI GI
BLAST score
                   85
                   2.0e-40
E value
                   165
Match length
                   88
% identity
                   Glycine max 7S seed globulin precursor, mRNA, complete cds
NCBI Description
Seq. No.
                   crh700852467.h1
Seq. ID
                   BLASTN
Method
                   q3097320
NCBI GI
BLAST score
                   183
                    1.0e-98
E value
                    195
Match length
                    99
 % identity
                   Glycine max gene for Bd 30K, complete cds
 NCBI Description
                    43552
 Seq. No.
 Seq. ID
                    crh700852475.h1
 Method
                    BLASTN
                    g170009
 NCBI GI
```



```
2.0e-10
E value
                   59
Match length
                   90
% identity
                   Soybean late embryogenesis abundant (LEA) protein mRNA,
NCBI Description
                   complete cds
                   43553
Seq. No.
                   crh700852486.h1
Seq. ID
                   BLASTN
Method
                   g1401239
NCBI GI
                   73
BLAST score
                   5.0e-33
E value
                   214
Match length
                   91
% identity
                  Glycine max 7S seed globulin precursor, mRNA, complete cds
NCBI Description
                   43554
Seq. No.
                   crh700852504.h1
Seq. ID
                   BLASTN
Method
                   g18542
NCBI GI
BLAST score
                   36
                   6.0e-11
E value
                   36
Match length
                   100
% identity
                   Soybean Bg gene for basic 7S globulin
NCBI Description
                   43555
Seq. No.
                   crh700852561.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q16508
BLAST score
                   72
                   2.0e-32
E value
Match length
                   156
                   87
% identity
                   A.thaliana DNA for S-adenosylmethionine synthetase gene
NCBI Description
                   sam-1 >gi 166871 gb M55077_ATHSAM A.thaliana
                   S-adenosylmethionine synthetase gene, complete cds
                   43556
Seq. No.
Seq. ID
                   crh700852565.h1
Method
                   BLASTN
                   q169090
NCBI GI
BLAST score
                   82
                               ..-
                   2.0e-38
E value
                   166
Match length
                   87
 % identity
                   Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA,
NCBI Description
                   complete cds
 Seq. No.
                   43557
                   crh700852602.h1
 Seq. ID
                   BLASTN
 Method
```

6928

g1326160

68 5.0e-30

122

93

NCBI GI BLAST score

E value

Match length % identity



178

84

3.0e-13

```
NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No. 43558
Seq. ID crh700852606.h1
Method BLASTX
NCBI GI q2244940
```

% identity 54
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 43559

 Seq. ID
 crh700852613.h1

 Method
 BLASTX

 NCBI GI
 g4539452

 BLAST score
 373

 E value
 3.0e-36

Match length 87 % identity 80

BLAST score

Match length

E value

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No. 43560

Seq. ID crh700852614.h1

Method BLASTX
NCBI GI g135416
BLAST score 162
E value 2.0e-11
Match length 39
% identity 74

NCBI Description TUBULIN ALPHA-3 CHAIN >gi 85174 pir C26488 tubulin alpha-3

chain - fruit fly (Drosophila melanogaster) >gi_158735

(M14645) alpha-tubulin 3 [Drosophila melanogaster]

Seq. No. 43561

Seq. ID crh700852622.h1

Method BLASTX
NCBI GI g3478637
BLAST score 282
E value 2.0e-25
Match length 86
% identity 59

NCBI Description (AC005546) R29425_1 [Homo sapiens]

Seq. No. 43562

Seq. ID crh700852652.h1

Method BLASTX
NCBI GI g127046
BLAST score 214
E value 1.0e-17
Match length 67
% identity 64

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_304637 (M61882) S-adenosylmethionine synthetase [Dianthus caryophyllus] >gi_228314_prf__1802406A Met(S-adenosyl)

Seq. No.

Seq. ID

Method



synthetase [Dianthus caryophyllus]

```
Seq. No.
                  crh700852656.h1
Seq. ID
                  BLASTN
Method
                  g311697
NCBI GI
BLAST score
                  121
                  1.0e-61
E value
                  233
Match length
                  57
% identity
NCBI Description G.max Lea protein mRNA, complete CDS
Seq. No.
                  43564
                  crh700852733.hl
Seq. ID
                  BLASTN
Method
                  g22073
NCBI GI
BLAST score
                  44
                  3.0e-16
E value
Match length
                  44
                  100
% identity
NCBI Description Mung bean 25S rRNA - 18S rDNA spacer region
                  43565
Seq. No.
Seq. ID
                  crh700852749.hl
                  BLASTX
Method
                  q1172635
NCBI GI
                   398
BLAST score
                   3.0e-39
E value
                   80
Match length
                   96
% identity
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                   PROTEIN HOMOLOG 2) >gi 556558_dbj_BAA04615_ (D17789) rice
                   homologue of Tat binding protein [Oryza sativa]
                   43566
Seq. No.
                   crh700852761.h1
Seq. ID
Method
                   BLASTX
                   q2853086
NCBI GI
                   208
BLAST score
E value
                   6.0e-17
                   80
Match length
                   47
% identity
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]
Seq. No.
                   43567
                   crh700852772.hl
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4204858
BLAST score
                   86
E value
                   6.0e-41
                   190
Match length
                   86
% identity
NCBI Description Triticum aestivum heat shock protein 80 mRNA, complete cds
```

6930

43568

BLASTX

crh700852781.h1

NCBI GI

BLAST score

g18731

113



```
g3850569
NCBI GI
                   164
BLAST score
                   8.0e-12
E value
                   68
Match length
                   54
% identity
                   (AC005278) ESTs gb T21276, gb T45403, and gb AA586113 come
NCBI Description
                   from this gene. [Arabidopsis thaliana]
                   43569
Seq. No.
                   crh700852809.h1
Seq. ID
                   BLASTX
Method
                   g3445204
NCBI GI
                   196
BLAST score
                   2.0e-18
E value
Match length
                   86
                    56
% identity
                   (AC004786) putative GTP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                    43570
Seq. No.
                    crh700852844.h1
Seq. ID
                    BLASTX
Method
                    g2909420
NCBI GI
                    174
BLAST score
                    7.0e-13
E value
Match length
                    60
                    37
% identity
                   (AJ224518) LEA protein [Cicer arietinum]
NCBI Description
                    43571
Seq. No.
                    crh700852880.h1
Seq. ID
                    BLASTX
Method
                    g2565010
NCBI GI
                    249
BLAST score
                    1.0e-21
E value
                    85
Match length
                    55
% identity
                    (AC002983) putative microfibril-associated protein
NCBI Description
                    [Arabidopsis thaliana] >gi_3377811 (AF076275) contains similarity to ATP synthase B/B' (Pfam: ATP-synt_B.hmm,
                    score: 11.71) [Arabidopsis thaliana]
                    43572
Seq. No.
                    crh700852895.hl
Seq. ID
Method
                    BLASTN
                    q18542
NCBI GI
                    125
BLAST score
                    4.0e-64
E value
Match length
                    207
                    99
% identity
NCBI Description Soybean Bg gene for basic 7S globulin
Seq. No.
                    crh700852904.h1
Seq. ID
Method
                    BLASTN
```

Match length

% identity

66

```
3.0e-57
E value
                  136
Match length
% identity
                  96
                  Soybean RPB1-B1 gene for the largest subunit of RNA
NCBI Description
                  polymerase II (EC 2.7.7.6)
                  43574
Seq. No.
                  crh700852907.h1
Seq. ID
                  BLASTN
Method
                   g1401239
NCBI GI
BLAST score
                   35
                   1.0e-10
E value
                   35
Match length
                   100
% identity
NCBI Description Glycine max 7S seed globulin precursor, mRNA, complete cds
Seq. No.
                   43575
Seq. ID
                   crh700852911.hl
                   BLASTN
Method
                   q2347089
NCBI GI
                   57
BLAST score
                   1.0e-23
E value
                   144
Match length
                   90
% identity
                  Phaseolus vulgaris low molecular weight heat shock protein
NCBI Description
                   PvHSP17-19 (Pvhsp17-19) mRNA, partial cds
                   43576
Seq. No.
Seq. ID
                   crh700852953.h1
                   BLASTN
Method
                   q555890
NCBI GI
                   46
BLAST score
                   4.0e-17
E value
                   134
Match length
% identity
                   84
                   Glycine max 7S storage protein alpha subunit mRNA, complete
NCBI Description
                   43577
Seq. No.
                   crh700852989.h1
Seq. ID
                   BLASTN
Method
                   g479059
NCBI GI
BLAST score
                   140
                   5.0e-73
E value
                   240
Match length
                   97
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                   43578
 Seq. No.
                   crh700853003.hl
 Seq. ID
                   BLASTX
 Method
                   g1086249
 NCBI GI
 BLAST score
                   267
                   9.0e-24
 E value
                   83
```

NCBI Description subtilisin-like protease - Alnus glutinosa



>gi_757522_emb_CAA59964_ (X85975) subtilisin-like protease
[Alnus glutinosa]

Seq. No. 43579

Seq. ID crh700853006.h1

Method BLASTN
NCBI GI g2275194
BLAST score 85
E value 3.0e-40
Match length 213
% identity 85

% identity 85
NCBI Description Arabidopsis thaliana chromosome II BAC T08I13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 43580

Seq. ID crh700853009.h1

Method BLASTN
NCBI GI g169928
BLAST score 254
E value 1.0e-141
Match length 258
% identity 100

% identity 100
NCBI Description Glycine max alpha'-type beta conglycinin storage protein

gene, complete cds, clone ch4A

Seq. No. 43581

Seq. ID crh700853016.h1

Method BLASTN
NCBI GI g414976
BLAST score 127
E value 3.0e-65
Match length 127
% identity 47

NCBI Description Glycine max Shi-shi 51 kDa seed maturation protein

(pGmPM10) mRNA, complete cds

Seq. No. 43582

Seq. ID crh700853019.hl

Method BLASTX
NCBI GI g4314365
BLAST score 191
E value 7.0e-15
Match length 80
% identity 49

NCBI Description (AC006340) putative copia-like retrotransposon Hopscotch

[Arabidopsis thaliana]

Seq. No. 43583

Seq. ID crh700853030.h1

Method BLASTX
NCBI GI g3492803
BLAST score 181
E value 1.0e-13
Match length 59
% identity 58

NCBI Description (AJ002479) ENBP1 [Medicago truncatula]



```
43584
  Seq. No.
                    crh700853125.hl
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q4234953
  BLAST score
                    189
                    1.0e-14
  E value
                    72
 Match length
                    `53 ~
. % identity
                    (AF098970) NBS-LRR-like protein cD7 [Phaseolus vulgaris]
  NCBI Description
                     43585
  Seq. No.
                    crh700853130.hl
  Seq. ID
  Method
                    BLASTX
                     q126078
  NCBI GI
  BLAST score
                     199
  E value
                     7.0e-16
                     55
  Match length
                     41
  % identity
                    LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
  NCBI Description
                     >gi_81554_pir__S04046 embryonic abundant protein gD-34 -
                     upland cotton >gi 18501_emb_CAA31594_ (X13206) D-34 Lea
                     protein [Gossypium hirsutum] >gi_167385 (M19389) storage
                     protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea
                     D-34 gene [Saguinus oedipus]
  Seq. No.
                     43586
                     crh700853148.h1
  Seq. ID
                     BLASTN
  Method
                     g3097320
  NCBI GI
                     217
  BLAST score
                     1.0e-119
  E value
                     240
  Match length
                     98
  % identity
  NCBI Description Glycine max gene for Bd 30K, complete cds
                     43587
  Seq. No.
                     crh700853194.h1
  Seq. ID
                     BLASTN
  Method
                     g170019
  NCBI GI
                     234
  BLAST score
                     1.0e-129
  E value
                     234
  Match length
                     88
  % identity
  NCBI Description Soybean maturation protein (MAT1) gene, complete cds
                     43588
  Seq. No.
                     crh700853241.h1
  Seq. ID
  Method
                     BLASTX
```

Method BLASTX
NCBI GI g2842704
BLAST score 143
E value 2.0e-09
Match length 51
% identity 55

NCBI Description HYPOTHETICAL 73.3 KD PROTEIN C6G9.14 IN CHROMOSOME I >qi 1644326 emb CAB03616_ (Z81317) serine rich pumilio

family rna binding domain protein [Schizosaccharomyces

pombe]



```
43589
Seq. No.
                  crh700853302.hl
Seq. ID
Method
                  BLASTN
                  g479059
NCBI GI
                  246
BLAST score
                  1.0e-136
E value
                  246
Match length
                  100
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                  43590
Seq. No.
                  crh700853308.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3096949
BLAST score
                  171
                  5.0e-16
E value
Match length
                  68
                   62
% identity
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
                   43591
Seq. No.
                   crh700853316.h1
Seq. ID
Method
                   BLASTX
                   q799369
NCBI GI
BLAST score
                   167
                   3.0e-12
E value
                   58
Match length
% identity
                   59
                  (U25111) metalloendopeptidase [Pisum sativum]
NCBI Description
                   43592
Seq. No.
                   crh700853355.h1
Seq. ID
                   BLASTN
Method
                   g4115336
NCBI GI
                   149
BLAST score
                   2.0e-78
E value
                   239
Match length
                   17
% identity
NCBI Description Pisum sativum (Alaska) ubiquitin (PUB3) gene, complete cds
                   43593
Seq. No.
                   crh700853375.h1
Seq. ID
                   BLASTX
Method
                   q3935183
NCBI GI
                   189
BLAST score
                   1.0e-14
 E value
                   57
Match length
                   72
 % identity
 NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]
```

43594

BLASTN

g170007

crh700853380.h1

Seq. No.

Seq. ID

Method

NCBI GI



```
166
BLAST score
                  1.0e-88
E value
                  234
Match length
% identity
                  92
                  Soybean 18 kD late embryogenesis abundant (Lea) protein
NCBI Description
                  mRNA, complete cds
                   43595
Seq. No.
                   crh700853383.h1
Seq. ID
                  BLASTN
Method
                   g18542
NCBI GI
                   135
BLAST score
                   4.0e-70
E value
                   231
Match length
% identity
                   90
                  Soybean Bg gene for basic 7S globulin
NCBI Description
                   43596
Seq. No.
                   crh700853396.h1
Seq. ID
                   BLASTX
Method
                   g3915037
NCBI GI
                   145
BLAST score
                   1.0e-09
E value
                   46
Match length
                   63
% identity
                   SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi 2570067 emb_CAA04512_ (AJ001071) second sucrose
                   synthase [Pisum sativum]
                   43597
Seq. No.
                   crh700853403.hl
Seq. ID
                   BLASTX
Method
                   g4417304
NCBI GI
                   328
BLAST score
                   6.0e-31
E value
                   85
Match length
                   67
% identity
                   (AC006446) putative beta-1,4-mannosyl-glycoprotein
NCBI Description
                   beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
                   thaliana]
                   43598
Seq. No.
                   crh700853422.h1
Seq. ID
                   BLASTX
Method
                   g4539291
NCBI GI
                   268
BLAST score
                   7.0e-24
E value
                   85
Match length
                   60
 % identity
                   (ALO49480) putative protein [Arabidopsis thaliana]
NCBI Description
                   43599
 Seq. No.
```

Seq. ID

crh700853452.h1

Method NCBI GI BLAST score E value

BLASTN g1401239 89 1.0e-42



```
174
Match length
                  94
% identity
NCBI Description Glycine max 7S seed globulin precursor, mRNA, complete cds
Seq. No.
                  43600
                  crh700853507.h1
Seq. ID
                  BLASTN
Method
                  q311697
NCBI GI
                  133
BLAST score
E value
                  8.0e-69
                  169
Match length
                   96
% identity
NCBI Description G.max Lea protein mRNA, complete CDS
                   43601
Seq. No.
                   crh700853533.h1
Seq. ID
Method
                   BLASTX
                   q2842490
NCBI GI
BLAST score
                   277
                   6.0e-25
E value
                   80
Match length
% identity
                   68
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   43602
Seq. No.
                   crh700853582.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4185146
BLAST score
                   214
                   9.0e-18
E value
Match length
                   42
                   86
% identity
                   (AC005724) putative xyloglucan endotransglycosylase
NCBI Description
                   [Arabidopsis thaliana]
                   43603
Seq. No.
                   crh700853617.hl
Seq. ID
                   BLASTX
Method
                   g3249110
NCBI GI
                   263
BLAST score
                   3.0e-23
E value
Match length
                   70
                   74
% identity
                   (AC003114) T12M4.6 [Arabidopsis thaliana]
NCBI Description
                   43604
 Seq. No.
                   crh700853629.h1
 Seq. ID
                   BLASTN
Method
                   g18662
NCBI GI
BLAST score
                   68
```

2.0e-30 E value Match length 100 92 % identity

NCBI Description Glycine max hsp 70 gene

43605 Seq. No.

crh700853656.h1 Seq. ID

6937



```
BLASTX
Method
                   g2245004
NCBI GI
                   292
BLAST score
                   1.0e-26
E value
                   87
Match length
% identity
                   64
                   (Z97341) similarity to membrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   43606
Seq. No.
                   crh700853766.h1
Seq. ID
                   BLASTN
Method
                   q479059
NCBI GI
                   77
BLAST score
                   9.0e-36
E value
Match length
                   109
% identity
                   93
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                   43607
Seq. No.
Seq. ID
                   crh700853820.hl
Method
                   BLASTX
                   q4567220
NCBI GI
BLAST score
                   141
                   5.0e-09
E value
                   82
Match length
% identity
                   (AC007119) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                   thaliana]
                   43608
Seq. No.
Seq. ID
                   crh700853826.h1
Method
                   BLASTX
                   q2132302
NCBI GI
BLAST score
                   211
                   3.0e-17
E value
Match length
                   81
% identity
                   52
                   hypothetical protein YPR144c - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_1066493 (U40829) Weak similarity near
                   C-terminus to \overline{\text{RNA}} Polymerase beta subunit (Swiss Prot.
                   accession number P11213) and CCAAT-binding transcription
                   factor (PIR accession number A36368) [Saccharomyces
                   cerevisiae]
                    43609
 Seq. No.
                   crh700853838.h1
 Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g4415923
BLAST score 140
E value 6.0e-09
Match length 74
% identity 36

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 43610

BLAST score

E value

138 7.0e-72



```
crh700853840.h1
Seq. ID
                  BLASTX
Method
                  g1173624
NCBI GI
                  156
BLAST score
                  8.0e-11
E value
                  80
Match length
                  44
% identity
                  (U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid
NCBI Description
                  SM9108']
                  43611
Seq. No.
                  crh700854010.h1
Seq. ID
                  BLASTN
Method
                  g510546
NCBI GI
                  150
BLAST score
                  5.0e-79
E value
                  250
Match length
                   90
% identity
NCBI Description P.sativum mRNA for starch branching enzyme II
                   43612
Seq. No.
                   crh700854025.hl
Seq. ID
                  BLASTN
Method
                   g311697
NCBJ GI
BLAST score
                   49
                   8.0e-19
E value
Match length
                   106
                   96
% identity
NCBI Description G.max Lea protein mRNA, complete CDS
                   43613
Seq. No.
                   crh700854053.hl
Seq. ID
                   BLASTN
Method
                   g256428
NCBI GI
BLAST score
                   90
                   3.0e-43
E value
                   200
Match length
                   86
% identity
NCBI Description KTi3 (KTi3+)=Kunitz trypsin inhibitor [soybeans, Dare and
                   Forrest, mRNA, 1259 nt]
                   43614
Seq. No.
                   crh700854057.h1
Seq. ID
                   BLASTN
Method
                   g479059
NCBI GI
                   69
BLAST score
                   7.0e-31
E value
                   164
Match length
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                   43615
Seq. No.
                   crh700854108.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4102691
```

6939



Match length 154 % identity 97

NCBI Description Glycine max late-embryogenesis abundant protein mRNA,

complete cds

Seq. No. 43616

Seq. ID crh700854111.h1

Method BLASTN
NCBI GI g18674
BLAST score 85
E value 1.0e-40
Match length 121
% identity 93

NCBI Description G.max mRNA for lipoxygenase

Seq. No. 43617

Seq. ID crh700854133.h1

Method BLASTN
NCBI GI g170007
BLAST score 204
E value 1.0e-111
Match length 276
% identity 95

NCBI Description Soybean 18 kD late embryogenesis abundant (Lea) protein

mRNA, complete cds

Seq. No. 43618

Seq. ID crh700854183.hl

Method BLASTN
NCBI GI g414976
BLAST score 95
E value 3.0e-46
Match length 206
% identity 87

NCBI Description Glycine max Shi-shi 51 kDa seed maturation protein

(pGmPM10) mRNA, complete cds

Seq. No. 43619

Seq. ID crh700854216.h1

Method BLASTX
NCBI GI g4106395
BLAST score 190
E value 9.0e-15
Match length 51
% identity 63

NCBI Description (AF073744) raffinose synthase [Cucumis sativus]

Seq. No. 43620

Seq. ID crh700854226.h1

Method BLASTN
NCBI GI g402635
BLAST score 135
E value 5.0e-70
Match length 223
% identity 90

NCBI Description L.albus gene for beta-tubulin

Method NCBI GI

g18542



```
Seq. No.
                   43621
Seq. ID
                   crh700854237.h1
Method
                  BLASTN
NCBI GI
                   g497416
BLAST score
                   170
E value
                   6.0e - 91
                   247
Match length
                   96
% identity
NCBI Description Glycine max Essex dehydrin-like protein mRNA, complete cds
Seq. No.
                   43622
                   crh700854393.h1
Seq. ID
Method
                   BLASTX
                   g2909420
NCBI GI
BLAST score
                   169
E value
                   2.0e-12
Match length
                   47
% identity
                   40
                   (AJ224518) LEA protein [Cicer arietinum]
NCBI Description
                   43623
Seq. No.
Seq. ID
                   crh700854417.h1
Method
                   BLASTX
NCBI GI
                   g1001719
BLAST score
                   223
                   9.0e-19
E value
Match length
                   73
                   59
% identity
                   (D64004) ATP-dependent RNA helicase DeaD [Synechocystis
NCBI Description
                   sp.]
Seq. No.
                   43624
                   crh700854478.h1
Seq. ID
                   BLASTX
Method
                   g2462781
NCBI GI
                   244
BLAST score
                   3.0e-21
E value
Match length
                   60
                   73
% identity
                   (U73175) carbamoyl phosphate synthetase small subunit
NCBI Description
                   [Arabidopsis thaliana]
                   43625
Seq. No.
                   crh700854559.h1
Seq. ID
                   BLASTX
Method
                   g4204308
NCBI GI
                   210
BLAST score
                   7.0e-20
E value
                   70
Match length
                   70
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   43626
Seq. No.
                   crh700854609.h1
Seq. ID
                   BLASTN
```



BLAST score 116 E value 1.0e-58 Match length 191 % identity 98

NCBI Description Soybean Bg gene for basic 7S globulin

Seq. No. 43627

Seq. ID crh700854789.h1

Method BLASTN
NCBI GI g256426
BLAST score 237
E value 1.0e-131
Match length 252
% identity 99

NCBI Description CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic,

3840 nt]

Seq. No. 43628

Seq. ID crh700854796.h1

Method BLASTN
NCBI GI g1046277
BLAST score 85
E value 3.0e-40
Match length 211
% identity 86

NCBI Description Phaseolus vulgaris embryo-specific acidic transcriptional

activator PvAlf mRNA, complete cds

Seq. No. 43629

Seq. ID crh700854826.hl

Method BLASTN
NCBI GI g3452136
BLAST score 183
E value 1.0e-98
Match length 199
% identity 99

NCBI Description Glycine max mRNA for glucose-6-phosphate-dehydrogenase,

partial

Seq. No. 43630

Seq. ID crh700854857.h1

Method BLASTX
NCBI GI g3219937
BLAST score 160
E value 2.0e-11
Match length 77
% identity 45

NCBI Description HYPOTHETICAL 35.1 KD PROTEIN C57A10.07 IN CHROMOSOME I

>gi_2058374_emb_CAB08170_ (Z94864) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 43631

Seq. ID crh700854873.h1

Method BLASTX NCBI GI g738309 BLAST score 166 E value 5.0e-12



```
Match length
                  46
% identity
NCBI Description nucler protein GRB1 [Homo sapiens]
                  43632
Seq. No.
                  crh700854907.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g479059
BLAST score
                  244
                  1.0e-135
E value
                  244
Match length
                  100
% identity
NCBI Description G.max (Fiskeby V) mRNA for cysteine endopeptidase
                  43633
Seq. No.
                  crh700854981.h1
Seq. ID
Method
                  BLASTX
                  q4490330
NCBI GI
BLAST score
                  414
                  5.0e-41
E value
                  82
Match length
                  95
% identity
                  (AL035656) splicing factor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   43634
Seq. No.
                   crh700855058.h1
Seq. ID
                  BLASTN
Method
                   g2281586
NCBI GI
BLAST score
                   213
                   1.0e-116
E value
                   229
Match length
                   98
% identity
                  Plasmid pAMS with hybrid amphotropic/Moloney murine
NCBI Description
                   leukemia virus, complete sequence
                   43635
Seq. No.
                   crh700855193.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q256426
BLAST score
                   104
E value
                   1.0e-51
                   168
Match length
                   91
% identity
                   CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic,
NCBI Description
                   3840 nt]
                   43636
Seq. No.
                   crh700855238.h1
```

Seq. ID

Method BLASTN q169069 NCBI GI 55 BLAST score 2.0e-22 E value 59 Match length % identity 98

NCBI Description Pea Cu-Zn superoxide dismutase mRNA, complete cds



```
Seq. No.
                  43637
                  crh700855248.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3982595
                  140
BLAST score
                  5.0e-73
E value
                  240
Match length
                  90
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                  43638
Seq. No.
                  crh700855257.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3152618
BLAST score
                   203
                   2.0e-16
E value
                   63
Match length
                   63
% identity
                   (AC004482) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   >gi 3242724 (AC003040) putative pectinesterase [Arabidopsis
                   thaliana]
                   43639
Seq. No.
                   crh700855314.h1
Seq. ID
                   BLASTN
Method
                   g256426
NCBI GI
                   99
BLAST score
                   1.0e-48
E value
                   153
Match length
                   92
% identity
                  CG4 beta-conglycinin [soybeans, Forrest and Dare, Genomic,
NCBI Description
                   3840 nt]
                   43640
Seq. No.
                   crh700855340.h1
Seq. ID
                   BLASTN
Method
                   g18542
NCBI GI
BLAST score
                   95
                   2.0e-46
E value
                   171
Match length
% identity
                   89
NCBI Description Soybean Bg gene for basic 7S globulin
                   43641
Seq. No.
                   crh700855428.h1
Seq. ID
                   BLASTX
Method
                   g4539293
NCBI GI
                   277
BLAST score
E value
                   6.0e-25
Match length
                   75
% identity
                   71
                   (AL049480) putative membrane transporter [Arabidopsis
NCBI Description
                   thaliana]
```

 Seq. No.
 43642

 Seq. ID
 crh700855518.hl

 Method
 BLASTX

Match length

% identity

116

95



```
g3386600
NCBI GI
                  196
BLAST score
                  1.0e-15
E value
Match length
                  41
% identity
                  88
                  (AC004665) putative glycoprotein [Arabidopsis thaliana]
NCBI Description
                  43643
Seq. No.
                  crh700855530.hl
Seq. ID
Method
                  BLASTN
                  g434060
NCBI GI
BLAST score
                  61
                  3.0e-26
E value
Match length
                  103
                  94
% identity
NCBI Description Soybean DNA for basic 7S globulin, complete cds
                  43644
Seq. No.
                  crh700855554.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128223
BLAST score
                  151
                  4.0e-10
E value
Match length
                  52
                  48
% identity
                  (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 3337369 (AC004481) unknown protein [Arabidopsis
                  thaliana]
                  43645
Seq. No.
                  crh700855615.h1
Seq. ID
Method
                  BLASTN
                  q3982595
NCBI GI
                  74
BLAST score
                  5.0e-34
E value
                  110
Match length
% identity
                  92
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   43646
Seq. No.
                  crh700855716.hl
Seq. ID
                  BLASTN
Method
                  g18535
NCBI GI
                   82
BLAST score
                   2.0e-38
E value
                  122
Match length
                   93
% identity
NCBI Description Soybean mRNA for: the alpha subunit of beta-conglycinin
                   43647
Seq. No.
                   crh700855768.h1
Seq. ID
Method
                   BLASTN
                   g210811
NCBI GI
                   54
BLAST score
                   7.0e-22
E value
```

6945



NCBI Description Bean pod mottle virus coat protein gene, complete cds, complete middle component (M) RNA

Seq. No. 43648

Seq. ID crh700855863.h1

Method BLASTX
NCBI GI g126078
BLAST score 181
E value 9.0e-14
Match length 55

% identity 69

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)

>gi_81554_pir__S04046 embryonic abundant protein gD-34 upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea
protein [Gossypium hirsutum] >gi_167385 (M19389) storage
protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea

D-34 gene [Saguinus oedipus]

Seq. No. 43649

Seq. ID crh700856064.h1

Method BLASTN
NCBI GI g310569
BLAST score 83
E value 5.0e-39
Match length 191
% identity 89

NCBI Description Glycine max seed maturation protein (GmPM3) mRNA, complete

cds

Seq. No. 43650

Seq. ID crh700856115.h1

Method BLASTN
NCBI GI g4115332
BLAST score 53
E value 2.0e-21
Match length 159
% identity 29

NCBI Description Pisum sativum (Alaska) ubiquitin (PUB1) gene, complete cds

Seq. No. 43651

Seq. ID crh700856122.h1

Method BLASTX
NCBI GI g2673919
BLAST score 162
E value 1.0e-11
Match length 81
% identity 51

NCBI Description (AC002561) putative protein kinase, 5' partial [Arabidopsis

thaliana]

43652

Seq. No.

Seq. ID crh700856191.h1

Method BLASTX
NCBI GI g4558566
BLAST score 196
E value 9.0e-24
Match length 73



```
% identity
                  (AC007138) putative raffinose synthase or seed imbibition
NCBI Description
                  protein [Arabidopsis thaliana]
                  43653
Seq. No.
                  crh700856201.h1
Seq. ID
                  BLASTN
Method
                  g2351062
NCBI GI
                  32
BLAST score
                  1.0e-08
E value
                  48
Match length
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAH20, complete sequence [Arabidopsis thaliana]
                   43654
Seq. No.
                  crh700856209.h1
Seq. ID
                  BLASTN
Method
                   g479059
NCBI GI
                   98
BLAST score
                   2.0e-48
E value
                   98
Match length
                   100
% identity
                  G.max (Fiskeby V) mRNA for cysteine endopeptidase
NCBI Description
                   43655
Seq. No.
                   crh700856338.h1
Seq. ID
                   BLASTX
Method
                   g2370232
NCBI GI
                   161
BLAST score
                   1.0e-16
E value
                   53
Match length
                   81
% identity
                  (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]
NCBI Description
                   43656
Seq. No.
                   crh700856440.h1
Seq. ID
                   BLASTN
Method
                   g414976
NCBI GI
BLAST score
                   47
                   1.0e-17
E value
                   135
Match length
                   53
% identity
                   Glycine max Shi-shi 51 kDa seed maturation protein
NCBI Description
                   (pGmPM10) mRNA, complete cds
                   43657
Seq. No.
                   crh700856442.h1
Seq. ID
Method
                   BLASTN
                   g1399563
NCBI GI
BLAST score
                   63
                   2.0e-27
E value
```

Match length 123 % identity 89

NCBI Description Hydrastis canadensis nuclear 26S ribosomal RNA gene,

partial sequence



```
43658
Seq. No.
Seq. ID
                  crh700856474.hl
                  BLASTN
Method
                  g169903
NCBI GI
BLAST score
                  39
                  8.0e-13
E value
                  123
Match length
                  83
% identity
NCBI Description soybean 7s seed storage protein alpha subunit mrna (c),
                  from gmc-alpha'-alpha 21
                  43659
Seq. No.
                  crh700856487.h1
Seq. ID
Method
                  BLASTN
                  g170019
NCBI GI
                  52
BLAST score
                  1.0e-20
E value
                  148
Match length
% identity
                  90
NCBI Description Soybean maturation protein (MAT1) gene, complete cds
                  43660
Seq. No.
                  crh700856502.h1
Seq. ID
                  BLASTN
Method
                  g18764
NCBI GI
                  172
BLAST score
                  3.0e-92
E value
                  211
Match length
                  96
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   43661
Seq. No.
                  crh700856534.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g18764
BLAST score
                   59
                   7.0e-25
E value
Match length
                   167
                   85
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
Seq. No.
                   43662
                   crh700856580.hl
Seq. ID
                   BLASTX
Method
                   g1730109
NCBI GI
                   190
BLAST score
                   3.0e-15
E value
                   79
Match length
% identity
                   65
                   LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                   HYDROXYLASE) >qi 499022 emb CAA53580 (X75966)
                   leucoanthocyanidin dioxygenase [Vitis vinifera]
```

Seq. No. 43663

Seq. ID crh700856585.h1

Method BLASTX NCBI GI g126078



```
BLAST score
                   3.0e-13
E value
                   62
Match length
                   65
% identity
                   LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
NCBI Description
                   >gi_81554_pir__S04046 embryonic abundant protein gD-34 -
                   upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea protein [Gossypium hirsutum] >gi_167385 (M19389) storage
                   protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea
                   D-34 gene [Saguinus oedipus]
                   43664
Seq. No.
                   crh700856629.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2832659
                   158
BLAST score
                   4.0e-11
E value
                   56
Match length
                   59
% identity
                   (AL021710) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   43665
Seq. No.
                   crh700856695.h1
Seq. ID
                   BLASTX
Method
                   g4567286
NCBI GI
BLAST score
                   169
                   2.0e-12
E value
                   71
Match length
% identity
                    (AC006841) putative coatomer alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
                   43666
Seq. No.
                   djj700605926.h2
Seq. ID
                   BLASTN
Method
                   g476213
NCBI GI
                   128
BLAST score
                    8.0e-66
E value
Match length
                    250
% identity
                   Glycine max Century 84 p24 oleosin isoform A gene, complete
NCBI Description
                    43667
Seq. No.
                    djj700605969.h2
Seq. ID
                    BLASTX
Method
                    g2832658
NCBI GI
                    270
BLAST score
                    4.0e-24
E value
Match length
                    61
% identity
                   (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. djj700605971.h2 Seq. ID

Method BLASTX NCBI GI g3548808



```
287
BLAST score
                  4.0e-26
E value
Match length
                  72
% identity
                  76
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                  43669
Seq. No.
                  djj700605972.h2
Seq. ID
                  BLASTN
Method
                  g18676
NCBI GI
                  175
BLAST score
                  7.0e-94
E value
                  267
Match length
% identity
                   97
                  Soybean lox-3 gene for seed lipoxygenase-3 gene (EC
NCBI Description
                   1.13.11.12
                   43670
Seq. No.
                   djj700605994.h2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q18676
BLAST score
                   180
                   7.0e-97
E value
Match length
                   184
% identity
                   99
                   Soybean lox-3 gene for seed lipoxygenase-3 gene (EC
NCBI Description
                   1.13.11.12)
Seq. No.
                   43671
                   djj700606004.h2
Seq. ID
                   BLASTN
Method
                   q169972
NCBI GI
                   268
BLAST score
                   1.0e-149
E value
                   272
Match length
                   100
% identity
                  Soybean glycinin A-la-B-x subunit mRNA, complete cds
NCBI Description
                   43672
Seq. No.
                   djj700606007.h2
Seq. ID
Method
                   BLASTN
                   g3097320
NCBI GI
BLAST score
                   267
                   1.0e-149
E value
Match length
                   267
                   100
% identity
                  Glycine max gene for Bd 30K, complete cds
NCBI Description
                   43673
Seq. No.
                   djj700606027.h2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g169972
                   268
BLAST score
                   1.0e-149
E value
                   268
Match length
                   100
% identity
NCBI Description Soybean glycinin A-1a-B-x subunit mRNA, complete cds
```



```
43674
Seq. No.
                  djj700606044.h2
Seq. ID
Method
                  BLASTN
                  q2605509
NCBI GI
                  265
BLAST score
                  1.0e-147
E value
                  265
Match length
% identity
                   100
                  Glycine max mRNA for alpha subunit of beta conglycinin,
NCBI Description
                   complete cds
                   43675
Seq. No.
                   djj700606074.h2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3617770
                   226
BLAST score
                   6.0e-19
E value
                   58
Match length
                   78
% identity
                   (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                   43676
Seq. No.
                   djj700606080.h2
Seq. ID
                   BLASTN
Method
NCBI GI
                   q18634
                   143
BLAST score
                   9.0e-75
E value
Match length
                   250
                   94
% identity
NCBI Description Soybean Gyl gene for glycinin subunit G1
                   43677
Seq. No.
                   dkc700967913.h1
Seq. ID
                   BLASTX
Method
                   g3342552
NCBI GI
                   239
BLAST score
                   2.0e-20
E value
Match length
                   81
                   52
% identity
                   (AF076979) putative strictosidine synthase [Arabidopsis
NCBI Description
                   thaliana]
                   43678
Seq. No.
                   dkc700968009.h1
Seq. ID
                   BLASTN
Method
                   g349436
NCBI GI
BLAST score
                   32
                   1.0e-08
E value
                   40
Match length
                   95
% identity
NCBI Description Carrot EP1 mRNA, complete cds
                   43679
Seq. No.
```

NCBI GI g464630

BLASTX

Seq. ID Method

dkc700968047.h1



```
142
BLAST score
                   3.0e-09
E value
Match length
                  30
% identity
                   93
NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi_20768_emb_CAA50035_ (X70702)
                  ribosomal protein L27 [Pisum sativum]
                   43680
Seq. No.
                   dkc700968093.hl
Seq. ID
Method '
                  BLASTN
                   g2225884
NCBI GI
BLAST score
                   101
                   9.0e-50
E value
                   189
Match length
% identity
                   88
                   Solanum tuberosum mRNA for eukaryotic initiation factor
NCBI Description
                   5A5, complete cds
                   43681
Seq. No.
                   dpv701096922.h1
Seq. ID
Method
                   BLASTX
                   q4510401
NCBI GI
BLAST score
                   138
                   9.0e-17
E value
Match length
                   60
                   70
% identity
                   (AC006587) putative general negative regulator of
NCBI Description
                   transcription [Arabidopsis thaliana]
                   43682
Seq. No.
                   dpv701096926.h1
Seq. ID
Method
                   BLASTN
                   q4567193
NCBI GI
                   44
BLAST score
                   1.0e-15
E value
                   56
Match length
                   95
% identity
                   Arabidopsis thaliana chromosome II BAC T26C19 genomic
NCBI Description
                   sequence, complete sequence
                   43683
Seq. No.
                   dpv701096945.hl
Seq. ID
                   BLASTX
Method
                   g807698
NCBI GI
                   288
BLAST score
                   4.0e-26
E value
Match length
                   92
                   58
% identity
                  (D32206) prepro-cucumisin [Cucumis melo]
NCBI Description
                   43684
Seq. No.
                   dpv701096987.h1
Seq. ID
                   BLASTX
Method
                   q4559346
NCBI GI
                   153
BLAST score
```

2.0e-10

71

E value Match length



```
% identity
                  (AC006585) early nodulin 16 [Arabidopsis thaliana]
NCBI Description
                  43685
Seq. No.
Seq. ID
                  dpv701097014.hl
Method
                  BLASTX
NCBI GI
                  q3738302
BLAST score
                  216
                  4.0e-26
E value
                  83
Match length
% identity
                  (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4249398 (AC006072) putative tubby protein [Arabidopsis
                  thaliana]
Seq. No.
                  43686
Seq. ID
                  dpv701097023.hl
Method
                  BLASTN
                  g2342717
NCBI GI
BLAST score
                  39
E value
                  1.0e-12
Match length
                  58
                  93
% identity
                  Arabidopsis thaliana chromosome II BAC T14G11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   43687
Seq. ID
                   dpv701097029.h1
Method
                   BLASTX
NCBI GI
                   g4455276
BLAST score
                   160
E value
                   2.0e-11
Match length
                   52
% identity
                   60
                   (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   43688
Seq. No.
                   dpv701097044.hl
Seq. ID
                   BLASTX
Method
                   g3044212
NCBI GI
BLAST score
                   327
                   1.0e-32
E value
                   82
Match length
                   88
% identity
                   (AF057043) acyl-CoA oxidase [Arabidopsis thaliana]
NCBI Description
                   43689
Seq. No.
                   dpv701097082.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1808591
BLAST score
                   98
                   6.0e-48
E value
Match length
                   165
```

NCBI Description C.arietinum mRNA for SAM-synthetase

% identity

Seq. ID Method

NCBI GI



```
43690
Seq. No.
                  dpv701097117.h1
Seq. ID
                  BLASTX
Method
                  g3928084
NCBI GI
                  281
BLAST score
                  2.0e-25
E value
                  58
Match length
                  83
% identity
                   (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   43691
Seq. No.
                   dpv701097150.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3426048
                   160
BLAST score
                   3.0e-11
E value
                   48
Match length
                   67
% identity
                   (AC005168) putative hydroxymethylglutaryl-CoA lyase
NCBI Description
                   precursor [Arabidopsis thaliana]
                   43692
Seq. No.
                   dpv701097169.h1
Seq. ID
                   BLASTX
Method
                   q2245020
NCBI GI
                   264
BLAST score
                   2.0e-23
E value
Match length
                   68
                   76
% identity
                  (Z97341) growth regulator homolog [Arabidopsis thaliana]
NCBI Description
                   43693
Seq. No.
                   dpv701097203.h1
Seq. ID
Method
                   BLASTX
                   g3702343
NCBI GI
                   163
BLAST score
                   4.0e-25
E value
                   86
Match length
                   70
% identity
                   (AC005397) putative homeotic gene regulator [Arabidopsis
NCBI Description
                   thaliana]
                   43694
Seq. No.
                   dpv701097212.h1
Seq. ID
Method
                   BLASTX
                   g4204793
NCBI GI
                   99
BLAST score
E value
                   7.0e-11
                   69
Match length
% identity
                   23
                   (U52079) P-glycoprotein [Solanum tuberosum]
NCBI Description
Seq. No.
                   43695
```

6954

dpv701097234.hl

BLASTX

g3292829



```
BLAST score
                  1.0e-36
E value
                  88
Match length
% identity
                  79
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  dpv701097261.h1
Seq. ID
                  BLASTX
Method
                  g4206196
NCBI GI
BLAST score
                  123
                  1.0e-15
E value
                  75
Match length
                  47
% identity
                  (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  43697
Seq. ID
                  dpv701097303.hl
                  BLASTN
Method
                   q497899
NCBI GI
                   83
BLAST score
E value
                   5.0e-39
                   167
Match length
                   87
% identity
                  Populus trichocarpa * Populus deltoides (clone
NCBI Description
                   sam.Pdx.Pt.2) S-adenosyl methionine synthetase mRNA,
                   complete cds
                   43698
Seq. No.
Seq. ID
                   dpv701097317.h1
Method
                   BLASTN
NCBI GI
                   q438898
BLAST score
                   101
                   7.0e-50
E value
                   120
Match length
                   97
% identity
                   Soybean glutamine phosphoribosylpyrophosphate
NCBI Description
                   amidotransferase mRNA, complete cds
                   43699
Seq. No.
                   dpv701097319.hl
Seq. ID
                   BLASTX
Method
                   q396384
NCBI GI
                   204
BLAST score
                   2.0e-16
E value
                   85
Match length
                   55
% identity
                   (U00006) No definition line found [Escherichia coli]
NCBI Description
                   43700
Seq. No.
                   dpv701097334.h1
Seq. ID
Method
                   BLASTX
                   g2262114
NCBI GI
                   151
BLAST score
                   4.0e-10
E value
                   84
Match length
% identity
                   42
```



```
(AC002343) cellulose synthase isolog [Arabidopsis thaliana]
NCBI Description
                  43701
Seq. No.
                  dpv701097350.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3176965
                  106
BLAST score
                   4.0e-11
E value
                   63
Match length
                   67
% identity
                   (AF067967) pyrroline-5-carboxylate synthetase
NCBI Description
                   [Mesembryanthemum crystallinum]
                   43702
Seq. No.
                   dpv701097366.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q255407
BLAST score
                   42
                   7.0e-15
E value
                   78
Match length
% identity
                   repetitive proline-rich protein {cDNA clone 1A10-2}
NCBI Description
                   [Glycine max=soybeans, axes germinated for 31 hours, mRNA,
                   943 nt]
                   43703
Seq. No.
                   dpv701097374.h1
Seq. ID
                   BLASTN
Method
                   q403326
NCBI GI
BLAST score
                   43
                   3.0e-15
E value
                   127
Match length
% identity
                   83
                   T.repens TrMT1A mRNA for metallothionein-like protein
NCBI Description
                   43704
Seq. No.
                   dpv701097375.hl
Seq. ID
                   BLASTN
Method
                   g1163180
NCBI GI
BLAST score
                   33
E value
                   3.0e-09
Match length
                   115
% identity
                   Glycine max arginine decarboxylase mRNA, complete cds
NCBI Description
                   43705
Seq. No.
                   dpv701097383.h1
Seq. ID
Method
                   BLASTX
                   g3779218
NCBI GI
                   408
BLAST score
                   3.0e-40
E value
Match length
                   86
 % identity
                   90
                   (AF030879) protein kinase CPK1 [Solanum tuberosum]
NCBI Description
```

43706

dpv701097405.h1

Seq. No.

Seq. ID

BLAST score

187



```
BLASTX
Method
NCBI GI
                  g3367576
BLAST score
                  138
                  1.0e-08
E value
Match length
                  61
% identity
                  54
                  (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
NCBI Description
                  43707
Seq. No.
Seq. ID
                  dpv701097409.h1
Method
                  BLASTN
                  q4469002
NCBI GI
BLAST score
                  37
                  1.0e-11
E value
                  97
Match length
% identity
                  85
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
NCBI Description
                   (ESSA project)
                   43708
Seq. No.
                  dpv701097416.h1
Seq. ID
Method
                  BLASTX
                  g2062169
NCBI GI
BLAST score
                   173
                   8.0e-13
E value
                   52
Match length
% identity
                   (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                   thaliana]
                   43709
Seq. No.
Seq. ID
                   dpv701097419.h1
Method
                   BLASTX
                   g3114901
NCBI GI
BLAST score
                   143
                   3.0e-09
E value
Match length
                   70
                   47
% identity
                   (AJ005804) pcbere [Populus balsamifera subsp. trichocarpa]
NCBI Description
                   >qi 3114905 emb CAA06709 (AJ005806) pceberh [Populus
                   balsamifera subsp. trichocarpa]
Seq. No.
                   43710
                   dpv701097472.h1
Seq. ID
                   BLASTN
Method
                   g872115
NCBI GI
BLAST score
                   37
                   1.0e-11
E value
                   97
Match length
                   85
% identity
NCBI Description G.max gmsti mRNA
Seq. No.
                   43711
                   dpv701097503.h1
Seq. ID
                   BLASTX
Method
                   g3258637
NCBI GI
```



```
2.0e-14
E value
Match length
                  57
% identity
                   58
                   (AF041050) 4-coumarate:CoA ligase [Populus tremuloides]
NCBI Description
                   43712
Seq. No.
                   dpv701097595.h1
Seq. ID
                   BLASTN
Method
                   q1326160
NCBI GI
BLAST score
                   36
                   5.0e-11
E value
Match length
                   36
                   100
% identity
                  Phaseolus vulgaris dehydrin mRNA, complete cds
NCBI Description
Seq. No.
                   43713
                   dpv701097624.h1
Seq. ID
                   BLASTN
Method
                   g2529228
NCBI GI
BLAST score
                   69
E value
                   1.0e-30
Match length
                   173
                   86
% identity
                   Glycine max mRNA for 6-phosphogluconate dehydrogenase,
NCBI Description
                   complete cds
Seq. No.
                   43714
Seq. ID
                   dpv701097644.hl
Method
                   BLASTX
                   g3873408
NCBI GI
BLAST score
                   163
                   1.0e-11
E value
                   44
Match length
                   68
% identity
                   (L76926) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   43715
Seq. No.
                   dpv701097654.hl
Seq. ID
                   BLASTX
Method
                   g4056416
NCBI GI
BLAST score
                   141
                   5.0e-09
E value
                   63
Match length
                   51
% identity
                   (AC005322) Strong similarity to Dsor1 protein kinase
NCBI Description
                   gb_D13782 from Drosophila melanogaster. [Arabidopsis
                   thaliana]
```

43716 Seq. No.

dpv701097689.h1 Seq. ID

Method BLASTX g3273202 NCBI GI 279 BLAST score 2.0e-25 E value Match length 67 78 % identity

6958

NCBI Description

43722

Seq. No.



```
NCBI Description (AB010918) responce reactor4 [Arabidopsis thaliana]
                  43717
Seq. No.
Seq. ID
                  dpv701097735.h1
                  BLASTN
Method
NCBI GI
                  g166802
BLAST score
                  34
                  3.0e-10
E value
                  38
Match length
                  97
% identity
NCBI Description Arabidopsis thaliana phosphoprotein phosphatase-type 1
                  catalytic site mRNA, complete cds
                  43718
Seq. No.
Seq. ID
                  dpv701097741.h1
Method
                  BLASTX
NCBI GI
                  q4185136
BLAST score
                  158
E value
                  3.0e-11
Match length
                  49
% identity
                  67
                  (AC005724) putative trehalose-6-phosphate synthase
NCBI Description
                  [Arabidopsis thaliana]
                  43719
Seq. No.
                  dpv701097750.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20755
BLAST score
                  39
E value
                  5.0e-13
Match length
                  67
                  91
% identity
NCBI Description P.sativum mRNA rab for ras-related GTP-binding protein
Seq. No.
                  43720
Seq. ID
                  dpv701097923.h1
Method
                  BLASTX
NCBI GI
                  g1710518
BLAST score
                  183
                  6.0e-14
E value
Match length
                  62
                  65
% identity
                  60S RIBOSOMAL PROTEIN L22 >gi 1124998 emb CAA63927
NCBI Description
                   (X94243) ribosomal protein homologue to human L22 [Xenopus
                  laevis]
                  43721
Seq. No.
                  dpv701097961.h1
Seq. ID
Method
                  BLASTX
                  g3075390
NCBI GI
BLAST score
                  238
E value
                  1.0e-20
Match length
                  56
% identity
                  80
```

6959

(AC004484) protein kinase ARSK1 [Arabidopsis thaliana]



```
dpv701097963.h1
Seq. ID
                  BLASTN
Method
                  g456713
NCBI GI
                  242
BLAST score
                  1.0e-134
E value
                  258
Match length
                  25
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
                  43723
Seq. No.
                  dpv701098049.hl
Seq. ID
                  BLASTN
Method
                  g1066498
NCBI GI
BLAST score
                  118
                  7.0e-60
E value
                  253
Match length
                   87
% identity
                  Medicago sativa (clone GG16-1) NADH-dependent glutamate
NCBI Description
                   synthase gene, complete cds
                   43724
Seq. No.
                   dpv701098073.h1
Seq. ID
                   BLASTN
Method
                   g3021337
NCBI GI
BLAST score
                   73
                   5.0e-33
E value
Match length
                   168
                   86
% identity
NCBI Description Cicer arietinum mRNA for cytosolic
                   fructose-1,6-bisphosphate aldolase
                   43725
Seq. No.
                   dpv701098106.h1
Seq. ID
Method
                   BLASTN
                   q2895197
NCBI GI
BLAST score
                   170
                   6.0e-91
E value
                   170
Match length
                   100
% identity
                   Glycine max DNA polymerase delta (Pol delta) mRNA, complete
NCBI Description
                   cds
                   43726
Seq. No.
                   dpv701098210.h1
Seq. ID
Method
                   BLASTX
                   g2673905
NCBI GI
                   152
BLAST score
                   3.0e-10
E value
Match length
                   38
                   76
% identity
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
                   43727
Seq. No.
```

Seq. ID dpv701098286.h1

Method BLASTX NCBI GI g4539525 BLAST score 297



```
E value
                  3.0e-27
Match length
                  82
% identity
NCBI Description
                  (AJ012370) NAALADase II protein [Homo sapiens]
Seq. No.
                  43728
Seq. ID
                  dpv701098295.hl
Method
                  BLASTN
NCBI GI
                  q516853
BLAST score
                  48
                  2.0e-18
E value
Match length
                  68
% identity
                  53
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
                  43729
Seq. No.
Seq. ID
                  dpv701098312.h1
                  BLASTN
Method
                  g18764
NCBI GI
BLAST score
                  167
E value
                  4.0e-89
Match length
                  207
                  95
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                  43730
Seq. No.
Seg. ID
                  dpv701098331.h1
Method
                  BLASTX
NCBI GI
                  g1871196
BLAST score
                  149
E value
                  6.0e-10
Match length
                  47
% identity
                  66
                  (U90439) GMP kinase isolog [Arabidopsis thaliana]
NCBI Description
                  >gi 2335091 (AC002339) putative GMP kinase [Arabidopsis
                  thaliana]
Seq. No.
                  43731
                  dpv701098424.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738325
BLAST score
                  242
E value
                  7.0e-21
Match length
                  71
                  72
% identity
NCBI Description
                  (AC005170) putative CaMB-channel protein [Arabidopsis
                  thaliana]
Seq. No.
                  43732
```

dpv701098487.h1 Seq. ID Method BLASTN

NCBI GI g170089 BLAST score 166 E value 1.0e-88 Match length 250 % identity 92

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds



```
43733
Seq. No.
                   dpv701098514.h1
Seq. ID
Method
                   BLASTX
                    g3913437
NCBI GI
                    460
BLAST score
                    2.0e-46
E value
                    93
Match length
                    97
% identity
                    PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                    HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase
[Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)
                    HELICASE >gi_1402875_emb_CAA66825
                    RNA helicase [Arabidopsis Thaliana]
Seq. No.
                    43734
                    dpv701098522.hl
Seq. ID
                    BLASTX
Method
                    g2191194
NCBI GI
                    198
BLAST score
                    1.0e-15
E value
Match length
                    87
                    49
% identity
                    (AF007271) contains weak to the SAPB protein (TR:E236624)
NCBI Description
                    [Arabidopsis thaliana]
                    43735
Seq. No.
                    dpv701098561.hl
Seq. ID
Method
                    BLASTX
                    g3367572
NCBI GI
                    197
BLAST score
                    2.0e-15
E value
Match length
                    87
                    46
% identity
                    (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                    43736
Seq. No.
                    dpv701098579.h1
Seq. ID
                    BLASTX
Method
                    g1871177
NCBI GI
                    174
BLAST score
                    8.0e-13
 E value
                    48
Match length
                    69
 % identity
                    (U90439) unknown protein [Arabidopsis thaliana]
 NCBI Description
                     43737
 Seq. No.
                    dpv701098645.h1
 Seq. ID
                    BLASTN
 Method
                     q2494106
 NCBI GI
                     47
 BLAST score
                     1.0e-17
 E value
                     90
 Match length
                     88
 % identity
```

Seq. No. 43738

NCBI Description

complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,

BLAST score

E value

365 3.0e-35



```
dpv701098728.h2
Seq. ID
                  BLASTX
Method
                  g558925
NCBI GI
                   305
BLAST score
                   3.0e-28
E value
                   88
Match length
                   76
% identity
                   (U15778) geranylgeranyl pyrophosphate synthase [Lupinus
NCBI Description
                   albus]
                   43739
Seq. No.
                   dpv701098825.hl
Seq. ID
                   BLASTX
Method
                   g2055228
NCBI GI
                   153
BLAST score
                   2.0e-16
E value
                   79
Match length
                   37
% identity
                  (AB000129) SRC1 [Glycine max]
NCBI Description
                   43740
Seq. No.
                   dpv701099003.h1
Seq. ID
                   BLASTX
Method
                   g4544409
NCBI GI
                   350
BLAST score
                   2.0e-33
E value
                   92
Match length
                   72
% identity
                   (AC006955) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   43741
Seq. No.
                   dpv701099009.h1
Seq. ID
                   BLASTX
Method
                   g2914703
NCBI GI
                   231
BLAST score
                   2.0e-19
E value
                   52
Match length
 % identity
                   85
                   (AC003974) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   43742
 Seq. No.
                   dpv701099017.hl
 Seq. ID
                    BLASTX
 Method
                    g1871187
 NCBI GI
                    156
 BLAST score
                    1.0e-11
 E value
                    60
 Match length
                    57
 % identity
                   (U90439) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    43743
 Seq. No.
                    dpv701099096.h1
 Seq. ID
                    BLASTX
 Method
                    q3450842
 NCBI GI
```



```
89
Match length
                  78
% identity
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
                  43744
Seq. No.
                  dpv701099143.h1
Seq. ID
                  BLASTX
Method
                  g2618686
NCBI GI
                  191
BLAST score
                  7.0e-15
E value
                  77
Match length
                   47
% identity
                   (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43745
                   dpv701099211.hl
Seq. ID
                   BLASTX
Method
                   g2384675
NCBI GI
BLAST score
                   191
E value
                   7.0e-15
Match length
                   43
                   86
% identity
                   (AF012659) putative potassium transporter AtKT4p
NCBI Description
                   [Arabidopsis thaliana]
                   43746
Seq. No.
                   dpv701099248.h1
Seq. ID
                   BLASTX
Method
                   q2668492
NCBI GI
                   205
BLAST score
                   2.0e-16
E value
                   77
Match length
                   57
% identity
                   (D89981) metal-transporting P-type ATPase [Arabidopsis
NCBI Description
                   thaliana]
                   43747
Seq. No.
                   dpv701099289.h1
Seq. ID
                   BLASTN
Method
                   q3860322
NCBI GI
                   92
BLAST score
                   2.0e-44
E value
                   204
Match length
                   86
 % identity
                   Cicer arietinum mRNA for hypothetical protein, clone
NCBI Description
                   Can40-1
                   43748
 Seq. No.
                   dpv701099314.h1
 Seq. ID
Method
                   BLASTN
                   g2687432
NCBI GI
 BLAST score
                   40
                   2.0e-13
 E value
                   40
Match length
                   100
 % identity
NCBI Description Plumbago auriculata large subunit 26S ribosomal RNA gene,
```

Seq. No.

Seq. ID

43754

dpv701099448.h1



partial sequence

```
43749
Seq. No.
                  dpv701099336.h1
Seq. ID
                  BLASTX
Method
                  g4106970
NCBI GI
                  140
BLAST score
                  7.0e-09
E value
                  86
Match length
                  14
% identity
                   (AF113948) resistance protein candidate RGC2B [Lactuca
NCBI Description
                   sativa]
                   43750
Seq. No.
                   dpv701099396.h1
Seq. ID
                   BLASTX
Method
                   q4204095
NCBI GI
                   214
BLAST score
                   9.0e-18
E value
                   62
Match length
% identity
                   63
                   (AF030260) CYP94A1 [Vicia sativa]
NCBI Description
                   43751
Seq. No.
                   dpv701099411.hl
Seq. ID
                   BLASTN
Method
                   g2264318
NCBI GI
                   98
BLAST score
                   6.0e-48
E value
                   229
Match length
                   86
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUP24, complete sequence [Arabidopsis thaliana]
                   43752
Seq. No.
                   dpv701099429.h1
Seq. ID
                   BLASTN
Method
                   g3668068
NCBI GI
BLAST score
                   46
                   6.0e-17
E value
                   98
Match length
                   87
% identity
                   Lycopersicon esculentum Pto kinase interactor 1 (Pti1)
NCBI Description
                   mRNA, complete cds
                   43753
Seq. No.
                   dpv701099447.hl
Seq. ID
                   BLASTX
Method
                   q1200256
NCBI GI
                   169
BLAST score
E value
                   2.0e-12
                   43
Match length
 % identity
                   (X90990) stpk1 protein kinase [Solanum tuberosum]
NCBI Description
```

NCBI GI

BLAST score



```
BLASTN
Method
                  g3176097
NCBI GI
                  73
BLAST score
                  5.0e-33
E value
                  200
Match length
                  85
% identity
                  Medicago truncatula mRNA for annexin
NCBI Description
                  43755
Seq. No.
                  dpv701099488.h1
Seq. ID
                  BLASTX
Method
                  g1172584
NCBI GI
                   182
BLAST score
                   8.0e-26
E value
Match length
                   86
% identity
                   65
                  POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE)
NCBI Description
                   >gi 1076478_pir__S52984 catechol oxidase (EC 1.10.3.1)
                   precursor - apple tree >gi_507280 (L29450) polyphenol
                   oxidase [Malus domestica]
                   43756
Seq. No.
                   dpv701099506.hl
Seq. ID
                   BLASTN
Method
                   g170073
NCBI GI
                   201
BLAST score
                   1.0e-109
E value
                   228
Match length
                   97
% identity
                   Soybean calmodulin (SCaM-3) mRNA, complete cds
NCBI Description
                   43757
Seq. No.
                   dpv701099567.h1
Seq. ID
                   BLASTX
Method
                   g3122673
NCBI GI
                   157
BLAST score
                   4.0e-11
E value
                   36
Match length
% identity
                   83
                   60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   43758
Seq. No.
                   dpv701099578.h1
Seq. ID
                   BLASTN
Method
                   g169980
NCBI GI
                   180
BLAST score
                   7.0e-97
E value
                   254
Match length
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   43759
Seq. No.
                   dpv701099624.h1
 Seq. ID
                   BLASTX
Method
```

g4415934 163



```
5.0e-18
E value
                    81
Match length
% identity
                    (AC006418) putative auxin response factor 1 [Arabidopsis
NCBI Description
                    thaliana]
                    43760
Seq. No.
                                                                           s( *
                    dpv701099676.h1
Seq. ID
                   BLASTX
Method
                    g2529707
NCBI GI
                    141
BLAST score
                    5.0e-09
E value
                    44
Match length
% identity
                    61
                    (AF001434) Hpast [Homo sapiens]
NCBI Description
                    43761
Seq. No.
                    dpv701099725.h1
Seq. ID
                    BLASTX
Method
                    q2262149
NCBI GI
BLAST score
                    226
                    7.0e-19
E value
                    90
Match length
                    50
% identity
                    (ACO02330) LUMINIDEPENDENS protein [Arabidopsis thaliana]
NCBI Description
                    43762
Seq. No.
                    dpv701099758.hl
Seq. ID
Method
                    BLASTX
                    g1669599
NCBI GI
                    213
BLAST score
                    2.0e-17
E value
                    88
Match length
                    48
% identity
                    (D88746) AR791 [Arabidopsis thaliana]
NCBI Description
                    43763
Seq. No.
                    dpv701099762.h1
Seq. ID
                    BLASTX
Method
                    g123656
NCBI GI
BLAST score
                    181
                    8.0e-14
E value
                    50
Match length
                    70
% identity
                    CHLOROPLAST ENVELOPE MEMBRANE 70 KD HEAT SHOCK-RELATED
NCBI Description
                    PROTEIN >gi_285407_pir__A42582 heat shock protein SCE70 - spinach >gi_21338_emb_CAA43711_ (X61491) 70 kDa heat shock
                    protein [Spinacia oleracea]
Seq. No.
                    43764
                    dpv701099772.h1
Seq. ID
                    BLASTX
Method
                    q3236253
NCBI GI
                    253
BLAST score
```

4.0e-22

89 56

E value Match length

% identity



```
NCBI Description
                   (AC004684) receptor-like protein kinase [Arabidopsis
                  thaliana]
                  43765
Seq. No.
Seq. ID
                  dpv701099786.h1
Method
                  BLASTN
NCBI GI
                  g2852444
BLAST score
                  66
E value
                  8.0e-29
Match length
                  182
% identity
                  84
                 Salix bakko mRNA for SUI1 homolog, complete cds
NCBI Description
                  43766
Seq. No.
Seq. ID
                  dpv701099788.h1
                  BLASTX
Method
NCBI GI
                  g4544431
BLAST score
                  283
                  1.0e-25
E value
Match length
                  60
                  88
% identity
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  43767
                  dpv701099869.h1
Seq. ID
Method
                  BLASTX
                  q3717946
NCBI GI
BLAST score
                  151
E value
                   4.0e-10
                  52
Match length
                   62
% identity
                  (AJ005901) vag1 [Arabidopsis thaliana]
NCBI Description
                   43768
Seq. No.
                  dpv701099955.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q461736
BLAST score
                   245
                  1.0e-31
E value
                  95
Match length
                  84
% identity
NCBI Description
                  MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
                  >gi_478786_pir__S29316 chaperonin 60 - cucurbit
                  >gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita
                   sp.]
Seq. No.
                   43769
Seq. ID
                  dpv701099977.h1
Method
                  BLASTX
NCBI GI
                   g4432855
BLAST score
                  333
E value
                  2.0e-31
Match length
                  92
                  75
% identity
NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]
```

43770

Seq. No.



```
dpv701099980.hl
Seq. ID
                  BLASTX
Method
                  q3075391
NCBI GI
                  279
BLAST score
                  4.0e-25
E value
Match length
                  65
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
                  43771
Seq. No.
                  dpv701100005.h2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3970652
                  192
BLAST score
                   3.0e-21
E value
                   69
Match length
% identity
                  (X77499) amino acid permease [Arabidopsis thaliana]
NCBI Description
                   43772
Seq. No.
                   dpv701100060.h2
Seq. ID
                   BLASTN
Method
                   q829118
NCBI GI
                   107
BLAST score
                   2.0e-53
E value
                   211
Match length
                   88
% identity
NCBI Description P.vulgaris gene for cyclophilin
                   43773
Seq. No.
                   dpv701100071.h2
Seq. ID
                   BLASTN
Method
                   q288187
NCBI GI
BLAST score
                   204
                   1.0e-111
E value
                   252
Match length
                   95
% identity
NCBI Description V.unguiculata cysteine proteinase inhibitor mRNA
                   43774
Seq. No.
                   dpv701100139.hl
 Seq. ID
                   BLASTN
Method
                   q1184122
NCBI GI
                   143
 BLAST score
                   8.0e-75
 E value
                   239
Match length
                   90
 % identity
                  Vigna radiata clone MII-4 auxin-induced protein mRNA,
 NCBI Description
                   partial cds
                    43775
 Seq. No.
                   dpv701100218.h1
 Seq. ID
                   BLASTX
 Method
                   g3193319
 NCBI GI
                   161
 BLAST score
```

6969

2.0e-11

83

E value

Match length



```
% identity
                  (AF069299) contains similarity to mouse brain protein E46
NCBI Description
                   (GB:X61506) [Arabidopsis thaliana]
                  43776
Seq. No.
                  dpv701100228.h1
Seq. ID
                  BLASTX
Method
                  g4432824
NCBI GI
                   309
BLAST score
                   1.0e-28
E value
                  74
Match length
                   77
% identity
                  (AC006593) putative membrane-associated salt-inducible
NCBI Description
                   protein [Arabidopsis thaliana]
                   43777
Seq. No.
                   dpv701100256.h1
Seq. ID
                   BLASTX
Method
                   g1710546
NCBI GI
                   156
BLAST score
                   7.0e-11
E value
                   54
Match length
                   41
% identity
                   60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative
NCBI Description
                   ribosomal protein [Daucus carota]
                   43778
Seq. No.
                   dpv701100278.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4415913
                   179
BLAST score
                   1.0e-13
E value
                   60
Match length
                   67
% identity
                   (AC006282) unknown protein [Arabidopsis thaliana]
NCBI Description
                   43779
Seq. No.
                   dpv701100293.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4467125
                   324
BLAST score
                   1.0e-30
E value
                   77
Match length
                   77
% identity
                   (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   43780
                   dpv701100370.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3540206
BLAST score
                   159
E value
                   4.0e-11
                   51
Match length
                   57
% identity
```

Seq. No. 43781

NCBI Description

(AC004260) Hypothetical protein [Arabidopsis thaliana]



```
dpv701100375.h1
Seq. ID
                  BLASTX
Method
                  g542200
NCBI GI
                  205
BLAST score
                  2.0e-16
E value
Match length
                  70
                   57
% identity
                  hypothetical protein - garden asparagus
NCBI Description
                  >gi 452714 emb CAA54526 (X77320) unknown [Asparagus
                   officinalis]
                   43782
Seq. No.
                   dpv701100415.hl
Seq. ID
                   BLASTX
Method
                   q346685
NCBI GI
BLAST score
                   290
E value
                   1.0e-26
                   78
Match length
% identity
                   developmentally-regulated GTP-binding protein - mouse
NCBI Description
                   43783
Seq. No.
Seq. ID
                   dpv701100417.hl
                   BLASTX
Method
NCBI GI
                   g4006900
                   157
BLAST score
                   8.0e-11
E value
                   65
Match length
% identity
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   43784
Seq. No.
                   dpv701100507.h1
Seq. ID
                   BLASTX
Method
                   g3785971
NCBI GI
                   112
BLAST score
                   3.0e-09
E value
                   45
Match length
                   71
 % identity
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4262248_gb_AAD14541_ (AC006200) hypothetical protein
                   [Arabidopsis thaliana]
                   43785
 Seq. No.
                   dpv701100543.hl
 Seq. ID
                   BLASTN
 Method
                   g170071
 NCBI GI
                   202
 BLAST score
                   1.0e-110
 E value
                   262
 Match length
 % identity
 NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds
```

Seq. No. 43786

Seq. ID dpv701100555.h1

Method BLASTN NCBI GI g1220521



```
BLAST score
                   7.0e-63
E value
                   225
Match length
                   99
% identity
NCBI Description
                  Glycine max TATA-box binding protein (STBP1) mRNA, complete
                   43787
Seq. No.
                   dpv701100617.h1
Seq. ID
Method
                   BLASTN
                   g218082
NCBI GI
BLAST score
                   108
                   7.0e-54
E value
                   274
Match length
% identity
                   86
                  Rice mRNA for initiation factor eIF-4D (225 gene), partial
NCBI Description
                   sequence
Seq. No.
                   43788
                   dpv701100724.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3831441
"BLAST score
                   170
E value
                   3.0e-12
Match length
                   63
% identity
                   67
NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   43789
Seq. ID
                   dpv701100772.h1
Method
                   BLASTX
NCBI GI
                   g2914703
BLAST score
                   179
                   2.0e-13
E value
                   88
Match length
                   48
% identity
NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]
                   43790
Seq. No.
Seq. ID
                   dpv701100811.h1
Method
                   BLASTX
NCBI GI
                   q3056595
BLAST score
                   211
                   4.0e-17
E value
Match length
                   67
% identity
                   55
NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]
Seq. No.
                   43791
                   dpv701100916.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1514643
BLAST score
                   212
```

Method BLASTX
NCBI GI g1514643
BLAST score 212
E value 3.0e-17
Match length 49
% identity 86

NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]



Seq. No. 43792

Seq. ID dpv701100925.h1

Method BLASTX
NCBI GI g1076348
BLAST score 205
E value 2.0e-16
Match length 92
% identity 47

NCBI Description myosin MYA1, class V - Arabidopsis thaliana

>gi 433663 emb CAA82234 (Z28389) myosin [Arabidopsis

thaliana]

Seq. No. 43793

Seq. ID dpv701100934.h1

Method BLASTX
NCBI GI g4206122
BLAST score 156
E value 5.0e-11
Match length 32
% identity 84

NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum

crystallinum]

Seq. No. 43794

Seq. ID dpv701100943.h1

Method BLASTX
NCBI GI g131026
BLAST score 225
E value 9.0e-19
Match length 85
% identity 49

NCBI Description PATHOGENESIS-RELATED PROTEIN STH-2 >gi_479691_pir__S35161

STH-2 protein - potato >gi 169551 (M25155) pSTH-2 protein

[Solanum tuberosum] >gi 169576 (M29041) STH-2 protein

[Solanum tuberosum]

Seq. No. 43795

Seq. ID dpv701100983.h1

Method BLASTN
NCBI GI g166411
BLAST score 130
E value 5.0e-67
Match length 278
% identity 87

NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds

Seq. No. 43796

Seq. ID dpv701100987.h1

Method BLASTN
NCBI GI g516853
BLAST score 195
E value 1.0e-106
Match length 283
% identity 27

NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. ID

NCBI GI

Method



```
43797
Seq. No.
                  dpv701101016.hl
Seq. ID
Method
                  BLASTX
                  g3859659
NCBI GI
                   326
BLAST score
                   1.0e-30
E value
                   70
Match length
                   87
% identity
                   (AL031394) putative potassium transporter AtKT5p (AtKT5)
NCBI Description
                   [Arabidopsis thaliana]
                   43798
Seq. No.
                   dpv701101038.h1
Seq. ID
                   BLASTX
Method
                   g2702284
NCBI GI
                   157
BLAST score
                   7.0e-11
E value
                   47
Match length
                   68
% identity
                   (AC003033) Argonaute (AGO1)-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   43799
Seq. No.
                   dpv701101047.hl
Seq. ID
                   BLASTX
Method
                   g2832623
NCBI GI
                   188
BLAST score
                   1.0e-14
E value
                   88
Match length
                   48
% identity
                   (AL021711) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   43800
Seq. No.
                   dpv701101127.h1
Seq. ID
                   BLASTN
Method
                   g169930
NCBI GI
                   114
BLAST score
                   9.0e-58
E value
                   154
Match length
 % identity
                   94
NCBI Description Glycine max calcium dependent protein kinase mRNA
                   43801
 Seq. No.
                   dpv701101148.h1
 Seq. ID
                   BLASTN
Method
                   g1771478
 NCBI GI
                   35
 BLAST score
                   1.0e-10
 E value
                   47
 Match length
 % identity
                   94
 NCBI Description P.sativum hsp70 gene
                   43802
 Seq. No.
```

6974

dpv701101149.hl

BLASTN

g508602



BLAST score 45 E value 1.0e-16 Match length 65 % identity 92

NCBI Description Glycine max stearoyl-acyl carrier protein desaturase

(SACPD) mRNA, complete cds

Seq. No. 43803

Seq. ID dpv701101234.h1

Method BLASTN
NCBI GI g968986
BLAST score 146
E value 1.0e-76
Match length 206
% identity 100

NCBI Description Glycine max ferritin gene, nuclear gene encoding

chloroplast protein, complete cds

Seq. No. 43804

Seq. ID dpv701101260.h1

Method BLASTX
NCBI GI g4309737
BLAST score 161
E value 1.0e-11
Match length 43
% identity 72

NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No. 43805

Seq. ID dpv701101269.h1

Method BLASTN
NCBI GI g3318610
BLAST score 69
E value 7.0e-31
Match length 111
% identity 95

NCBI Description Glycine max mRNA for mitochondrial phosphate transporter,

complete cds

Seq. No. 43806

Seq. ID dpv701101284.h1

Method BLASTN
NCBI GI g18764
BLAST score 110
E value 3.0e-55
Match length 144
% identity 94

NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No. 43807

Seq. ID dpv701101328.h1

Method BLASTN
NCBI GI g16508
BLAST score 45
E value 2.0e-16
Match length 89
% identity 88



43808

43809

NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene sam-1 >gi 166871 gb M55077 ATHSAM A.thaliana S-adenosylmethionine synthetase gene, complete cds

dpv701101370.h1 Seq. ID Method BLASTN NCBI GI g3334662 BLAST score 254 1.0e-141 E value Match length 254 100 % identity

Seq. No.

NCBI Description G.max mRNA for putative cytochrome P450, clone CP4

Seq. No. Seq. ID dpv701101372.h1 Method BLASTX g4454019 NCBI GI BLAST score 228 E value 3.0e-19 Match length 79

% identity 49

NCBI Description (AL035396) SRG1-like protein [Arabidopsis thaliana]

43810 Seq. No.

Seq. ID dpv701101394.h1

Method BLASTX NCBI GI g2245136 390 BLAST score 3.0e-38 E value Match length 86

% identity 84

NCBI Description (Z97344) trehalose-6-phosphate synthase homolog

[Arabidopsis thaliana]

Seq. No. 43811

Seq. ID dpv701101538.h1

Method BLASTX NCBI GI g3152572 BLAST score 252 E value 5.0e-22 Match length 81 53 % identity

(AC002986) Contains homology to DNAJ heatshock protein NCBI Description

gb U32803 from Haemophilus influenzae. [Arabidopsis

thaliana]

43812 Seq. No.

Seq. ID dpv701101549.h1

Method BLASTX g3080441 NCBI GI BLAST score 193 E value 5.0e-15 Match length 74

% identity

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

NCBI GI

BLAST score



```
43813
Seq. No.
                  dpv701101564.h1
Seq. ID
                  BLASTX
Method
                  g2632103
NCBI GI
                  351
BLAST score
                  1.0e-33
E value
                  89
Match length
                  74
% identity
NCBI Description (Z98759) arginyl-tRNA synthetase [Arabidopsis thaliana]
                  43814
Seq. No.
                  dpv701101675.hl
Seq. ID
                  BLASTX
Method
                  g2443887
NCBI GI
BLAST score
                   238
                   2.0e-20
E value
                   85
Match length
                   59
% identity
                  (AC002294) Similar to transcription factor
NCBI Description
                   gb_Z46606_1658307 and others [Arabidopsis thaliana]
                   43815
Seq. No.
                   dpv701101691.h1
Seq. ID
                   BLASTX
Method
                   g4039155
NCBI GI
                   200
BLAST score
                   7.0e-16
E value
                   72
Match length
                   49
% identity
                   (AF104258) putative copper-inducible 35.6 kDa protein
NCBI Description
                   [Festuca rubra]
                   43816
Seq. No.
                   dpv701101721.h1
Seq. ID
                   BLASTX
Method
                   g1514643
NCBI GI
                   141
BLAST score
                   3.0e-09
E value
                   44
Match length
                   57
 % identity
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                   43817
 Seq. No.
                   dpv701101736.h1
 Seq. ID
                   BLASTX
 Method
                   g2737894
 NCBI GI
                   208
 BLAST score
                   4.0e-17
 E value
                   54
 Match length
                   70
 % identity
                   (U59151) Cbf5p homolog [Homo sapiens]
 NCBI Description
                   43818
 Seq. No.
                   dpv701101801.hl
 Seq. ID
                   BLASTN
 Method
                    q4193387
```



E value 1.0e-39 Match length 184 % identity 86

NCBI Description Hevea brasiliensis translationally controlled tumor protein

(TCTP) mRNA, complete cds

Seq. No. 43819

Seq. ID dpv701101811.h1

Method BLASTX
NCBI GI g2501195
BLAST score 239
E value 2.0e-20
Match length 82
% identity 59

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (NSL-TP)

(STEROL CARRIER PROTEIN 2) (SCP-2) (STEROL CARRIER PROTEIN X) (SCP-X) (SCPX) >gi_479569_pir__S34744 sterol carrier protein - chicken >gi_304423 (L09231) sterol carrier

protein-2 [Gallus gallus]

Seq. No. 43820

Seq. ID dpv701101846.h1

Method BLASTX
NCBI GI g1174626
BLAST score 186
E value 2.0e-14
Match length 73
% identity 56

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

(P23) >gi_1072463_pir__A38959 IgE-dependent histamine-releasing factor homolog - potato

>gi_587546_emb_CAA85519_ (Z37160) P23 protein [Solanum

tuberosum]

Seq. No. 43821

Seq. ID dpv701101868.h1

Method BLASTX
NCBI GI g3850587
BLAST score 379
E value 6.0e-37
Match length 83
% identity 87

NCBI Description (AC005278) Strong similarity to gi_2244780 hypothetical

protein from Arabidopsis thaliana chromosome 4 contig

gb Z97335. [Arabidopsis thaliana]

Seq. No. 43822

Seq. ID dpv701101873.h1

Method BLASTX
NCBI GI g2224911
BLAST score 161
E value 2.0e-11
Match length 66
% identity 47

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

carota]



```
43823
Seq. No.
                  dpv701101907.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629692
                   233
BLAST score
                  9.0e-20
E value
                  84
Match length
                  56
% identity
                  hypothetical protein - common tobacco
NCBI Description
                  >gi_506471_emb_CAA56189_ (X79794) unnamed protein product
                   [Nicotiana tabacum]
                   43824
Seq. No.
                   dpv701101920.hl
Seq. ID
Method
                   BLASTX
                   g3776029
NCBI GI
BLAST score
                   363
                   2.0e-36
E value
                   87
Match length
                   85
% identity
                   (AJ010476) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   43825
Seq. No.
                   dpv701102010.h1
Seq. ID
                   BLASTX
Method
                   q541954
NCBI GI
                   170
BLAST score
                   2.0e-12
E value
Match length
                   38
                   79
% identity
                   ubiquitin extension protein - white lupine
NCBI Description
                   >gi 438111_emb_CAA80334_ (Z22613) ubiquitin extension
                   protein [Lupinus albus]
                   43826
Seq. No.
                   dpv701102133.hl
Seq. ID
                   BLASTN
Method
                   g170042
NCBI GI
                   56
BLAST score
                   6.0e-23
E value
                   118
Match length
                   96
% identity
                   Glycine max cv Prize protein kinase mRNA
NCBI Description
                   43827
Seq. No.
                   dpv701102158.h1
 Seq. ID
                   BLASTN
Method
                   g2245073
NCBI GI
                    63
 BLAST score
                    5.0e-27
 E value
Match length
                    107
                    56
```

% identity

Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description fragment No

43828

Seq. No. dpv701102164.hl Seq. ID

Method

NCBI GI

BLASTX q3402754



```
BLASTX
  Method
                     g1762144
  NCBI GI
                     153
  BLAST score
                                                                                  Æ.
                     7.0e-11
E value
                     59
  Match length
                     64
  % identity
  NCBI Description (U48435) putative cytochrome P450 [Solanum chacoense]
                     43829
  Seq. No.
                     dpv701102184.h1
  Seq. ID
                     BLASTX
  Method
                     g1353157
  NCBI GI
                     141
  BLAST score
                      6.0e-09
  E value
  Match length
                     51
                      45
  % identity
                     HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II
  NCBI Description
                      >gi_3878900_emb_CAA86774_ (Z46794) similar to vacuolar
biogenesis protein (pep5); cDNA EST EMBL:D27614 comes from
                      this gene; cDNA EST EMBL: D34974 comes from this gene
                      [Caenorhabditis elegans]
                      43830
  Seq. No.
                      dpv701102187.h1
  Seq. ID
                      BLASTX
  Method
                      g3395436
  NCBI GI
  BLAST score
                      148
                      8.0e-10
  E value
                      40
  Match length
                      72
  % identity
                     (AC004683) unknown protein [Arabidopsis thaliana]
  NCBI Description
                      43831
  Seq. No.
                      dpv701102219.h1
  Seq. ID
                      BLASTN
  Method
                      g2149954
  NCBI GI
                      103
  BLAST score
                      6.0e-51
  E value
                      210
  Match length
                      92
   % identity
                     Phaseolus vulgaris putative aquaporin-1 (Mip-1) mRNA,
  NCBI Description
                      complete cds
                      43832
   Seq. No.
                      dpv701102287.h1
   Seq. ID
                      BLASTX
   Method
                      g4539295
   NCBI GI
                      169
   BLAST score
                      3.0e-12
   E value
   Match length
                      72
   % identity
                      47
                      (AL049480) putative protein [Arabidopsis thaliana]
   NCBI Description
                      43833
   Seq. No.
                      dpv701102289.h1
   Seq. ID
```

6980

```
BLAST score
                   163
E value
                   4.0e-13
Match length
                   67
                   59
% identity
NCBI Description
                  (AL031187) putative protein [Arabidopsis thaliana]
Seq. No.
                   43834
Seq. ID
                  dpv701102365.h1
Method
                  BLASTX
NCBI GI
                  g3953466
BLAST score
                   304
E value
                   4.0e-28
Match length
                  88
% identity
                   64
NCBI Description
                  (AC002328) F20N2.11 [Arabidopsis thaliana]
                  43835
Seq. No.
                  dpv701102369.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115373
BLAST score
                   235
                  5.0e-20
E value
Match length
                  84
% identity
                   63
NCBI Description
                   (AC005967) receptor-like protein kinase [Arabidopsis
                   thaliana]
                   43836
Seq. No.
```

Seq. ID dpv701102430.h1

Method BLASTN NCBI GI g2264306 35 BLAST score E value 2.0e-10 71 Match length

87 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MBK5, complete sequence [Arabidopsis thaliana]

43837 Seq. No.

dpv701102435.h1 Seq. ID

Method BLASTN g3021337 NCBI GI BLAST score 65 3.0e-28 E value Match length 176 85 % identity

NCBI Description Cicer arietinum mRNA for cytosolic fructose-1,6-bisphosphate aldolase

Seq. No. 43838

dpv701102477.h1 Seq. ID

Method BLASTX NCBI GI g4185136 BLAST score 211 2.0e-36 E value 83 Match length % identity 67



```
NCBI Description (AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No. 43839
Seq. ID dpv701102509.h1
Method BLASTN
```

NCBI GI g2656031
BLAST score 39
E value 6.0e-13
Match length 59
% identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC20

Seq. No. 43840

Seq. ID dpv701102520.h1

Method BLASTX
NCBI GI g3023443
BLAST score 202
E value 2.0e-16
Match length 49
% identity 73

NCBI Description CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5

(CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi 2258455 (AF008563) centromere-binding factor 5

[Kluyveromyces lactis]

Seq. No. 43841

Seq. ID dpv701102577.h1

Method BLASTX
NCBI GI g2252839
BLAST score 139
E value 6.0e-09
Match length 52
% identity 52

NCBI Description (AF013293) Similar to receptor-like protein kinase precusor

[Arabidopsis thaliana]

Seq. No. 43842

Seq. ID dpv701102691.h1

Method BLASTX
NCBI GI g2660670
BLAST score 195
E value 1.0e-15
Match length 66
% identity 64

NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis

thaliana]

Seq. No. 43843

Seq. ID dpv701102718.h1

Method BLASTN
NCBI GI g3452139
BLAST score 195
E value 1.0e-106
Match length 263
% identity 97

6982

Seq. ID

NCBI GI

Method



```
NCBI Description Glycine max mRNA for resistance protein, partial
                  43844
Seq. No.
                  dpv701102722.hl
Seq. ID
Method
                  BLASTN
                  q1808591
NCBI GI
                  109
BLAST score
                   2.0e-54
E value
                   172
Match length
                   91
% identity
NCBI Description C.arietinum mRNA for SAM-synthetase
                   43845
Seq. No.
                   dpv701102816.h1
Seq. ID
                   BLASTN
Method
                   g505584
NCBI GI
BLAST score
                   104
                   2.0e-51
E value
                   236
Match length
                   86
% identity
                  G.max mRNA for Glyoxalase I
NCBI Description
                   43846
Seq. No.
                   dpv701102845.h1
Seq. ID
                   BLASTX
Method
                   g4490306
NCBI GI
BLAST score
                   315
                   2.0e-29
E value
                   91
Match length
% identity
                   68
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   43847
 Seq. No.
                   dpv701102851.h1
 Seq. ID
                   BLASTX
Method
                   g2558938
NCBI GI
                   227
BLAST score
                   4.0e-19
 E value
                   93
Match length
                   55
 % identity
                   (AF024625) arm repeat containing protein [Brassica napus]
NCBI Description
                   43848
 Seq. No.
                   dpv701102854.h1
 Seq. ID
                   BLASTX
 Method
                   g4204304
 NCBI GI
                    279
 BLAST score
                    4.0e-25
 E value
                    74
 Match length
                    70
 % identity
                   (AC003027) lcl_prt seq No definition line found
 NCBI Description
                    [Arabidopsis thaliana]
                    43849
 Seq. No.
```

6983

dpv701102871.h1

BLASTN

g3168839



BLAST score 33 E value 4.0e-09 Match length 81 % identity 85

NCBI Description Arabidopsis thaliana copper homeostasis factor (CCH) mRNA,

complete cds

Seq. No. 43850

Seq. ID dpv701102904.h1

Method BLASTX
NCBI GI 9710626
BLAST score 207
E value 1.0e-16
Match length 53
% identity 68

NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis

thaliana]

Seq. No. 43851

Seq. ID dpv701102915.h1

Method BLASTX
NCBI GI g3420052
BLAST score 249
E value 1.0e-21
Match length 79
% identity 58

NCBI Description (AC004680) putative ubiqinone reductase [Arabidopsis

thaliana]

Seq. No. 43852

Seq. ID dpv701102977.h1

Method BLASTX
NCBI GI g2498731
BLAST score 176
E value 4.0e-13
Match length 45
% identity 73

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1

>gi_1362013_pir__S57611 zeta-crystallin homolog Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 43853

Seq. ID dpv701102985.h1

Method BLASTX
NCBI GI g2827555
BLAST score 318
E value 9.0e-30
Match length 84
% identity 71

NCBI Description (AL021635) Translation factor EF-1 alpha - like protein

[Arabidopsis thaliana]

Seq. No. 43854

Seq. ID dpv701103006.h1



```
Method
                  BLASTX
NCBI GI
                  g1871182
BLAST score
                  275
                  1.0e-24
E value
Match length
                  69
% identity
                  75
                 (U90439) phospholipase D isolog [Arabidopsis thaliana]
NCBI Description
                  43855
Seq. No.
Seq. ID
                  dpv701103010.h1
Method
                  BLASTN
NCBI GI
                  g170065
BLAST score
                  210
E value
                  1.0e-115
Match length
                  238
% identity
                  13
NCBI Description Soybean (G.max) proline-rich cell wall protein (SbPRP2)
                  gene, complete cds
                  43856
Seq. No.
                  dpv701103080.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080420
BLAST score
                  182
E value
                  8.0e-14
Match length
                . 86
% identity
                  44
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  43857
Seq. No.
Seq. ID
                  dpv701103091.h1
Method
                  BLASTX
NCBI GI
                  q4539306
BLAST score
                  304
                  4.0e-28
E value
Match length
                  82
                  20
% identity
NCBI Description (AL049480) pumilio-like protein [Arabidopsis thaliana]
                  43858
Seq. No.
Seq. ID
                  dpv701103094.h1
Method
                  BLASTX
                  g2499931
NCBI GI
BLAST score
                  150
E value
                  5.0e-10
Match length
                  38
% identity
                  71
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
                  >gi 2129534 pir S71272 adenine phosphoribosyltransferase
                  (EC 2.4.2.7) - Arabidopsis thaliana
                  >qi 1321681 emb CAA65609 (X96866) adenine
                  phosphoribosyltransferase [Arabidopsis thaliana]
```

6985

43859

BLASTN

dpv701103144.hl

Seq. No. Seq. ID

Method

Match length

% identity

50

66



```
NCBI GI
                   g1619902
BLAST score
                   57
E value
                  7.0e-24
                  97
Match length
                  90
% identity
NCBI Description Glycine max thiol protease isoform B mRNA, partial cds
                  43860
Seq. No.
Seq. ID
                  dpv701103156.h1
Method
                  BLASTX
NCBI GI
                  q4038030
BLAST score
                  202
E value
                  3.0e-16
                  80
Match length
% identity
                  49
NCBI Description
                  (AC005936) putative protein kinase, 5' partial [Arabidopsis
                  thaliana]
Seq. No.
                  43861
Seq. ID
                  dpv701103159.h1
Method
                  BLASTX
NCBI GI
                  g2511693
BLAST score
                  323
E value
                  3.0e-30
Match length
                  72
                  76
% identity
NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
                  43862
Seq. No.
Seq. ID
                  dpv701103169.h1
Method
                  BLASTX
NCBI GI
                  g1857944
BLAST score
                  139
                  2.0e-15
E value
Match length
                  70
% identity
                  60
                  (U88666) serine kinase SRPK2 [Homo sapiens]
NCBI Description
                  >gi 4507221 ref NP 003129.1 pSRPK2 SFRS protein kinase
                  43863
Seq. No.
Seq. ID
                  dpv701103236.h1
Method
                  BLASTN
NCBI GI
                  q3322492
BLAST score
                  36
E value
                  6.0e-11
Match length
                  44
% identity
                  95
NCBI Description Treponema pallidum section 20 of 87 of the complete genome
Seq. No.
                  43864
                  dpv701103251.h1
Seq. ID
Method
                  BLASTX
                  g499301
NCBI GI
BLAST score
                  173
                  6.0e-13
E value
```

6986



NCBI Description (X77116) ABI1 [Arabidopsis thaliana] >gi_549981 (U12856) abscisic acid insensitive protein [Arabidopsis thaliana] >gi_4538937_emb_CAB39673.1_ (AL049483) protein phosphatase ABI1 [Arabidopsis thaliana]

Seq. No. 43865

Seq. ID dpv701103335.h1

Method BLASTN
NCBI GI g166421
BLAST score 32
E value 7.0e-09
Match length 44
% identity 93

NCBI Description Medicago sativa ubiquitin carrier protein mRNA, complete

cds

Seq. No. 43866

Seq. ID dpv701103337.h1 Method BLASTN

NCBI GI g3892698 BLAST score 37 E value 1.0e-11 Match length 53 % identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2

(ESSAII project)

Seq. No. 43867

Seq. ID dpv701103464.h1

Method BLASTN
NCBI GI g21012
BLAST score 53
E value 4.0e-21
Match length 106
% identity 93

NCBI Description Phaseolus vulgaris mRNA (pR-2) for glutamine synthetase

(GS,EC 6.3.1.2)

Seq. No. 43868

Seq. ID dpv701103496.h1

Method BLASTN
NCBI GI g21012
BLAST score 121
E value 1.0e-61
Match length 169
% identity 93

NCBI Description Phaseolus vulgaris mRNA (pR-2) for glutamine synthetase

(GS, EC 6.3.1.2)

Seq. No. 43869

Seq. ID dpv701103553.h1

Method BLASTX
NCBI GI g323230
BLAST score 142
E value 2.0e-09
Match length 66
% identity 45

6987

% identity

93



```
NCBI Description (M96687) polyprotein [Bovine viral diarrhea virus]
Seq. No.
                  43870
Seq. ID
                  dpv701103557.h1
Method
                  BLASTX
NCBI GI
                  g2887437
BLAST score
                  107
E value
                  5.0e-12
                  76
Match length
% identity
                  60
NCBI Description (AB007893) KIAA0433 [Homo sapiens]
                  43871
Seq. No.
Seq. ID
                  dpv701103559.h1
                  BLASTX
Method
NCBI GI
                  g4388826
BLAST score
                  201
E value
                  4.0e-16
Match length
                  79
                  48
% identity
NCBI Description (AC006528) hypothetical protein [Arabidopsis thaliana]
                  43872
Seq. No.
                  dpv701103566.h1
Seq. ID
                  BLASTX
Method
                  g3935168
NCBI GI
BLAST score
                  206
E value
                  1.0e-16
Match length
                  77
% identity
                  64
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]
                  43873
Seq. No.
Seq. ID
                  dpv701103639.h1
Method
                  BLASTX
NCBI GI
                  g3377507
BLAST score
                  210
E value
                  6.0e-33
                  84
Match length
                  89
% identity
                  (AF056026) auxin transport protein EIR1 [Arabidopsis
NCBI Description
                  thaliana] >gi 3661620 (AF093241) putative auxin efflux
                  carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459)
                  polar-auxin-transport efflux component AGRAVITROPIC 1
                  [Arabidopsis thaliana] >gi 4206709 (AF086906) root
                  gravitropism control protein [Arabidopsis thaliana]
Seq. No.
                  43874
Seq. ID
                  eep700863717.h1
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  407
                  3.0e-40
E value
                  80
Match length
```

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

BLAST score

Match length

E value

301

63

8.0e-28



```
Seq. No.
                   43875
Seq. ID
                  eep700863814.h1
                  {\tt BLASTX}
Method
NCBI GI
                  g2444174
BLAST score
                  370
                  7.0e-36
E value
                  78
Match length
                   91
% identity
                  (U94781) unconventional myosin [Helianthus annuus]
NCBI Description
Seq. No.
                   43876
Seq. ID
                   eep700863838.h1
Method
                  BLASTX
NCBI GI
                   g3885342
BLAST score
                   362
E value
                   6.0e-35
Match length
                  84
% identity
                  88
                  (AC005623) putative DNA polymerase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  43877
                  eep700863907.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760327
BLAST score
                  154
E value
                  1.0e-10
Match length
                  74
% identity
                  39
NCBI Description
                  (AC002130) F1N21.12 [Arabidopsis thaliana]
Seq. No.
                   43878
                   eep700863940.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4097880
BLAST score
                   290
E value
                  1.0e-26
                  70
Match length
                  74
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   43879
Seq. No.
Seq. ID
                  eep700863948.h1
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                   283
E value
                   9.0e-26
Match length
                  76
% identity
                  74
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   43880
                  eep700864006.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1223926
```

6989



```
% identity
NCBI Description
                  (U49741) Vigna radiata carboxypeptidase II mRNA, partial
                  cds [Vigna radiata]
                  43881
Seq. No.
Seq. ID
                  eep700864077.h1
                  BLASTX
Method
NCBI GI
                  q2388580
BLAST score
                  155
                  1.0e-10
E value
Match length
                  65
                  52
% identity
                 (AC000098) Similar to Sequence 10 from patent 5477002
NCBI Description
                  (gb 1253956). [Arabidopsis thaliana]
Seq. No.
                  43882
                  eep700864121.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023432
BLAST score
                  219
                  3.0e-18
E value
Match length
                  64
                  67
% identity
                  CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA
NCBI Description
                  3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT)
                  >gi 1785477 dbj BAA19102 (AB000408) caffeoyl-CoA
                  3-0-methyltransferase [Populus kitakamiensis]
Seq. No.
                  43883
Seq. ID
                  eep700864136.h1
Method
                  BLASTX
NCBI GI
                  g2266947
BLAST score
                  306
E value
                  2.0e-28
Match length
                  78
                  73
% identity
                  (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium
NCBI Description
                  hirsutum]
                  43884
Seq. No.
Seq. ID
                  eep700864158.h1
                  BLASTX
Method
NCBI GI
                  q4097880
BLAST score
                  437
E value
                  1.0e-43
Match length
                  86
% identity
                  98
                 (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  43885
Seq. No.
```

eep700864196.h1 Seq. ID

Method BLASTX NCBI GI g138364 BLAST score 198 E value 7.0e-16 Match length 62 66 % identity



NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi 210812 (M62738) coat protein [Bean pod mottle virus]

Seq. No. 43886

Seq. ID eep700864209.h1

Method BLASTX NCBI GI g138364 BLAST score 348 E value 3.0e-33 Match length 88 % identity 80

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 43887

eep700864284.h1 Seq. ID

Method BLASTX NCBI GI q4097880 BLAST score 215 E value 1.0e-17 45 Match length 91 % identity

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 43888

Seq. ID eep700864308.h1

Method BLASTX g416884 NCBI GI BLAST score 192 5.0e-15 E value Match length 75

% identity 48

NCBI Description GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (GAD-67) (67 KD GLUTAMIC ACID DECARBOXYLASE) >gi 482463 pir A46758

glutamate decarboxylase (EC 4.1.1.15) 1 - cat >gi 163859

(M18629) glutamic acid decarboxylase [Felis catus]

Seq. No. 43889

eep700864345.h1 Seq. ID

Method BLASTX NCBI GI g138364 BLAST score 150 4.0e-10 E value Match length 35 % identity 86

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 43890

Seq. ID eep700864439.h1

Method BLASTX



```
NCBI GI
                  q138364
BLAST score
                  116
E value
                  2.0e-12
Match length
                  71
                  66
% identity
NCBI Description
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >qi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  43891
Seq. ID
                  eep700864477.h1
Method
                  BLASTX
NCBI GI
                  g3158474
BLAST score
                  142
E value
                  3.0e-09
Match length
                  49
                  59
% identity
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
Seq. No.
                  43892
                  eep700864509.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3150410
BLAST score
                  211
E value
                  3.0e-17
Match length
                  87
% identity
                  56
NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]
                  43893
Seq. No.
Seq. ID
                  eep700864560.h1
Method
                  BLASTX
NCBI GI
                  g1279222
BLAST score
                  278
                  4.0e-25
E value
                 85
Match length
                  7
% identity
NCBI Description (X97455) specific tissue protein 2 [Cicer arietinum]
                  43894
Seq. No.
Seq. ID
                  eep700864721.h1
Method
                  BLASTX
                  g138365
NCBI GI
BLAST score
                  134
                  6.0e-19
E value
Match length
                  78
% identity
                  67
                  GENOME POLYPROTEIN M [CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23] >gi 75638 pir GNWEC genome polyprotein M -
                  cowpea aphid-borne mosaic virus >gi 58911 emb CAA25314
```

Seq. No. 43895

Seq. ID eep700864749.h1

Method BLASTX NCBI GI g229708

(X00729) precursor polypeptide [Cowpea mosaic virus]



BLAST score E value 4.0e-21 Match length 78 68 % identity

NCBI Description Bean pod mottle virus

Seq. No.

43896

eep700864781.h1 Seq. ID

BLASTX Method g138364 NCBI GI 155 BLAST score 2.0e-13 E value 59 Match length 66 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

43897 Seq. No.

eep700864784.h1 Seq. ID

Method BLASTX NCBI GI q138364 BLAST score 139 1.0e-17 E value Match length 61 % identity 84

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 43898

Seq. ID eep700864815.h1

BLASTX Method g1723182 NCBI GI BLAST score 257 1.0e-23 E value Match length 71 80 % identity

SUGAR CARRIER PROTEIN A >gi 169736 (L08197) sugar carrier NCBI Description

protein [Ricinus communis]

Seq. No. 43899

Seq. ID eep700864876.h1

Method BLASTX NCBI GI g1346520 BLAST score 414 5.0e-41E value Match length 81 95 % identity

S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE NCBI Description

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)

>gi 790978 emb CAA56590 (X80362) S-adenosyl-L-methionine

synthetase [Brassica juncea]

43900 Seq. No.



```
eep700864890.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097880
BLAST score
                  403
E value
                  9.0e-40
Match length
                  81
% identity
                 (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                  43901
                  eep700864933.hl
Seq. ID
Method
                  BLASTX
                  g2623248
NCBI GI
BLAST score
                  322
E value
                  8.0e-33
Match length
                  81
                  83
% identity
                  (AF030882) SU1 isoamylase [Zea mays]
NCBI Description
Seq. No.
                  43902
                  eep700865035.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1209756
BLAST score
                  361
                  8.0e-35
E value
Match length
                  76
                  88
% identity
                  (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
Seq. No.
                  43903
                  eep700865072.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g138364
                  373
BLAST score
E value
                  3.0e-36
                  87
Match length
                  78
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  43904
Seq. ID
                  eep700865090.hl
Method
                  BLASTX
NCBI GI
                  q2194142
BLAST score
                  156
                  5.0e-22
E value
Match length
                  68
                  78
% identity
                  (AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from
NCBI Description
                  this gene. [Arabidopsis thaliana]
```

Seq. No. 43905

Seq. ID eep700865106.h1

Method BLASTX NCBI GI g3738295



```
BLAST score
                   2.0e-21
E value
Match length
                   71
% identity
                   70
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                   43906
Seq. No.
                   eep700865143.hl
Seq. ID
                   BLASTX
Method
                   g2635195
NCBI GI
BLAST score
                   164
                   8.0e-12
E value
Match length
                   53
                   55
% identity
                   (Z99117) similar to hypothetical proteins [Bacillus
NCBI Description
                   subtilis] >gi_2635213_emb_CAB14708_ (Z99118) similar to
                   hypothetical proteins [Bacillus subtilis]
                   43907
Seq. No.
                   eep700865146.h1
Seq. ID
Method
                   BLASTX
                   g1743354
NCBI GI
                   213
BLAST score
                   1.0e-17
E value
Match length
                   52
                   75
% identity
                   (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
NCBI Description
Seq. No.
                   43908
                   eep700865177.h1
Seq. ID
                   BLASTX
Method
                   q2959781
NCBI GI
                   297
BLAST score
                   2.0e-27
E value
                   71
Match length
                   77
% identity
                   (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                   43909
Seq. No.
                   eep700865210.h1
Seq. ID
                   BLASTX
Method
                   g4185511
NCBI GI
                   322
BLAST score
                   4.0e-30
E value
                   70
Match length
                   87
% identity
                    (AF102822) actin depolymerizing factor 4 [Arabidopsis
NCBI Description
                   thaliana]
                   43910
 Seq. No.
                   eep700865217.h1
 Seq. ID
 Method
                   BLASTX
                   q1076485
 NCBI GI
 BLAST score
                    361
                    1.0e-34
 E value
 Match length
                    70
```

6995

97

% identity



```
NCBI Description
                  SAM-synthetase - chickpea (fragment)
                  >gi 732576 emb CAA59508 (X85252) SAM-synthetase [Cicer
                  arietinum]
Seq. No.
                  43911
Seq. ID
                  eep700865243.h1
Method
                  BLASTX
NCBI GI
                  g2760327
BLAST score
                  178
                  2.0e-13
E value
Match length
                  68
                  29
% identity
NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]
Seq. No.
                  43912
Seq. ID
                  eep700865248.h1
Method
                  BLASTX
                  g229708
NCBI GI
BLAST score
                  489
                  1.0e-49
E value
                  96
Match length
                  96
% identity
NCBI Description Bean pod mottle virus
Seq. No.
                  43913
                  eep700865283.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q136098
BLAST score
                  260
                  7.0e-23
E value
Match length
                  71
                  77
% identity
                  TROPOMYOSIN, MUSCLE >gi 161677 (J04669) tropomyosin
NCBI Description
                   [Trichostrongylus colubriformis]
                  43914
Seq. No.
Seq. ID
                  eep700865304.h1
                  BLASTX
Method
NCBI GI
                  g4314391
BLAST score
                  328
E value
                  7.0e-31
Match length
                  88
% identity
NCBI Description
                  (AC006232) unknown protein [Arabidopsis thaliana]
                  43915
                  eep700865337.hl
Seq. ID
                  BLASTX
Method
```

Seq. No.

NCBI GI g229708 BLAST score 201 E value 3.0e-16 Match length 45 73 % identity

NCBI Description Bean pod mottle virus

Seq. No. 43916

Seq. ID eep700865340.h1

6996



Method BLASTX
NCBI GI g4097880
BLAST score 332
E value 2.0e-33
Match length 86
% identity 85
NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 43917 Seq. ID eep700865350.h1

Method BLASTX
NCBI GI g138364
BLAST score 204
E value 2.0e-16
Match length 75
% identity 66

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 43918

Seq. ID eep700865362.h1

Method BLASTX
NCBI GI g138364
BLAST score 192
E value 6.0e-15
Match length 85
% identity 56

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 43919

Seq. ID eep700865377.h1

Method BLASTX
NCBI GI g3953463
BLAST score 144
E value 2.0e-16
Match length 57
% identity 68

NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No. 43920

Seq. ID eep700865446.h1

Method BLASTX
NCBI GI g4097880
BLAST score 302
E value 6.0e-33
Match length 84
% identity 89

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 43921

Seq. ID eep700865489.h1

Method BLASTX



```
NCBI GI
                   g138364
BLAST score
                  204
E value
                   1.0e-16
Match length
                  62
% identity
                  39
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639 pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                  43922
Seq. No.
Seq. ID
                  eep700865515.h1
Method
                  BLASTX
NCBI GI
                  g2105487
                  177
BLAST score
E value
                  2.0e-13
Match length
                   39
% identity
                   69
NCBI Description
                  (AF003739) partial CDS [Caenorhabditis elegans]
Seq. No.
                  43923
                  eep700865531.h1
Seq. ID
Method
                  BLASTX
                  q4097880
NCBI GI
BLAST score
                   345
                  5.0e-33
E value
Match length
                  75
                  85
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   43924
Seq. No.
                   eep700865542.h1
Seq. ID
Method
                  BLASTX
                  g4097880
NCBI GI
BLAST score
                  257
                  5.0e-23
E value
                  74
Match length
                   67
% identity
NCBI Description
                  (U70866) polyprotein [Bean pod mottle vírus]
Seq. No.
                   43925
Seq. ID
                  eep700865556.h1
Method
                  BLASTX
NCBI GI
                  q4097880
BLAST score
                   272
E value
                   2.0e-24
Match length
                  75
                   69
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   43926
```

Seq. ID eep700865578.h1 BLASTX Method

NCBI GI q138364 BLAST score 162 E value 2.0e-23 76 Match length

Match length

% identity

59



```
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi 210812
                   (M62738) coat protein [Bean pod mottle virus]
                  43927
Seq. No.
Seq. ID
                  eep700865582.h1
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  148
E value
                  6.0e-10
                  32
Match length
                  91
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  43928
Seq. ID
                  eep700865583.h1
Method
                  BLASTX
NCBI GI
                  q3192042
BLAST score
                  239
E value
                  1.0e-20
Match length
                  75
                  57
% identity
NCBI Description (AL023796) phosphoglucomutase [Schizosaccharomyces pombe]
Seq. No.
                  43929
                  eep700865620.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3367568
BLAST score
                  306
E value
                  3.0e-28
Match length
                  86
% identity
                  66
NCBI Description
                   (AL031135) protein kinase - like protein [Arabidopsis
                  thaliana]
                  43930
Seq. No.
Seq. ID
                  eep700865690.h1
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  419
E value
                  1.0e-41
Match length
                  84
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  43931
                  eep700865730.h1
Seq. ID
Method
                  BLASTX
                  g4103959
NCBI GI
BLAST score
                  301
E value
                  9.0e-28
```

NCBI Description (AF030033) calmodulin [Phaseolus vulgaris]



```
Seq. No.
                  43932
Seq. ID
                  eep700865756.h1
Method
                  BLASTX
NCBI GI
                  g4097880
                  347
BLAST score
E value
                  3.0e-33
Match length
                  83
                  82
% identity
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  43933
Seq. ID
                  eep700865764.h1
Method
                  BLASTX
NCBI GI
                  g4415933
BLAST score
                  226
E value
                  6.0e-19
Match length
                  84
                  54
% identity
                  (AC006418) putative cellular apoptosis susceptibility
NCBI Description
                  protein [Arabidopsis thaliana]
                  >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative
                  cellular apoptosis susceptibility protein [Arabidopsis
                  thaliana]
Seq. No.
                  43934
                  eep700865774.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q229708
BLAST score
                  236
                  2.0e-20
E value
Match length
                  45
                  98
% identity
NCBI Description Bean pod mottle virus
                  43935
Seq. No.
Seq. ID
                  eep700865806.h1
Method
                  BLASTX
NCBI GI
                  g229708
BLAST score
                  368
E value
                  9.0e-36
Match length
                  75
% identity
                  91
NCBI Description Bean pod mottle virus
Seq. No.
                  43936
                  eep700865886.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2117700
BLAST score
                  286
E value
                  4.0e-26
Match length
                  61
% identity
NCBI Description transketolase (EC 2.2.1.1) precursor - potato (fragment)
```

Method BLASTX

43937

eep700865924.h1

Seq. No. Seq. ID



```
g138364
NCBI GI
BLAST score
                  444
                  1.0e-44
E value
                  81
Match length
% identity
                  98
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle vīrus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                   43938
Seq. No.
                   eep700865960.h1
Seq. ID
                   BLASTX
Method
                   q3298539
NCBI GI
BLAST score
                   207
E value
                   8.0e-17
Match length
                   80
% identity
                   55
                   (AC004681) NPK1-related protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   43939
Seq. No.
                   eep700865961.hl
Seq. ID
                   BLASTX
Method
                   g4097880
NCBI GI
BLAST score
                   383
                   2.0e-37
E value
Match length
                   80
                   93
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   43940
Seq. No.
                   eep700866038.h1
Seq. ID
                   BLASTX
Method
                   g2384669
NCBI GI
                   381
BLAST score
                   3.0e-37
E value
                   82
Match length
                   84
% identity
                   (AF012656) putative potassium transporter AtKT1p
NCBI Description
                   [Arabidopsis thaliana]
                   43941
Seq. No.
                   eep700866067.hl
Seq. ID
                   BLASTX
Method
                   g2317900
NCBI GI
                   381
BLAST score
                   3.0e-37
E value
                   74
Match length
                   95
% identity
NCBI Description (U89693) Sali3-2 [Glycine max]
```

Seq. No.

43942

eep700866068.hl Seq. ID

BLASTX Method NCBI GI g138364 321 BLAST score



3.0e - 30E value 79 Match length % identity 84 GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle vīrus (straīn Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus] 43943 Seq. No.

eep700866124.h1 Seq. ID BLASTX Method q3935138 NCBI GI 208 BLAST score 7.0e-17 E value 72 Match length 57 % identity

(AC005106) T25N20.2 [Arabidopsis thaliana] NCBI Description

43944 Seq. No. eep700866138.hl Seq. ID BLASTX Method g3913008 NCBI GI 273 BLAST score

2.0e-27 E value 74 Match length 93 % identity

FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME NCBI Description >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic

fructose-1,6-bisphosphate aldolase [Cicer arietinum]

43945 Seq. No.

eep700866148.hl Seq. ID

BLASTX Method q4580393 NCBI GI 178 BLAST score 2.0e-13 E value 66 Match length 53 % identity

(AC007171) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

eep700866154.h1 Seq. ID

BLASTX Method q138364 NCBI GI BLAST score 256 E value 1.0e-22 74 Match length 72 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

43947 Seq. No.

eep700866217.h1 Seq. ID

BLASTX Method g3334162 NCBI GI

```
BLAST score 106
E value 7.0e-09
Match length 51
% identity 61
NCBI Description DOWN SYNDROME CRITICAL REGION PROTEIN A
>gi_2588993_dbj_BAA23270_ (AB001990) Dcra [Mus musculus]
```

Seq. ID eep700866220.h1
Method BLASTX
NCBI GI g2501296
BLAST score 260
E value 6.0e-23
Match length 88
% identity 55

Seq. No.

43948

% identity 55
NCBI Description DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA

gyrase B subunit [Synechocystis sp.]

 Seq. No.
 43949

 Seq. ID
 eep700866368.h1

 Method
 BLASTX

 NCBI GI
 g4097880

 BLAST score
 388

BLAST score 388
E value 4.0e-38
Match length 83
% identity 93

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 43950

Seq. ID eep700866375.h1

Method BLASTX
NCBI GI g2335108
BLAST score 342
E value 1.0e-32
Match length 82
% identity 74

NCBI Description (AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No. 43951

Seq. ID eep700866402.h1

Method BLASTX
NCBI GI g2398525
BLAST score 177
E value 3.0e-13
Match length 53
% identity 62

NCBI Description (Y13722) Transcription factor [Arabidopsis thaliana]

Seq. No. 43952

Seq. ID eep700866411.hl

Method BLASTX
NCBI GI g729442
BLAST score 211
E value 2.0e-17
Match length 62
% identity 43

NCBI Description PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR



>gi_166380 (M80235) glucose-regulated endoplasmic reticular protein precursor [Medicago sativa]

43953 Seq. No. eep700866441.hl Seq. ID BLASTX Method g1176081 NCBI GI 168 BLAST score 3.0e-12E value Match length 80 % identity 42 HYPOTHETICAL PROTEIN HI0671 >gi_1074478_pir__F64156 NCBI Description hypothetical protein HI0671 - Haemophilus influenzae (strain Rd KW20) >gi_1573672 (U32750) conserved hypothetical protein [Haemophilus influenzae Rd] 43954 Seq. No. eep700866457.h1 Seq. ID BLASTX Method q4097880 NCBI GI BLAST score 291 E value 2.0e-32 76 Match length 91 % identity (U70866) polyprotein [Bean pod mottle virus] NCBI Description 43955 Seq. No. eep700866461.h1 Seq. ID Method BLASTX g138364 NCBI GI 273 BLAST score 2.0e-34 E value 81 Match length 100 % identity GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus] 43956 Seq. No. eep700866480.h1 Seq. ID BLASTX Method g3395431 NCBI GI 289 BLAST score 2.0e-26 E value 80 Match length 66 % identity NCBI Description (AC004683) unknown protein [Arabidopsis thaliana] 43957 Seq. No. eep700866484.hl Seq. ID BLASTX Method q505100 NCBI GI 158 BLAST score

4.0e-11

61

56

E value

Match length % identity



(D31886) KIAA0066 [Homo sapiens] NCBI Description

43958 Seq. No.

eep700866514.hl Seq. ID

BLASTX Method g138364 NCBI GI 160 BLAST score 3.0e-15 E value 62 Match length 73 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle vīrus (straīn Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

43959 Seq. No.

eep700866518.hl Seq. ID

BLASTX Method q4371296 NCBI GI 225 BLAST score 4.0e-19 E value 64 Match length 72 % identity

(AC006260) putative receptor protein kinase [Arabidopsis NCBI Description

thaliana]

43960 Seq. No.

eep700866539.hl Seq. ID

BLASTX Method q138364 NCBI GI 250 BLAST score 9.0e-22 E value 83 Match length 66 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

43961 Seq. No.

eep700866542.h1 Seq. ID

BLASTX Method q4097880 NCBI GI 207 BLAST score E value 6.0e-17 62 Match length 65 % identity

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

43962 Seq. No.

eep700866546.hl Seq. ID

BLASTX Method q138364 NCBI GI 250 BLAST score 1.0e-24 E value Match length 76 82 % identity

7005



GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

43963 Seq. No.

NCBI Description

eep700866612.h1 Seq. ID

BLASTX Method g4097880 NCBI GI 161 BLAST score 2.0e-11 E value 48 Match length 71 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

43964 Seq. No.

eep700866623.h1 Seq. ID

BLASTX Method g4097880 NCBI GI 318 BLAST score 8.0e-30 E value 79 Match length 84 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

43965 Seq. No.

eep700866627.h1 Seq. ID

BLASTX Method g2980774 NCBI GI 182 BLAST score 8.0e-14 E value 46 Match length

76 % identity

(AL022198) leucyl aminopeptidase - like protein NCBI Description

[Arabidopsis thaliana]

43966 Seq. No.

eep700866632.h1 Seq. ID

BLASTX Method g2194126 NCBI GI 196 BLAST score 2.0e-15 E value 73 Match length 48 % identity

(AC002062) EST gb_T43335 comes from this gene. [Arabidopsis NCBI Description

thaliana]

43967 Seq. No.

eep700866704.h1 Seq. ID

BLASTX Method NCBI GI q138364 331 BLAST score 3.0e - 31E value 88 Match length 80 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -





bean pod mottle virus (strain Kentucky G7) >gi_210812 (M62738) coat protein [Bean pod mottle virus]

 Seq. No.
 43968

 Seq. ID
 eep700866793.h1

 Method
 BLASTX

 NCBI GI
 g4115905

 BLAST score
 210

E value 4.0e-17 Match length 78 % identity 89

NCBI Description (AF072131) secondary xylem cellulose synthase [Populus

tremuloides]

Seq. No. 43969

Seq. ID eep700866804.h1

Method BLASTX
NCBI GI g3176662
BLAST score 276
E value 8.0e-25
Match length 68
% identity 74

NCBI Description (AC004393) Similar to mannosyl-oligosaccharide glucosidase

gb X87237 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 43970

Seq. ID eep700866811.hl

Method BLASTX
NCBI GI g2829923
BLAST score 383
E value 2.0e-37
Match length 86
% identity 33

NCBI Description (AC002291) Similar to uridylyl transferases [Arabidopsis

thaliana]

Seq. No. 43971

Seq. ID eep700866832.h1

Method BLASTX
NCBI GI g1888357
BLAST score 180
E value 1.0e-13
Match length 68
% identity 49

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 43972

Seq. ID eep700866838.h1

Method BLASTX
NCBI GI g3292829
BLAST score 277
E value 4.0e-25
Match length 58
% identity 88

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]



```
Seq. No.
                  43973
                  eep700866857.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244913
BLAST score
                  217
E value
                  6.0e-18
Match length
% identity
                  56
NCBI Description
                  (Z97339) similar to SEN1 protein - yeast [Arabidopsis
                  thaliana]
Seq. No.
                  43974
Seq. ID
                  eep700866859.h1
Method
                  BLASTX
NCBI GI
                  a3142289
BLAST score
                  149
E value
                  6.0e-10
Match length
                  62
                  52
% identity
                  (AC002411) Strong similarity to beta-keto-Coa synthase
NCBI Description
                  gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
Seq. No.
                  43975
                  eep700866876.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  a138364
BLAST score
                  269
E value
                  5.0e-24
Match length
                  81
% identity
                  70
NCBI Description
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                  43976
Seq. ID
                  eep700866905.hl
Method
                  BLASTX
                  g229708
NCBI GI
BLAST score
                  241
E value
                  8.0e-21
Match length
                  53
% identity
                  92
NCBI Description Bean pod mottle virus
Seq. No.
                  43977
Seq. ID
                  eep700866915.hl
Method
                  BLASTX
                  q3850588
NCBI GI
```

Method BLASTX

NCBI GI g3850588

BLAST score 229

E value 2.0e-19

Match length 75

% identity 57

NCBI Description (AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come



from this gene. [Arabidopsis thaliana]

```
43978
Seq. No.
                  eep700866966.hl
Seq. ID
                  BLASTX
Method
                  q2624383
NCBI GI
BLAST score
                  403
                  9.0e-40
E value
                  80
Match length
                  96
% identity
                  (Y09447) cinnamate 4-hydroxylase [Phaseolus vulgaris]
NCBI Description
                  43979
Seq. No.
                  eep700867030.hl
Seq. ID
Method
                  BLASTX
                  g2980794
NCBI GI
                  200
BLAST score
                  6.0e-16
E value
                  47
Match length
                  79
% identity
                  (AL022197) myb - like protein [Arabidopsis thaliana]
NCBI Description
                  43980
Seq. No.
                  eep700867066.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538911
                  370
BLAST score
                  6.0e-36
E value
Match length
                  82
% identity
                  83
                  (ALO49482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   43981
Seq. No.
                  eep700867067.hl
Seq. ID
                  BLASTX
Method
                  g3367534
NCBI GI
BLAST score
                   395
                   7.0e-39
E value
                   79
Match length
                   30
% identity
                   (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                   (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                   thaliana]
Seq. No.
                   43982
                   eep700867082.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q138364
BLAST score
                   311
E value
                   5.0e-29
                   78
Match length
% identity
                   81
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                   PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
```

(M62738) coat protein [Bean pod mottle virus]

bean pod mottle virus (strain Kentucky G7) >gi_210812



```
43983
Seq. No.
                  eep700867143.h1
Seq. ID
                  BLASTX
Method
                  g2288985
NCBI GI
                  159
BLAST score
                  4.0e-11
E value
                  75
Match length
                  44
% identity
                  (AC002335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  43984
Seq. No.
                  eep700867158.h1
Seq. ID
                  BLASTX
Method
                  g138364
NCBI GI
BLAST score
                  441
                  3.0e-44
E value
Match length
                  88
                  99
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle vīrus (straīn Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
                  43985
Seq. No.
                  eep700867423.h1
Seq. ID
                  BLASTX
Method
                  g4097880
NCBI GI
                  291
BLAST score
                  1.0e-26
E value
Match length
                  57
                  100
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   43986
Seq. No.
                   eep700867485.h1
Seq. ID
                   BLASTX
Method
                   q4097880
NCBI GI
BLAST score
                   326
                   9.0e-31
E value
                   79
Match length
% identity
                   85
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   43987
Seq. No.
                   eep700867504.h1
Seq. ID
                   BLASTX
Method
                   q3805849
NCBI GI
```

225 BLAST score E value 6.0e-19 63 Match length % identity 68

(AL031986) cytoplasmatic aconitate hydratase (citrate NCBI Description hydro-lyase) (aconitase) (EC 4.2.1.3) [Arabidopsis thaliana]

43988 Seq. No.

Seq. ID eep700867510.hl

Method BLASTX



```
NCBI GI g4097880
BLAST score 453
E value 2.0e-45
Match length 91
% identity 96
```

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No. 43989

Seq. ID eep700867516.hl

Method BLASTX
NCBI GI g138364
BLAST score 313
E value 4.0e-29
Match length 88
% identity 98

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 43990

Seq. ID eep700867557.h1

Method BLASTX
NCBI GI g138364
BLAST score 232
E value 1.0e-19
Match length 78
% identity 62

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 43991

Seq. ID eep700867562.h1

Method BLASTX
NCBI GI g138364
BLAST score 199
E value 6.0e-28
Match length 87
% identity 79

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 43992

Seq. ID eep700867572.h1

Method BLASTX
NCBI GI g138364
BLAST score 254
E value 1.0e-22
Match length 77
% identity 81

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi_210812

Seq. ID

Method

NCBI GI





(M62738) coat protein [Bean pod mottle virus]

```
43993
Seq. No.
                   eep700867582.hl
Seq. ID
Method
                  BLASTX
                   g4097880
NCBI GI
                   320
BLAST score
                   3.0e-30
E value
                   73
Match length
                   86
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   43994
Seq. No.
                   eep700867612.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3158476
BLAST score
                   292
                   9.0e-27
E value
Match length
                   69
                   84
% identity
                  (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
                   43995
Seq. No.
                   eep700867665.hl
Seq. ID
                   BLASTX
Method
                   g4580517
NCBI GI
                   140
BLAST score
                   6.0e-09
E value
Match length
                   71
                   48
% identity
                  (AF036302) scarecrow-like 5 [Arabidopsis thaliana]
NCBI Description
                   43996
Seq. No.
                   eep700867711.h1
Seq. ID
                   BLASTX
Method
                   g4558550
NCBI GI
                   355
BLAST score
                   3.0e-34
E value
                   79
Match length
                   84
% identity
                   (AC007138) putative protein transport factor [Arabidopsis
NCBI Description
                   thaliana]
                   43997
Seq. No.
                   eep700867817.h1
Seq. ID
                   BLASTX
Method
                   g4262179
NCBI GI
                   220
BLAST score
                   3.0e-18
E value
Match length
                   92
                   21
% identity
NCBI Description (AC005508) 27668 [Arabidopsis thaliana]
                   43998
Seq. No.
```

eep700867835.hl

BLASTX

g4097880

```
BLAST score
                   3.0e-46
E value
                   89
Match length
                   98
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   43999
Seq. No.
                   eep700867863.h1
Seq. ID
                   BLASTX
Method
                   g4204276
NCBI GI
                   227
BLAST score
                   5.0e-19
E value
                   74
Match length
                   57
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   44000
Seq. No.
                   eep700867867.hl
Seq. ID
                   BLASTX
Method
                   g2598575
NCBI GI
                   159
BLAST score
                   4.0e-11
E value
                   53
Match length
                   55
% identity
                  (Y15293) MtN21 [Medicago truncatula]
NCBI Description
                   44001
Seq. No.
                   eep700867875.h1
Seq. ID
                   BLASTX
Method
                   g1076914
NCBI GI
                   198
BLAST score
                   6.0e-16
E value
                   71
Match length
                   55
% identity
                   protein phosphatase 2C - fission yeast (Schizosaccharomyces
NCBI Description
                   pombe) >gi_609658 (L34882) protein phosphatase 2C (ptc3+)
                   [Schizosaccharomyces pombe]
                   44002
Seq. No.
                   eep700867876.hl
Seq. ID
                   BLASTX
Method
                   q4539324
NCBI GI
                   180
BLAST score
                   2.0e-13
E value
                   44
Match length
                   75
% identity
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]
                   44003
Seq. No.
                   eep700867907.hl
Seq. ID
Method
                   BLASTX
                   q3763925
NCBI GI
```

Method BLASTX
NCBI GI g3763925
BLAST score 156
E value 8.0e-11
Match length 38
% identity 84

NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]



```
44004
Seq. No.
                    eep700867951.h1
Seq. ID
                    BLASTX
Method
                    g138364
NCBI GI
                    364
BLAST score
                    3.0e-35
E value
                    80
Match length
                    93
% identity
                    GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                    PROTEIN VP23) >gi 75639_pir__GNWXG7 genome polyprotein M -
                    bean pod mottle virus (strain Kentucky G7) >gi_210812
                    (M62738) coat protein [Bean pod mottle virus]
 Seq. No.
                    44005
                    eep700867971.hl
 Seq. ID
                    BLASTX
 Method
                    q3367574
 NCBI GI
                    157
BLAST score
                    4.0e-11
E value
                    77
 Match length
                    48
 % identity
                    (AL031135) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    44006
 Seq. No.
                    eep700867974.h1
 Seq. ID
                    BLASTX
 Method
                    g1169533
 NCBI GI
                    245
 BLAST score
                    2.0e-21
 E value
                    57
 Match length
                    79
 % identity
                    ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
 NCBI Description
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                    >gi 515827_emb_CAA56645_ (X80474) enolase [Neocallimastix
                    frontalis]
                    44007
 Seq. No.
                    eep700868013.h1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q114974
                    242
 BLAST score
                    7.0e-21
 E value
                    72
 Match length
                    62
 % identity
                    NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR
 NCBI Description
                    >gi_67491_pir__GLJY31 beta-glucosidase (EC 3.2.1.21)
                    precursor (clone TRE361) - white clover
>gi_21955_emb_CAA40058.1_ (X56734) beta-glucosidase
                     [Trifolium repens]
```

Seq. ID eep700868032.h1

Method BLASTX
NCBI GI g2832694
BLAST score 174
E value 7.0e-13



```
Match length
                  20
% identity
                  (AL021713) putative protein [Arabidopsis thaliana]
NCBI Description
                  44009
Seq. No.
                  eep700868050.h1
Seq. ID
                  BLASTX
Method
                  q2244973
NCBI GI
BLAST score
                  253
                  4.0e-22
E value
                  81
Match length
                  58
% identity
                  (Z97340) similarity to extensin class 1 protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  44010
                  eep700868113.h1
Seq. ID
Method
                  BLASTX
                  g4097880
NCBI GI
BLAST score
                  142
                  6.0e-22
E value
Match length
                  80
% identity
                  82
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   44011
Seq. No.
                   eep700868186.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3341679
BLAST score
                   273
                   1.0e-24
E value
Match length
                   77
% identity
                   66
                  (AC003672) dynamin-like protein phragmoplastin 12
NCBI Description
                   [Arabidopsis thaliana]
                   44012
Seq. No.
                   eep700868226.hl
Seq. ID
                   BLASTX
Method
                   g3738257
NCBI GI
BLAST score
                   316
E value
                   1.0e-29
                   70
Match length
                   87
% identity
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                   nigra]
                   44013
Seq. No.
                   eep700868237.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3046815
BLAST score
                   188
```

NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]

1.0e-14

67

61

E value Match length

% identity



```
44014
Seq. No.
                   eep700868302.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4097880
BLAST score
                   402
                   1.0e-39
E value
Match length
                   81
% identity
                   96
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   44015
Seq. No.
                   eep700868320.hl
Seq. ID
Method
                   BLASTX
                   g2827516
NCBI GI
BLAST score
                   238
E value
                   2.0e-20
Match length
                   59
% identity
                   78
                  (ALO21633) DNA topoisomerase like- protein [Arabidopsis
NCBI Description
                   thaliana]
                   44016
Seq. No.
Seq. ID
                   eep700868419.h1
Method
                   BLASTX
NCBI GI
                   g3913008
BLAST score
                   246
E value
                   2.0e-21
                   61
Match length
                   80
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                   >qi 3021338 emb CAA06308_ (AJ005041) cytosolic
                   fructose-1,6-bisphosphate aldolase [Cicer arietinum]
                   44017
Seq. No.
                   eep700868424.h1
Seq. ID
                   BLASTX
Method
                   g1653619
NCBI GI
                   221
BLAST score
                   2.0e-18
E value
                   87
Match length
% identity
                   48
                  (D90915) spermidine/putrescine-binding periplasmic protein
NCBI Description
                   [Synechocystis sp.]
                   44018
Seq. No.
                   eep700868433.hl
Seq. ID
                   BLASTX
Method
```

g4097880 NCBI GI BLAST score 157 3.0e-14E value 78 Match length % identity 63

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

44019 Seq. No.

Seq. ID eep700868442.h1

Method BLASTX

```
q4097880
NCBI GI
                  307
BLAST score
                  1.0e-28
E value
                  79
Match length
                  71
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  44020
Seq. No.
                  eep700868463.hl
Seq. ID
                  BLASTX
Method
                  g137091
NCBI GI
                  466
BLAST score
                  4.0e-47
E value
                  89
Match length
% identity
                   99
                  UREASE (UREA AMIDOHYDROLASE) >gi 170084 (M16772) urease
NCBI Description
                   [Glycine max]
                   44021
Seq. No.
                   eep700868471.h1
Seq. ID
Method
                  BLASTX
                   g2104949
NCBI GI
                   134
BLAST score
                   4.0e-12
E value
Match length
                  76
                   64
% identity
                  (U96716) MAP kinase-like protein [Selaginella lepidophylla]
NCBI Description
                   44022
Seq. No.
                   eep700868475.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4097880
                   301
BLAST score
                   8.0e-28
E value
Match length
                   83
% identity
                   71
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
                   44023
Seq. No.
                   eep700868515.h1
Seq. ID
                   BLASTX
Method
                   q4006899
NCBI GI
                   163
BLAST score
                   2.0e-11
E value
Match length
                   54
% identity
                   56
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   44024
```

Seq. ID eep700868544.h1

Method BLASTX
NCBI GI g4097880
BLAST score 455
E value 8.0e-46
Match length 87
% identity 99

NCBI Description (U70866) polyprotein [Bean pod mottle virus]



eep700868586.h1 Seq. ID

Method BLASTX q138364 NCBI GI 284 BLAST score 8.0e-26 E value 79 Match length % identity 78

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. eep700868596.h1 Seq. ID

44026

BLASTX Method q138364 NCBI GI 240 BLAST score 1.0e-20 E value Match length 82 85 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

44027 Seq. No.

eep700868617.hl Seq. ID

BLASTX Method q138364 NCBI GI 489 BLAST score 9.0e-50 E value 89 Match length 99 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

44028 Seq. No.

eep700868620.h1 Seq. ID

BLASTX Method q2811029 NCBI GI BLAST score 300 1.0e-27 E value 78 Match length 72 % identity

NCBI Description ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT)

(ACETYLORNITHINE TRANSAMINASE) (AOTA)

>gi_1944511_emb_CAA69936_ (Y08680) acetylornithine

aminotransferase [Alnus glutinosa]

44029 Seq. No.

Seq. ID eep700868629.h1

Method BLASTX NCBI GI g138364



BLAST score 4.0e-39 E value 85 Match length % identity 89

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M -

bean pod mottle vīrus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

44030 Seq. No.

eep700868664.hl Seq. ID

BLASTX Method g417444 NCBI GI 252 BLAST score E value 6.0e-22 Match length 64

80 % identity

PHENYLALANINE AMMONIA-LYASE 2 >gi_217984_dbj_BAA00887_ NCBI Description

(D10003) phenylalanine ammonia-lyase [Pisum sativum]

Seq. No.

44031 eep700868689.h1 Seq. ID

BLASTXMethod g2317905 NCBI GI BLAST score 206 9.0e-17 E value 69 Match length % identity 62

(U89959) bZIP-like protein [Arabidopsis thaliana] NCBI Description

Seq. No.

eep700868691.h1 Seq. ID

44032

BLASTX Method g4097880 NCBI GI BLAST score 387 6.0e-38 E value Match length 82 90 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

44033 Seq. No.

eep700868717.h1 Seq. ID

BLASTX Method NCBI GI g138364 BLAST score 221 E value 3.0e-18 92 Match length 51 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

44034 Seq. No.

eep700868743.h1 Seq. ID

Method BLASTX NCBI GI g138364



BLAST score 340 E value 2.0e-32 Match length 80 % identity 82

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M - bean pod mottle virus (strain Kentucky G7) >gi 210812

Dean pod mottre virus (Strain Renducky G7) 291_4

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 44035

Seq. ID eep700868764.hl

Method BLASTX
NCBI GI g1332579
BLAST score 228
E value 2.0e-26
Match length 69
% identity 10

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 44036

Seq. ID eep700868786.h1

Method BLASTX
NCBI GI g1742953
BLAST score 132
E value 1.0e-11
Match length 55

Match length 55 % identity 69

NCBI Description (Z71445) CLC-a chloride channel protein [Arabidopsis

thaliana]

44037

Seq. No.

Seq. ID eep700868795.h1

Method BLASTX
NCBI GI g4097880
BLAST score 254
E value 2.0e-22
Match length 58
% identity 86

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

44038

Seq. ID eep700868867.h1

Method BLASTX
NCBI GI g3885334
BLAST score 188
E value 1.0e-14
Match length 56
% identity 64

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thaliana]

Seq. No. 44039

Seq. ID eep700868875.h1

Method BLASTX
NCBI GI g4539343
BLAST score 323
E value 2.0e-30



Match length 90 % identity

(AL035539) putative protein [Arabidopsis thaliana] NCBI Description

44040 Seq. No.

eep700868906.h1 Seq. ID

BLASTX Method g138364 NCBI GI BLAST score 342 1.0e-32 E value Match length 87 78 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

44041 Seq. No.

eep700868922.h1 Seq. ID

BLASTX Method g138364 NCBI GI 256 BLAST score 2.0e-31 E value 84 Match length 78 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle vīrus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 44042

eep700868936.h1 Seq. ID

BLASTX Method NCBI GI g4115915 BLAST score 141 5.0e-09 E value Match length 86 36 % identity

(AF118222) contains similarity to Helix pomatia br-1 NCBI Description

protein (GB: X96994) [Arabidopsis thaliana]

44043 Seq. No.

eep700868942.hl Seq. ID

BLASTX Method NCBI GI q138364 BLAST score 310 7.0e-29 E value 74 Match length 84 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

44044 Seq. No.

eep700868978.hl Seq. ID

Method BLASTX



```
q3355477
NCBI GI
BLAST score
                  326
E value
                  9.0e-31
Match length
                  72
% identity
                  (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis
NCBI Description
                  thaliana]
                  44045
Seq. No.
Seq. ID
                  eep700869016.h1
Method
                  BLASTX
NCBI GI
                  g4097880
BLAST score
                  396
                  5.0e-39
E value
                  80
Match length
% identity
                  95
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                  44046
Seq. No.
                  eep700869139.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2500354
BLAST score
                  295
                  2.0e-29
E value
                   65
Match length
                   98
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_
NCBI Description
                   (AB001891) QM family protein [Solanum melongena]
                   44047
Seq. No.
Seq. ID
                   eep700869156.h1
Method
                  BLASTX
                   q267069
NCBI GI
                   208
BLAST score
                   4.0e-17
E value
Match length
                   38
% identity
                   97
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   44048
Seq. No.
                   eep700869225.h1
Seq. ID
                   BLASTX
Method
                   g1906845
NCBI GI
BLAST score
                   298
                   2.0e-27
E value
Match length
                   81
                   65
% identity
                  (Y07550) cellulose 1,4-beta-cellobiosidase [Claviceps
NCBI Description
```

purpurea]

44049 Seq. No.

eep700869305.h1 Seq. ID

BLASTX Method NCBI GI g2342683



```
BLAST score
                  9.0e-30
E value
Match length
                  80
                  81
% identity
                  (AC000106) Contains similarity to Bos beta-mannosidase
NCBI Description
                  (gb U46067). [Arabidopsis thaliana]
                  44050
Seq. No.
                  eep700869321.h1
Seq. ID
Method
                  BLASTX
                  g2245065
NCBI GI
BLAST score
                  244
E value
                  4.0e-21
Match length
                  84
% identity
                  (Z97342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  44051
                  eep700869327.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2979552
BLAST score
                  187
                  4.0e-25
E value
Match length
                  81
% identity
                  (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   44052
Seq. No.
Seq. ID
                   eep700869389.h1
Method
                  BLASTX
                  g4097880
NCBI GI
BLAST score
                  209
                   3.0e-36
E value
                  80
Match length
                  93
% identity
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   44053
Seq. No.
                   eep700869390.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                   g229708
                   209
BLAST score
                   5.0e-17
E value
                   105
Match length
                   63
% identity
NCBI Description Bean pod mottle virus
                   44054
Seq. No.
                   eep700869483.h2
```

Seq. ID

Method BLASTX g229708 NCBI GI BLAST score 144 2.0e-09 E value Match length 32 91 % identity

NCBI Description Bean pod mottle virus



Seq. ID eep700869501.h1

Method BLASTX
NCBI GI g138364
BLAST score 429
E value 9.0e-43
Match length 84
% identity 100

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 44056

Seq. ID eep700869517.h1

Method BLASTX
NCBI GI g138364
BLAST score 419
E value 1.0e-41
Match length 84
% identity 99

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT

PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 44057

Seq. ID eep700869537.h1

Method BLASTX
NCBI GI g421843
BLAST score 255
E value 2.0e-22
Match length 67
% identity 78

NCBI Description protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana

>gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein

kinase [Arabidopsis thaliana]

Seq. No. 44058

Seq. ID eep700869547.h1

Method BLASTX
NCBI GI g138364
BLAST score 299
E value 1.0e-29
Match length 77

% identity 95

NCBI Description GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M -

bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

(Moz/38) Coat protein [Bean pod Mottle virus]

Seq. No. 44059

Seq. ID eep700869564.h1

Method BLASTX
NCBI GI g135460
BLAST score 409
E value 2.0e-40

```
Match length
                    96
% identity
                    TUBULIN BETA-2 CHAIN >gi_100933_pir__ S14702 tubulin beta-2 chain - maize >gi_22184_emb_CAA37061_ (X52879) beta 2
NCBI Description
                    tubulin (AA 1-444) [Zea mays]
                    44060
Seq. No.
                    eep700869617.hl
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2764949
                    303
BLAST score
                    6.0e-28
E value
Match length
                    67
% identity
                    84
                   (X98931) heat shock protein 70 [Emericella nidulans]
NCBI Description
                    44061
Seq. No.
                    eep700869681.h1
Seq. ID
                    BLASTX
Method
                    q4097880
NCBI GI
BLAST score
                    267
                    8.0e-24
E value
                    76
Match length
                    59
% identity
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                    44062
Seq. No.
                    eep700869710.h1
Seq. ID
Method
                    BLASTX
                    g4558591
NCBI GI
BLAST score
                    258
                    1.0e-22
E value
                    87
Match length
                    57
% identity
                    (AC006555) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                    thaliana]
                    44063
Seq. No.
                    eep700869712.h1
Seq. ID
                    BLASTX
Method
                    g4097880
NCBI GI
BLAST score
                    302
                    2.0e-30
E value
```

85 Match length 75 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

44064 Seq. No.

eep700869809.hl Seq. ID

Method BLASTX NCBI GI g2832606 233 BLAST score 8.0e-20 E value 80 Match length 57 % identity

(AL021635) predicted protein [Arabidopsis thaliana] NCBI Description >gi 3292810 emb_CAA19800_ (AL031018) putative protein

Seq. ID



[Arabidopsis thaliana]

```
44065
Seq. No.
Seq. ID
                  eep700869853.h1
Method
                  BLASTX
NCBI GI
                  q225282
                  297
BLAST score
E value
                  2.0e-27
                  64
Match length
                  88
% identity
                  RNA polymerase beta [Nicotiana tabacum]
NCBI Description
                  44066
Seq. No.
Seq. ID
                  eep700869909.h1
                  BLASTX
Method
NCBI GI
                  q2662343
BLAST score
                  317
E value
                  2.0e-29
                  84
Match length
                  74
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                   44067
Seq. No.
Seq. ID
                   eep700869967.h1
                  BLASTX
Method
                   g3201477
NCBI GI
BLAST score
                   146
                   2.0e-09
E value
                   82
Match length
% identity
                   40
                   (AJ006021) putative PRL1 associated protein [Arabidopsis
NCBI Description
                   thaliana]
                   44068
Seq. No.
Seq. ID
                   eep700870015.h1
Method
                   BLASTX
NCBI GI
                   g2944178
BLAST score
                   177
                   3.0e-13
E value
Match length
                   75
% identity
                   52
                   (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   44069
Seq. No.
                   eep700870087.hl
Seq. ID
                   BLASTX
Method
                   g3738325
NCBI GI
                   223
BLAST score
                   8.0e-19
E value
                   53
Match length
                   77
% identity
                   (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                   thaliana]
                   44070
Seq. No.
```

eep700870168.h1



```
Method
                   BLASTX
NCBI GI
                  g2745900
BLAST score
                   145
                   9.0e-17
E value
Match length
                   78
% identity
                   58
                  (AF039405) arsenite-translocating ATPase [Mus musculus]
NCBI Description
                   44071
Seq. No.
Seq. ID
                   eep700870172.h1
Method
                   BLASTX
NCBI GI
                   q1346769
BLAST score
                   145
                   2.0e-21
E value
                   81
Match length
% identity
                   PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)
NCBI Description
                   >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase
                   [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase
                   [Homo sapiens] >gi_4506043_ref_NP_002717.1_pPREP_ prolyl
                   endopeptidase
                   44072
Seq. No.
Seq. ID
                   eep700870251.hl
                   BLASTX
Method
NCBI GI
                   q4097880
BLAST score
                   323
                   2.0e-30
E value
Match length
                   77
% identity
                   81
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   44073
Seq. No.
                   eep700870268.h1
Seq. ID
Method
                   BLASTX
                   g1778370
NCBI GI
BLAST score
                   200
                   5.0e-16
E value
Match length
                   38
                   100
% identity
                  (U77678) asparagine synthetase 2 [Glycine max]
NCBI Description
                   44074
Seq. No.
                   eep700870280.h1
Seq. ID
                   BLASTX
Method
                   g138364
NCBI GI
BLAST score
                   389
```

4.0e-38 E value 79 Match length 99 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi_75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

44075 Seq. No.

eep700870293.h1 Seq. ID



```
Method
NCBI GI
                  q217995
BLAST score
                  311
                  5.0e-29
E value
Match length
                  75
% identity
                  77
                  (D13683) peroxidase [Populus kitakamiensis]
NCBI Description
                  44076
Seq. No.
Seq. ID
                  eep700870308.hl
Method
                  BLASTX
                  g3158476
NCBI GI
BLAST score
                  121
                  1.0e-14
E value
                  61
Match length
% identity
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
                  44077
Seq. No.
Seq. ID
                  eep700870331.h1
                  BLASTX
```

Method NCBI GI q3228517 BLAST score 277 5.0e-25 E value 83 Match length 64 % identity

(AF007788) ETTIN [Arabidopsis thaliana] NCBI Description

44078 Seq. No. Seq. ID eep700870353.hl Method BLASTX NCBI GI q138364 BLAST score 229 1.0e-19 E value Match length 70 % identity 69

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description PROTEIN VP23) >gi 75639_pir__GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi_210812

(M62738) coat protein [Bean pod mottle virus]

44079 Seq. No.

eep700870358.h1 Seq. ID

BLASTX Method q4249662 NCBI GI 307 BLAST score 2.0e-28 E value Match length 82 % identity

(AF089810) Altered Response to Gravity [Arabidopsis NCBI Description

thaliana]

44080 Seq. No.

eep700870361.h1 Seq. ID

BLASTX Method g2252634 NCBI GI BLAST score 208



```
6.0e-17
E value
Match length
                  65
% identity
                  (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  44081
                  eep700870363.hl
Seq. ID
                  BLASTX
Method
                  q138364
NCBI GI
                  355
BLAST score
E value
                  4.0e-34
                  79
Match length
                  92
% identity
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi_75639_pir GNWXG7 genome polyprotein M -
                  bean pod mottle virus (strain Kentucky G7) >gi_210812
                  (M62738) coat protein [Bean pod mottle virus]
                  44082
Seq. No.
                  eep700870403.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3641252
                  202
BLAST score
                  2.0e-16
E value
                  69
Match length
% identity
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                  domestica]
                  44083
Seq. No.
                  eep700870407.h1
Seq. ID
Method
                  BLASTX
                  g138364
NCBI GI
BLAST score
                  369
E value
                  1.0e-35
Match length
                  88
% identity
                  83
                  GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT
NCBI Description
                  PROTEIN VP23) >gi 75639_pir__GNWXG7 genome polyprotein M -
                  bean pod mottle vīrus (strain Kentucky G7) >gi_210812
                   (M62738) coat protein [Bean pod mottle virus]
Seq. No.
                   44084
                  eep700870423.h1
Seq. ID
                  BLASTX
Method
                  g283004
NCBI GI
BLAST score
                  188
                  2.0e-14
E value
                  59
Match length
                   36
% identity
                  DNA-binding protein Gt-2 - rice >gi_20249_emb_CAA48328_
NCBI Description
                   (X68261) gt-2 [Oryza sativa]
```

Seq. ID eep700870483.h1

Method BLASTX NCBI GI g3688173



```
BLAST score
                  1.0e-09
E value
Match length
                  72
                  64
% identity
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                  44086
Seq. No.
                  ejt700606103.h2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832629
BLAST score
                  130
E value
                  3.0e-10
Match length
                  85
                  42
% identity
                  (ALO21711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  44087
Seq. ID
                  ejt700606110.h2
Method
                  BLASTN
NCBI GI
                  q2811197
BLAST score
                  33
E value
                  4.0e-09
Match length
                  112
                  92
% identity
                  Gleditsia delavayi ribosomal protein 16 large subunit
NCBI Description
                   (rpl16) gene, chloroplast gene encoding chloroplast
                  protein, partial cds
                   44088
Seq. No.
                   ejt700606116.h2
Seq. ID
Method
                  BLASTX
                  q3860264
NCBI GI
BLAST score
                  233
                   5.0e-20
E value
Match length
                   51
% identity
                  82
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   44089
Seq. No.
                   ejt700606148.h2
Seq. ID
Method
                  BLASTX
                  q309673
NCBI GI
                  138
BLAST score
                   7.0e-09
E value
                  53
Match length
% identity
                   66
                  (L19651) light harvesting protein [Pisum sativum]
NCBI Description
                   44090
Seq. No.
                   ejt700606191.h2
Seq. ID
```

Method BLASTN g984307 NCBI GI BLAST score 123 7.0e-63 E value Match length 230 % identity 96



NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso

Seq. No. 44091

Seq. ID ejt700606196.h2

Method BLASTN
NCBI GI g18764
BLAST score 239
E value 1.0e-132
Match length 250
% identity 99

NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No.

Seq. ID ejt700606220.h1

44092

Method BLASTX
NCBI GI 94539344
BLAST score 153
E value 4.0e-20
Match length 70
% identity 73

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 44093

Seq. ID ejt700606255.h1

Method BLASTX
NCBI GI g1174745
BLAST score 201
E value 3.0e-22
Match length 94
% identity 76

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM) >gi 1363523 pir S53761 triose-phosphate isomerase (EC

5.3.1.1) precursor, chloroplast - rye

>gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
[Secale cereale] >gi_1095494_prf__2109226B triosephosphate

isomerase [Secale cereale]

Seq. No. 44094

Seq. ID ekl700968118.h1

Method BLASTX
NCBI GI g3152595
BLAST score 148
E value 5.0e-10
Match length 33
% identity 85

NCBI Description (AC002986) Similar to D. melanogaster sno gene gb_U95760.

EST gb N97148 and gb Z26221 come from this gene.

[Arabidopsis thaliana]

Seq. No. 44095

Seq. ID ekl700968173.hl

Method BLASTX NCBI GI g3176098



```
BLAST score
                  6.0e-17
E value
Match length
                  66
                  57
% identity
                  (Y15036) annexin [Medicago truncatula]
NCBI Description
                  44096
Seq. No.
                  ek1700968176.h1
Seq. ID
Method -
                  BLASTN
NCBI GI
                  g3982595
BLAST score
                  153
                  7.0e-81
E value
                  224
Match length
                  92
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
Seq. No.
                  44097
Seq. ID
                  ek1700968207.h1
                  BLASTN
Method
                  q609224
NCBI GI
                  63
BLAST score
E value
                  4.0e-27
                  151
Match length
                  85
% identity
                  P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB
NCBI Description
                   Pisum sativum S-adenosylmethionine synthase mRNA, complete
                   44098
Seq. No.
                   ek1700968209.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2435517
BLAST score
                   326
                   9.0e-31
E value
Match length
                   81
                   74
% identity
NCBI Description (AF024504) contains similarity to peptidase family A1
                   [Arabidopsis thaliana]
                   44099
Seq. No.
Seq. ID
                   ek1700968235.h1
Method
                   BLASTX
NCBI GI
                   g4580575
                   194
BLAST score
                   2.0e-15
E value
Match length
                   66
                   58
% identity
                  (AF082176) auxin response factor 9 [Arabidopsis thaliana]
NCBI Description
```

ek1700968258.h1 Seq. ID

BLASTX Method NCBI GI q4468986 161 BLAST score 2.0e-11 E value Match length 72 % identity 46





```
(AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44101
Seq. ID
                   ek1700968270.h1
Method
                  BLASTN
                   q3982595
NCBI GI
BLAST score
                   46
                   6.0e-17
E value
                   128
Match length
% identity
                   84
                  Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
NCBI Description
                   44102
Seq. No.
                   epx701103702.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2654108
BLAST score
                   379
                   8.0e-37
E value
Match length
                   98
                   74
% identity
                  (AF034419) cytosine-5 DNA methyltransferase [Pisum sativum]
NCBI Description
                   44103
Seq. No.
Seq. ID
                   epx701103732.h1
Method
                   BLASTX
NCBI GI
                   g1076782
BLAST score
                   187
E value
                   3.0e-14
Match length
                   57
% identity
                   70
                  transcription factor HBP-1b(c1) - wheat (fragment)
NCBI Description
                   44104
Seq. No.
                   epx701103740.h1
Seq. ID
                   BLASTX
Method
                   g2388710
NCBI GI
BLAST score
                   200
                   8.0e-16
E value
Match length
                   69
                   58
% identity
                  (AF017150) betaine aldehyde dehydrogenase [Amaranthus
NCBI Description
                   hypochondriacus]
                   44105
Seq. No.
                   epx701103844.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2960358
                   182
BLAST score
                   8.0e-14
E value
```

Match length 42 76 % identity

(AJ224895) caffeoyl-CoA 3-O-methyltransferase [Populus NCBI Description balsamifera subsp. trichocarpa] >gi_2960360_emb_CAA12200_

(AJ224896) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa] >gi_3550590_emb_CAA11495_ (AJ223620) caffeoyl CoA 3-O-methyltransferase [Populus

balsamifera subsp. trichocarpa]



```
44106
Seq. No.
Seq. ID
                  epx701103858.h1
Method
                  BLASTX
NCBI GI
                  q4335745
BLAST score
                  168
E value
                   3.0e-12
Match length
                  74
                   43
% identity
                   (AC006284) putative hydrolase (contains an
NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                   (prosite: PS50187) [Arabidopsis thaliana]
                   44107
Seq. No.
Seq. ID
                   epx701103949.hl
Method
                   BLASTX
NCBI GI
                   q4558672
BLAST score
                   253
                   4.0e-22
E value
                   88
Match length
% identity
                   (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
NCBI Description
                   thaliana]
                   44108
Seq. No.
Seq. ID
                   epx701103953.h1
Method
                   BLASTX
NCBI GI
                   q3402694
BLAST score
                   271
E value
                   3.0e-24
Match length
                   91
                   53
% identity
                  (AC004697) putative Mlo-hi protein [Arabidopsis thaliana]
NCBI Description
                   44109
Seq. No.
                   epx701104007.h1
Seq. ID
Method
                   BLASTX
                   g2347088
NCBI GI
                   175
BLAST score
                   6.0e-13
E value
Match length
                   67
                   52
% identity
                   (U72765) non-specific lipid transfer protein PvLTP-24
NCBI Description
                   [Phaseolus vulgaris]
                   44110
Seq. No.
                   epx701104105.h1
Seq. ID
                   BLASTN
Method
                   g1183936
NCBI GI
                   72
BLAST score
                   2.0e-32
E value
Match length
                   174
```

% identity

NCBI Description

Seq. ID epx701104208.h1

86

P.sativum 5S rRNA gene

Seq. ID

Method NCBI GI



```
Method
                   BLASTX
NCBI GI
                   g2706515
BLAST score
                   262
                   4.0e-23
E value
Match length
                   90
% identity
                   54
                  (Y12689) isoflavone reductase-like protein [Citrus x
NCBI Description
                  paradisi]
                   44112
Seq. No.
Seq. ID
                   epx701104220.h1
                   BLASTN
Method
                   g392991
NCBI GI
                   109
BLAST score
                   2.0e-54
E value
                   285
Match length
% identity
                   85
                   Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete
NCBI Description
                   44113
Seq. No.
Seq. ID
                   epx701104227.h1
                   BLASTN
Method
                   g2511573
NCBI GI
                   61
BLAST score
                   8.0e-26
E value
                   177
Match length
% identity
                   84
                   Arabidopsis thaliana mRNA for proteasome subunit prc3
NCBI Description
                   >gi_3421074_gb_AF043520_AF043520 Arabidopsis thaliana 20S
                   proteasome subunit PAB1 (PAB1) mRNA, complete cds
Seq. No.
                   44114
Seq. ID
                   epx701104233.h1
                   BLASTX
Method
NCBI GI
                   g3420233
BLAST score
                   232
E value
                   1.0e-19
Match length
                   85
                   51
% identity
                  (AF058763) uroporphyrinogen decarboxylase [Zea mays]
NCBI Description
Seq. No.
                   44115
                   epx701104259.h1
Seq. ID
Method
                   BLASTX
                   g4262239
NCBI GI
BLAST score
                   430
E value
                   7.0e-43
                   90
Match length
                   93
% identity
                   (AC006200) putative membrane transporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   44116
```

epx701104269.h1

BLASTX

g3451072



```
BLAST score 289
E value 3.0e-26
Match length 79
% identity 66
```

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 44117

Seq. ID epx701104275.h1

Method BLASTN
NCBI GI g533691
BLAST score 59
E value 1.0e-24
Match length 186
% identity 83

NCBI Description Glycine max Essex protease inhibitor mRNA, complete cds

Seq. No. 44118

Seq. ID epx701104316.h1

Method BLASTN
NCBI GI g1518539
BLAST score 249
E value 1.0e-138
Match length 265
% identity 98

NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No. 44119

Seq. ID epx701104462.h1

Method BLASTN
NCBI GI g256142
BLAST score 144
E value 2.0e-75
Match length 256
% identity 89

NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var

Prize, mRNA, 1450 nt]

Seq. No. 44120

Seq. ID epx701104489.h1

Method BLASTX
NCBI GI g3914472
BLAST score 257
E value 1.0e-22
Match length 63
% identity 78

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

>gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No. 44121

Seq. ID epx701104531.h1

Method BLASTX
NCBI GI g3549654
BLAST score 159
E value 4.0e-11
Match length 46



% identity (AL031394) metal-transporting P-type ATPase (fragment) NCBI Description [Arabidopsis thaliana] Seq. No. 44122 Seq. ID epx701104548.hl Method BLASTX NCBI GI q4262155 BLAST score 142 E value 4.0e-09 Match length 88

(AC005275) putative D-type cyclin [Arabidopsis thaliana] NCBI Description

44123 Seq. No.

% identity

Seq. ID epx701104554.h1

39

Method BLASTN NCBI GI g169036 BLAST score 50 E value 3.0e-19 Match length 70 % identity 93

NCBI Description Pisum sativum L. aldolase gene, 3' end cds

44124 Seq. No.

Seq. ID epx701104556.h1

Method BLASTX NCBI GI q3269295 BLAST score 151 E value 3.0e-10 Match length 55 % identity 58

(AL030978) putative protein [Arabidopsis thaliana] NCBI Description

44125 Seq. No.

epx701104585.h1 Seq. ID

Method BLASTX NCBI GI g2827637 BLAST score 139 1.0e-08 E value Match length 41 % identity 61

(AL021636) putative protein [Arabidopsis thaliana] NCBI Description

44126 Seq. No.

epx701104642.h1 Seq. ID

BLASTN Method g14311 NCBI GI 98 BLAST score 6.0e-48 E value 257 Match length % identity 94

NCBI Description G.max chloroplast gene rps19 and flanking regions

44127 Seq. No.

epx701104706.h1 Seq. ID

Method BLASTX



```
NCBI GI
                  g1742955
                  337
BLAST score
                  7.0e-32
E value
Match length
                  95
% identity
                  62
                  (Z71446) CLC-b chloride channel protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  44128
                  epx701104710.h1
Seq. ID
                  BLASTX
Method
                  g282964
NCBI GI
BLAST score
                  222
                  2.0e-18
E value
Match length
                  46
% identity
                  87
                  transforming protein (myb) homolog (clone myb.Ph3) - garden
NCBI Description
                  petunia >gi 20563 emb CAA78386 (Z13996) protein 1 [Petunia
                  x hybrida]
Seq. No.
                  44129
                  epx701104726.hl
Seq. ID
                  BLASTX
Method
                  g3426046
NCBI GI
BLAST score
                  141
E value
                  6.0e-09
Match length
                  80
% identity
                  6
                  (AC005168) similar to salt-inducible protein [Arabidopsis
NCBI Description
                  thaliana]
                  44130
Seq. No.
                  epx701104777.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2352492
BLAST score
                  362
                  7.0e-35
E value
Match length
                  88
% identity
                  81
                  (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                  thaliana] >gi 2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
```

epx701104796.hl Seq. ID

Method BLASTX NCBI GI g1209703 BLAST score 254 4.0e-22 E value Match length 75 % identity 55

NCBI Description (U40489) maize gl1 homolog [Arabidopsis thaliana]

44132 Seq. No.

epx701104817.h1 Seq. ID

Method BLASTN NCBI GI g1150683



```
BLAST score
                  2.0e-35
E value
Match length
                  262
% identity
                   82
                  V.radiata atpB, rbcL and trnK genes
NCBI Description
Seq. No.
                   44133
                   epx701104844.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3236238
BLAST score
                   156
E value
                   5.0e-11
Match length
                   46
                   63
% identity
                   (ACO04684) putative ARF1 GTPase activating protein
NCBI Description
                   [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_
                   (AB017876) Aspl [Arabidopsis thaliana]
                   44134
Seq. No.
                   epx701104864.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3021374
BLAST score
                   114
                   1.0e-57
E value
                   166
Match length
                   92
% identity
NCBI Description Glycine max mRNA for profilin, PRO1
                   44135
Seq. No.
Seq. ID
                   epx701104883.hl
Method
                   BLASTX
                   q2129854
NCBI GI
BLAST score
                   203
E value
                   3.0e-16
Match length
                   59
                   64
% identity
                   early nodulin 8 precursor - alfalfa >gi_304037 (L18899)
NCBI Description
                   early nodulin [Medicago sativa]
Seq. No.
                   44136
Seq. ID
                   epx701104888.h1
Method
                   BLASTX
NCBI GI
                   q1723172
                   158
BLAST score
                   5.0e-11
E value
                   85
Match length
                   35
% identity
NCBI Description _ HYPOTHETICAL 70.4 KD PROTEIN SLR0551
                   >qi 1001381 dbj BAA10871 (D64006) hypothetical protein
                   [Synechocystis sp.]
```

epx701104935.hl Seq. ID

BLASTX Method g4469007 NCBI GI BLAST score 229 E value 3.0e-19



81

90

Match length

NCBI Description

% identity

```
Match length
% identity
                  (AL035602) UDP rhamnose-anthocyanidin-3-glucoside
NCBI Description
                  rhamnosyltransferase-like protein [Arabidopsis thaliana]
Seq. No.
                  44138
                  epx701105001.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3738298
                  232
BLAST score
E value
                  4.0e-22
                  96
Match length
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 4249394 (AC006072) unknown protein [Arabidopsis
                  thaliana]
                   44139
Seq. No.
                   epx701105029.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4314378
BLAST score
                  137
                   3.0e-09
E value
                   56
Match length
% identity
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]
                   44140
Seq. No.
                   epx701105054.h1
Seq. ID
Method
                   BLASTN
                   q2664201
NCBI GI
BLAST score
                   46
E value
                   7.0e-17
Match length
                   111
% identity
                   86
NCBI Description Arabidopsis thaliana GT2 gene
Seq. No.
                   44141
Seq. ID
                   epx701105110.hl
Method
                   BLASTN
NCBI GI
                   g2055227
BLAST score
                   117
E value
                   2.0e-59
Match length
                   117
% identity
                   100
NCBI Description Glycine max mRNA for SRC1, complete cds
                   44142
Seq. No.
                   epx701105159.h1
Seq. ID
Method
                   BLASTX
                   g3913808
NCBI GI
BLAST score
                   370
E value
                   9.0e-36
```

FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME

SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120)



ferrochelatase [Oryza sativa]

```
44143
Seq. No.
Seq. ID
                  epx701105162.h1
Method
                  BLASTX
NCBI GI
                  g3341684
                  250
BLAST score
                  1.0e-21
E value
                  94
Match length
                  56
% identity
                  (AC003672) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  44144
Seq. No.
                  epx701105389.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1902893
BLAST score
                  102
                  2.0e-50
E value
Match length
                  246
                  85
% identity
                  Solanum melongena mRNA for QM family protein, complete cds
NCBI Description
                  44145
Seq. No.
                  epx701105407.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539422
BLAST score
                  176
E value
                   4.0e-13
Match length
                   48
                   67
% identity
                  (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44146
Seq. ID
                   epx701105410.hl
                   BLASTX
Method
NCBI GI
                   g1174549
BLAST score
                   260
E value
                   6.0e-23
                   79
Match length
                   52
% identity
                  VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
NCBI Description
                   >gi_1075441 pir__G64121 valine--tRNA ligase (EC 6.1.1.9) -
                   Haemophilus influenzae (strain Rd KW20) >gi_1574225
                   (U32819) valyl-tRNA synthetase (valS) [Haemophilus
                   influenzae Rd]
Seq. No.
                   44147
Seq. ID
                   epx701105426.h1
Method
                   BLASTX
NCBI GI
                   g2982303
BLAST score
                   189
E value
                   1.0e-14
Match length
                   57
% identity
                   61
                  (AF051236) hypothetical protein [Picea mariana]
NCBI Description
```

44148

Seq. No.

BLAST score

E value

212 1.0e-116



```
epx701105432.h1
Seq. ID
                  BLASTX
Method
                  g3461842
NCBI GI
                  191
BLAST score
                  8.0e-15
E value
Match length
                  84
% identity
                   42
                   (AC005315) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                   44149
Seq. No.
                   epx701105548.h1
Seq. ID
                   BLASTN
Method
                   g516853
NCBI GI
                   108
BLAST score
                   6.0e-54
E value
Match length
                   156
                   31
% identity
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
                   44150
Seq. No.
Seq. ID
                   epx701105581.h1
                   BLASTX
Method
                   g3269282
NCBI GI
                   161
BLAST score
                   3.0e-11
E value
                   79
Match length
                   43
% identity
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   44151
Seq. No.
Seq. ID
                   epx701105605.hl
Method
                   BLASTN
                   q1483172
NCBI GI
BLAST score
                   46
                   7.0e-17
E value
                   106
Match length
% identity
                   86
                   Japanese jack bean clone CgHMGY1 DNA for high mobility
NCBI Description
                   group protein, complete cds
Seq. No.
                   44152
Seq. ID
                   epx701105608.h1
Method
                   BLASTX
                   g2811224
NCBI GI
BLAST score
                   186
E value
                   3.0e-14
Match length
                   95
% identity
                   48
                   (AF042668) fimbrin 1 [Arabidopsis thaliana]
NCBI Description
                   44153
Seq. No.
Seq. ID
                   epx701105664.h1
Method
                   BLASTN
                   g1053215
NCBI GI
```

7042



Match length 259 % identity 96

NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 44154

Seq. ID epx701105702.h1

Method BLASTX
NCBI GI g4490323
BLAST score 175
E value 6.0e-14
Match length 70
% identity 58

NCBI Description (AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No. 44155

Seq. ID epx701105714.h1

Method BLASTX
NCBI GI g3510255
BLAST score 147
E value 1.0e-09
Match length 94
% identity 44

NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No. 44156

Seq. ID epx701105807.h1

Method BLASTX
NCBI GI g4454482
BLAST score 383
E value 2.0e-37
Match length 89
% identity 74

NCBI Description (AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No. 44157

Seq. ID epx701105855.h1

Method BLASTN
NCBI GI g18650
BLAST score 80
E value 3.0e-37
Match length 152
% identity 88

NCBI Description Soybean genomic fragment for heat-shock protein 6834 3'

terminus

Seq. No. 44158

Seq. ID epx701105864.h1

Method BLASTN
NCBI GI g18556
BLAST score 251
E value 1.0e-139
Match length 274
% identity 99

NCBI Description G.max DNA for Cab5

Seq. No. 44159



```
epx701105872.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q170067
BLAST score
                  251
E value
                  1.0e-139
Match length
                  259
                  99
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                  gene, complete cds
Seq. No.
                  44160
Seq. ID
                  epx701105875.hl
Method
                  BLASTN
NCBI GI
                  q506628
BLAST score
                  144
E value
                  2.0e-75
Match length
                  228
% identity
                  92
                  Glycine max cv. Dare photosystem II type I chlorophyll
NCBI Description
                  a/b-binding protein (lhcb1*7) gene, complete cds
Seq. No.
                  44161
                  epx701105941.h1
Seq. ID
                  BLASTX
Method
                  g4522009
NCBI GI
                  213
BLAST score
E value
                  2.0e-17
Match length
                  90
                  47
% identity
NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]
                  44162
Seq. No.
Seq. ID
                  epx701105945.hl
Method
                  BLASTX
NCBI GI
                  q4455217
BLAST score
                  181
E value
                   6.0e-18
Match length
                  74
% identity
                  (AL035440) Avr9 elicitor response like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   44163
                   epx701105966.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1619324
BLAST score
                   41
E value
                  3.0e-14
Match length
                   69
% identity
                  90
NCBI Description P.sativum mRNA for ADP-glucose pyrophosphorylase
```

Seq. No.

44164

Seq. ID epx701105972.h1

Method BLASTX
NCBI GI g2146731
BLAST score 193

4.0e-15 E value Match length 78 % identity 47 FK506-binding protein - Arabidopsis thaliana >gi_1354207 NCBI Description (U49453) rof1 [Arabidopsis thaliana] 44165 Seq. No. epx701106003.h1 Seq. ID Method BLASTX NCBI GI g117478 BLAST score 212 E value 2.0e-17 Match length 80 7 % identity NCBI Description CROOKED NECK PROTEIN 44166 Seq. No. Seq. ID epx701106013.hl Method BLASTX NCBI GI q2462751 BLAST score 189 E value 1.0e-14 Match length 39 95 % identity (AC002292) nearly identical to rice water stress induced NCBI Description protein gp D26537_537404 [Arabidopsis thaliana] 44167 Seq. No. epx701106018.hl Seq. ID Method BLASTX NCBI GI g4204287 BLAST score 239 2.0e-20 E value Match length 55 % identity 75

(AC003027) lcl prt seq No definition line found NCBI Description [Arabidopsis thaliana]

44168 Seq. No. epx701106147.h1 Seq. ID

Method BLASTX q1769897 NCBI GI BLAST score 168 8.0e-14 E value 56 Match length 70 % identity

(Y08010) lectin receptor kinase [Arabidopsis thaliana] NCBI Description

Seq. No.

44169

epx701106150.h1 Seq. ID

BLASTX Method NCBI GI g4467123 348 BLAST score 3.0e-33 E value Match length 91 75 % identity

(AL035538) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. ID

Method NCBI GI



```
44170
Seq. No.
Seq. ID
                   epx701106224.h1
                  BLASTN
Method
NCBI GI
                   g3075487
BLAST score
                   70
                   3.0e-31
E value
                   158
Match length
                   86
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
                   44171
Seq. No.
Seq. ID
                   epx701106230.h1
                   BLASTN
Method
NCBI GI
                   g22073
BLAST score
                   60
                   3.0e-25
E value
Match length
                   98
                   92
% identity
NCBI Description Mung bean 25S rRNA - 18S rDNA spacer region
                   44172
Seq. No.
                   epx701106242.h1
Seq. ID
                   BLASTX
Method
                   q4464185
NCBI GI
BLAST score
                   228
                   3.0e-19
E value
                   73
Match length
                   60
% identity
                  (U76687) lipoxygenase [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   44173
Seq. ID
                   epx701106314.hl
Method
                   BLASTX
NCBI GI
                   g2911079
BLAST score
                   190
E value
                   1.0e-14
Match length
                   41
                   80
% identity
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44174
                   epx701106331.h1
Seq. ID
Method
                   BLASTX
                   g4263704
NCBI GI
                   137
BLAST score
E value
                   1.0e-13
Match length
                   62
                   70
% identity
                   (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   44175
```

epx701106356.hl

BLASTX

q2275211



```
BLAST score
                   4.0e-09
E value
                   45
Match length
                   58
% identity
                  (ACO02337) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44176
Seq. ID
                   epx701106380.hl
                  BLASTX
Method
                   q1769556
NCBI GI
BLAST score
                   198
E value
                   1.0e-15
                   79
Match length
                   80
% identity
                   (U81158) Forsythia x intermedia
NCBI Description
                   (+)-pinoresinol/(+)-lariciresinol reductase (PLR) protein,
                   complete sequence [Forsythia x intermedia]
                   44177
Seq. No.
                   epx701106386.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4164576
                   211
BLAST score
                   6.0e-32
E value
                   95
Match length
                   82
% identity
                  (AF098946) CTF2A [Arabidopsis thaliana]
NCBI Description
                   44178
Seq. No.
Seq. ID
                   epx701106408.hl
Method
                   BLASTN
NCBI GI
                   q1370147
BLAST score
                   164
                   3.0e-87
E value
Match length
                   176
                   98
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB11D
                   44179
Seq. No.
                   epx701106423.h1
Seq. ID
Method
                   BLASTN
                   g1173641
NCBI GI
BLAST score
                   68
                   2.0e-30
E value
Match length
                   116
                   90
% identity
NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds
                   44180
Seq. No.
                   epx701106431.h1
Seq. ID
                   BLASTN
Method
                   g974781
NCBI GI
```

Method BLASTN
NCBI GI g974781
BLAST score 49
E value 1.0e-18
Match length 96
% identity 90

NCBI Description C.blumei kinetoplast met gene for cobalamine-independent



methionine synthase

```
44181
Seq. No.
                  epx701106540.hl
Seq. ID
Method
                  BLASTX
                  q4309698
NCBI GI
BLAST score
                  412
                  1.0e-40
E value
                  92
Match length
                  80
% identity
                  (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                   44182
Seq. No.
Seq. ID
                   epx701106638.hl
Method
                  BLASTX
                  g3914472
NCBI GI
                  259
BLAST score
                  8.0e-23
E value
Match length
                   63
                   79
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
NCBI Description
                   >gi_322764_pir_S32021 photosystem II 10K protein - common
                   tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana
                   tabacum]
                   44183
Seq. No.
                   epx701106643.h1
Seq. ID
Method
                   BLASTX
                   g2664210
NCBI GI
BLAST score
                   425
                   2.0e-42
E value
Match length
                   86
                   93
% identity
                  (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   44184
Seq. No.
                   epx701106671.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3063697
BLAST score
                   166
                   6.0e-12
E value
                   43
Match length
                   31
% identity
                  (AL022537) putative myb-protein (partial) [Arabidopsis
NCBI Description
                   thaliana]
                   44185
Seq. No.
                   epx701106678.h1
Seq. ID
Method
                   BLASTX
                   g3386611
NCBI GI
                   149
BLAST score
                   6.0e-10
E value
Match length
                   36
% identity
                   64
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
```



```
Seq. No.
                  44186
Seq. ID
                  epx701106737.hl
Method
                  BLASTN
NCBI GI
                  q3702315
BLAST score
                  70
                  3.0e-31
E value
Match length
                  270
                  81
% identity
                  Arabidopsis thaliana chromosome II BAC T3F17 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  44187
                  epx701106827.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760319
BLAST score
                  278
E value
                  5.0e-25
Match length
                  72
                  75
% identity
NCBI Description
                  (AC002130) F1N21.3 [Arabidopsis thaliana]
                  44188
Seq. No.
Seq. ID
                  epx701106870.h1
Method
                  BLASTX
NCBI GI
                  q399091
BLAST score
                  373
E value
                  3.0e-36
Match length
                  87
% identity
                  85
                  PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
NCBI Description
                   (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                   (H+-PPASE) >gi 282878 pir A38230 inorganic pyrophosphatase
                   (EC 3.6.1.1), H+-translocating pyrophosphate-energized -
                  Arabidopsis thaliana >gi 166634 (M81892) vacuolar
                  H+-phosphatase [Arabidopsis thaliana]
                  44189
Seq. No.
                  epx701106872.h1
Seq. ID
Method
                  BLASTN
                  g1370199
NCBI GI
BLAST score
                  150
                  5.0e-79
E value
                  229
Match length
                  92
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC1
                  44190
Seq. No.
                  epx701106909.h1
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI g3335363
BLAST score 154
E value 2.0e-10
Match length 78
% identity 23

NCBI Description (AC003028) hypothetical protein [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                  epx701106919.hl
                  BLASTX
Method
                   q2582822
NCBI GI
BLAST score
                   322
E value
                   3.0e-30
                   85
Match length
                   48
% identity
                  (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                   Protein of 32kDa) [Solanum tuberosum]
                   44192
Seq. No.
                   epx701107003.h1
Seq. ID
                   BLASTX
Method
                   g3776005
NCBI GI
                   264
BLAST score
                   2.0e-23
E value
                   77
Match length
% identity
                   (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   44193
Seq. No.
                   epx701107117.h1
Seq. ID
                   BLASTX
Method
                   q3328240
NCBI GI
                   230
BLAST score
                   2.0e-19
E value
                   83
Match length
% identity
                   (AF064775) early nodule-specific protein [Medicago
NCBI Description
                   truncatula]
                   44194
Seq. No.
Seq. ID
                   epx701107158.h1
                   BLASTN
Method
                   g18551
NCBI GI
                   167
BLAST score
```

E value 4.0e-89 259 Match length % identity

Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding NCBI Description

protein

44195

Seq. No.

Seq. ID epx701107161.h1

BLASTN Method NCBI GI q1707656

BLAST score 89 1.0e-42 E value Match length 229 % identity 85

P.sativum mRNA for DnaJ-like protein NCBI Description

Seq. No. 44196

epx701107296.hl Seq. ID

BLASTX Method q122007 NCBI GI



BLAST score 1.0e-15 E value 40 Match length 97 % identity HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley NCBI Description >gi_20448_emb_CAA37828_ (X $\overline{53}$ 831) H2A histone protein (AA 1 - 149) [Petroselinum crispum] 44197 Seq. No. epx701107302.h1 Seq. ID Method BLASTN g1944318 NCBI GI 77 BLAST score 2.0e-35 E value 161 Match length 87 % identity Glycine max mRNA for cysteine proteinase inhibitor, NCBI Description complete cds 44198 Seq. No. Seq. ID epx701107311.hl BLASTX Method q4249388 NCBI GI 190 BLAST score 1.0e-14 E value 60 Match length 63 % identity (AC005966) Similar to gb_AF025438 Opa-interacting protein NCBI Description (OIP2) from Homo sapiens. [Arabidopsis thaliana] 44199 Seq. No. Seq. ID epx701107363.h1 Method BLASTN NCBI GI q1408470 BLAST score 53 4.0e-21 E value Match length 121 % identity 86 Arabidopsis thaliana actin depolymerizing factor 1 (AtADF1) NCBI Description mRNA, complete cds 44200 Seq. No. Seq. ID epx701107377.h1 Method BLASTX g4455323 NCBI GI BLAST score 174 8.0e-13 E value Match length 60 57 % identity (AL035525) aminopeptidase-like protein [Arabidopsis NCBI Description thaliana]

Seq. No.

44201

epx701107385.h1 Seq. ID

BLASTX Method g131384 NCBI GI BLAST score 267



E value 9.0e-24
Match length 72
% identity 82
NCBI Description OXYGEN-

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132

photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA

-81 to 248) [Pisum satīvum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum satīvum] >gi_226937_prf_1611461A O2 evolving

complex 33kD protein [Arachis hypogaea]

Seq. No. 44202

Seq. ID epx701107434.h1

Method BLASTX
NCBI GI 94314378
BLAST score 239
E value 2.0e-20
Match length 76
% identity 51

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 44203

Seq. ID epx701107524.h1

Method BLASTX
NCBI GI g548337
BLAST score 172
E value 1.0e-12
Match length 73
% identity 44

NCBI Description NADPH-CYTOCHROME P450 REDUCTASE (CPR)

>gi_284738_pir__S27158 NADPH--ferrihemoprotein reductase
(EC 1.6.2.4) - guinea pig >gi_220557_dbj_BAA01385_ (D10498)
NADPH-cytochrome P450 oxidoreductase [Cavia porcellus]

Seq. No. 44204

Seq. ID epx701107604.h1

Method BLASTX
NCBI GI g2384863
BLAST score 165
E value 8.0e-12
Match length 80
% identity 44

NCBI Description (AF022976) Similar to lipase; R11G11.14 [Caenorhabditis

elegans]

44205

Seq. No.

Seq. ID epx701107611.h1

Method BLASTX
NCBI GI g4512708
BLAST score 183
E value 6.0e-14
Match length 80
% identity 35

NCBI Description (AC006569) putative glutaredoxin [Arabidopsis thaliana]



```
44206
Seq. No.
                  epx701107613.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1336081
                   86
BLAST score
                   6.0e-41
E value
                   93
Match length
                   99
% identity
                  Glycine max var. Century ascorbate peroxidase 2 (APx2)
NCBI Description
                  mRNA, complete cds
                   44207
Seq. No.
                   epx701107727.h1
Seq. ID
Method
                   BLASTX
                   g246248
NCBI GI
                   483
BLAST score
                   4.0e-49
E value
                   90
Match length
% identity
                   100
                   GmPK2=protein kinase [Glycine max L.=soybeans, Peptide, 119
NCBI Description
                   44208
Seq. No.
                   epx701107731.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18653
                   61
BLAST score
                   8.0e-26
E value
Match length
                   81
                   94
% identity
NCBI Description Soybean gene for heat shock protein Gmhsp18.5-C (class I)
                   44209
Seq. No.
Seq. ID
                   epx701107734.h1
                   BLASTN
Method
                   q18556
NCBI GI
BLAST score
                   260
                   1.0e-144
E value
                   279
Match length
                   99
% identity
NCBI Description G.max DNA for Cab5
                   44210
Seq. No.
Seq. ID
                   epx701107785.h1
                   BLASTN
Method
NCBI GI
                   q169974
BLAST score
                   167
                   4.0e-89
E value
Match length
                   227
% identity
                   93
NCBI Description Glycine max vspA gene, complete cds
                   44211
Seq. No.
Seq. ID
                   epx701107853.h1
Method
                   BLASTX
```

q4454048

203

NCBI GI BLAST score

```
2.0e-16
E value
Match length
                  65
% identity
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  44212
                  epx701107858.h1
Seq. ID
Method
                  BLASTN
                  q170493
NCBI GI
BLAST score
                  36
                  4.0e-11
E value
                  44
Match length
% identity
                  Tomato (L.esculentum) photosystem I protein mRNA, complete
NCBI Description
Seq. No.
                  44213
```

Seq. NO. 44213

Seq. ID epx701107882.h1

Method BLASTX

NCBI GI g2119719

BLAST score 201

E value 5.0e-16

Match length 52

E value 5.0e-16

Match length 52

% identity 75

NCRI Description beat-shock cogn

NCBI Description heat-shock cognate protein 70-3 - tomato >gi_762844 (L41253) Hsc70 [Lycopersicon esculentum]

 Seq. No.
 44214

 Seq. ID
 epx701107907.h1

 Method
 BLASTN

 NCBI GI
 g256142

 BLAST score
 276

BLAST score 276
E value 1.0e-154
Match length 280
% identity 100

NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No. 44215

Seq. ID epx701107933.h1

Method BLASTX
NCBI GI g1103318
BLAST score 298
E value 2.0e-27
Match length 59
% identity 90

NCBI Description (X78818) casein kinase I [Arabidopsis thaliana] >gi_2244791_emb_CAB10213.1_ (Z97336) casein kinase I

[Arabidopsis thaliana]

Seq. No. 44216

Seq. ID epx701107947.h1

Method BLASTX
NCBI GI g3096910
BLAST score 192
E value 3.0e-21
Match length 58



% identity (AJ005813) neoxanthin cleavage enzyme [Arabidopsis NCBI Description thaliana] 44217 Seq. No. Seq. ID epx701107958.h1 Method BLASTX g3482974 NCBI GI 390 BLAST score 3.0e-38 E value 88 Match length 84 % identity (AL031369) ATP-dependent Clp proteinase-like protein NCBI Description [Arabidopsis thaliana] 44218 Seq. No. Seq. ID epx701107973.h1 BLASTX Method g2129581 NCBI GI BLAST score 340 3.0e-32 E value 87 Match length 72 % identity envelope Ca2+-ATPase precursor - Arabidopsis thaliana NCBI Description >gi 471089 dbj_BAA03091_ (D13984) chloroplast envelope Ca2+-ATPase precursor [Arabidopsis thaliana] >gi 4165448 emb_CAA49558_ (X69940) envelope Ca2+-ATPase [Arabidopsis thaliana] 44219 Seq. No. Seq. ID epx701108251.h1 BLASTN Method NCBI GI q3738260 71 BLAST score 7.0e-32 E value 143 Match length % identity 87 Populus nigra PnChlPGK mRNA for chloroplast NCBI Description phosphoglycerate kinase, complete cds 44220 Seq. No. Seq. ID epx701108266.hl Method BLASTX NCBI GI q2865424 183 BLAST score 6.0e-14 E value

74 Match length

% identity

(AF039371) polyprotein [Arabidopsis thaliana] NCBI Description

44221 Seq. No.

epx701108272.h1 Seq. ID

BLASTN Method NCBI GI q587561 BLAST score 66 7.0e-29 E value Match length 146



```
% identity
                  S.tuberosum mRNA for alpha-II MPP
NCBI Description
                  44222
Seq. No.
                  epx701108344.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1055367
                  205
BLAST score
                  1.0e-112
E value
                  264
Match length
                  94
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                   44223
Seq. No.
Seq. ID
                   epx701108368.h1
                  {\tt BLASTN}
Method
                   g999189
NCBI GI
                   84
BLAST score
                   1.0e-39
È value
                   244
Match length
                   84
% identity
                  dihydrofolate reductase-thymidylate synthase=bifunctional
NCBI Description
                   enzyme [Glycine max, seedling, mRNA, 1794 nt]
                   44224
Seq. No.
                   epx701108407.h1
Seq. ID
                   BLASTN
Method
                   q1087112
NCBI GI
                   33
BLAST score
                   4.0e-09
E value
Match length
                   49
                   92
% identity
                   Rac9=21.5 kda GTP-binding protein [Gossypium
NCBI Description
                   hirsutum=cotton plants, cv. Acala SJ-2, boll fibers, mRNA
                   Partial, 840 nt]
                   44225
Seq. No.
                   epx701108441.h1
Seq. ID
                   BLASTN
Method
                   q169097
NCBI GI
BLAST score
                   57
E value
                   2.0e-23
Match length
                   201
                   82
% identity
NCBI Description
                  Pea histone H2A mRNA
                   44226
Seq. No.
                   epx701108468.h1
Seq. ID
                   BLASTN
Method
                   g3449327
NCBI GI
BLAST score
                   58
E value
                   5.0e-24
Match length
                   182
```

MCA23, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

83

% identity

NCBI Description

E value

Match length

% identity

2.0e-21 80

54



```
44227
Seq. No.
                  epx701108476.h1
Seq. ID
                  BLASTX
Method
                  g3450842
NCBI GI
                  227
BLAST score
                  4.0e-19
E value
                  48
Match length
% identity
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
                   44228
Seq. No.
                  epx701108528.h1
Seq. ID
                  BLASTX
Method
                   g133872
NCBI GI
                   294
BLAST score
                   7.0e-27
E value
Match length
                   90
% identity
                   67
                   30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
NCBI Description
                   >gi 282838 pir S26494 ribosomal protein S1, chloroplast -
                   spinach >gi 322404 pir_A44121 small subunit ribosomal
                   protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >gi 170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
                   44229
Seq. No.
                   epx701108532.hl
Seq. ID
                   BLASTX
Method
                   g3850630
NCBI GI
                   397
BLAST score
                   6.0e-39
E value
                   92
Match length
                   80
% identity
                  (AJ012581) cytochrome P450 [Cicer arietinum]
NCBI Description
                   44230
Seq. No.
                   epx701108616.h1
Seq. ID
                   BLASTN
Method
                   g3493646
NCBI GI
                   69
BLAST score
                   1.0e-30
E value
                   185
Match length
 % identity
                   84
                   Pimpinella brachycarpa transcription activator (MADS1)
NCBI Description
                   mRNA, complete cds
                   44231
 Seq. No.
                   epx701108631.h1
 Seq. ID
                   BLASTX
Method
                   g4262225
 NCBI GI
 BLAST score
                   247
```

7057



(AC006200) putative phosphatidic acid phosphatase NCBI Description [Arabidopsis thaliana] 44232 Seq. No. epx701108654.h1 Seq. ID Method BLASTN NCBI GI g2529228 BLAST score 103 E value 6.0e-51 Match length 231 % identity 86 Glycine max mRNA for 6-phosphogluconate dehydrogenase, NCBI Description complete cds 44233 Seq. No. epx701108714.h1 Seq. ID BLASTX Method g3176098 NCBI GI BLAST score 315 2.0e-29 E value 85 Match length % identity 68 (Y15036) annexin [Medicago truncatula] NCBI Description Seq. No. 44234 epx701108744.h1 Seq. ID BLASTN Method q4151065 NCBI GI 93 BLAST score E value 5.0e-45 244 Match length 85 % identity NCBI Description N.tabacum mRNA for ribonucleotide reductase, clone R1-1 Seq. No. 44235 epx701108783.h1 Seq. ID ${\tt BLASTN}$ Method NCBI GI g3452136 BLAST score 168 9.0e-90 E value Match length 184 99 % identity Glycine max mRNA for glucose-6-phosphate-dehydrogenase, NCBI Description partial 44236 Seq. No.

Seq. ID epx701108786.h1

BLASTX Method NCBI GI q3386605 BLAST score 251 6.0e-22 E value Match length 81 % identity

(AC004665) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

epx701108795.h1 Seq. ID

7058



```
BLASTN
Method
                  g170071
NCBI GI
BLAST score
                  168
                  7.0e-90
E value
                  200
Match length
                  96
% identity
                  Soybean calmodulin (SCaM-2) mRNA, complete cds
NCBI Description
                   44238
Seq. No.
                   epx701108796.h1
Seq. ID
                  BLASTX
Method
                   g2462750
NCBI GI
                   147
BLAST score
                   9.0e-10
E value
Match length
                   64
                   47
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                   44239
Seq. No.
                   epx701108822.h1
Seq. ID
                   BLASTN
Method
                   g1644387
NCBI GI
BLAST score
                   32
                   1.0e-08
E value
Match length
                   32
                   100
% identity
                   Eustoma grandiflorum flavonoid 3'5'-hydroxylase (F3'5'H)
NCBI Description
                   mRNA, complete cds
                   44240
Seq. No.
                   epx701108909.h1
Seq. ID
                   BLASTX
Method
                   g1173257
NCBI GI
BLAST score
                   382
                   4.0e-37
E value
                   77
Match length
                   91
% identity
                   40S RIBOSOMAL PROTEIN S4 >gi_1076674_pir__S47642 ribosomal
NCBI Description
                   protein S4 - potato >gi_457803 emb_CAA54095 (X76651)
                   ribosomal protein S4 [Solanum tuberosum]
                   44241
Seq. No.
                   epx701108920.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g100200
                   140
BLAST score
                   9.0e-09
E value
                   66
Match length
                   45
% identity
                  chlorophyll a/b-binding protein type I precursor - tomato
NCBI Description
                   44242
Seq. No.
                   epx701108934.hl
Seq. ID
                   BLASTX
Method
```

g3183077

242

NCBI GI

BLAST score



E value Match length 95 52 % identity

PROBABLE 1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE NCBI Description (DHNA-OCTAPRENYLTRANSFERASE) >gi 1653114 dbj_BAA18030 (D90911) menaquinone biosynthesis protein [Synechocystis

Seq. No. 44243

epx701108968.h1 Seq. ID

Method BLASTX q2494174 NCBI GI BLAST score 139 3.0e-16 E value 80 Match length % identity 64

GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi 497979 (U10034) NCBI Description

glutamate decarboxylase [Arabidopsis Thaliana]

44244 Seq. No.

Seq. ID epx701108989.h1

Method BLASTX NCBI GI g2621658 BLAST score 237 3.0e-20 E value Match length 91 % identity

(AE000840) conserved protein [Methanobacterium NCBI Description

thermoautotrophicum]

44245 Seq. No.

epx701109020.h1 Seq. ID

BLASTX Method g902938 NCBI GI 426 BLAST score 2.0e-42 E value 92 Match length 83 % identity

(D50866) beta-amylase [Glycine max] NCBI Description

>gi 2196550 dbj_BAA20453_ (AB004271) beta-amylase [Glycine

max]

44246 Seq. No.

epx701109025.hl Seq. ID

BLASTX Method NCBI GI g135103 BLAST score 179 2.0e-13 E value 43 Match length

65 % identity

NCBI Description MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [CONTAINS: GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE);

PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE)]

>gi_103253_pir__S18644 multifunctional amino acid--tRNA ligase (EC 6.1.1.-) - fruit fly (Drosophila melanogaster)

>qi 157564 (M74104) transfer RNA-Glu-Pro aminoacyl

synthetase [Drosophila melanogaster] >gi_1871360 (U59923)

NCBI Description





```
Seq. No.
                  44247
Seq. ID
                  epx701109058.h1
Method
                  BLASTN
NCBI GI
                  g2924653
BLAST score
                  41
E value
                  6.0e-14
Match length
                  73
% identity
                  30
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDA7, complete sequence [Arabidopsis thaliana]
                  44248
Seq. No.
Seq. ID
                  epx701109071.h1
Method
                  BLASTX
NCBI GI
                  q4164425
BLAST score
                  161
                  3.0e-11
E value
                  75
Match length
% identity
                  41
NCBI Description
                  (AL035247) hypothetical trp-asp repeat protein
                  [Schizosaccharomyces pombe]
Seq. No.
                  44249
Seq. ID
                  epx701109092.h1
Method
                  BLASTN
NCBI GI
                  g3873174
BLAST score
                  37
                  2.0e-11
E value
Match length
                  93
                  85
% identity
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F14N23,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  44250
Seq. ID
                  epx701109104.hl
Method
                  BLASTN
NCBI GI
                  g12158
BLAST score
                  64
                  1.0e-27
E value
Match length
                  196
% identity
                  84
                  Pea gpal gene for subunit A of chloroplast
NCBI Description
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13)
Seq. No.
                  44251
Seq. ID
                  epx701109114.h1
                  BLASTX
Method
                  g4218014
NCBI GI
BLAST score
                  332
E value
                  2.0e-31
Match length
                  76
% identity
                  47
```

protein) [Arabidopsis thaliana]

(AC006135) putative spliceosomal protein (RNA binding



Seq. No. 44252 Seq. ID epx701109175.h1 Method BLASTN

NCBI GI g4140690 BLAST score 72 E value 2.0e-32 Match length 164 % identity 86

NCBI Description Phaseolus lunatus zeatin O-glucosyltransferase (ZOG1) mRNA,

complete cds

Seq. No. 44253

Seq. ID epx701109190.h1

Method BLASTN
NCBI GI g2739043
BLAST score 57
E value 2.0e-23
Match length 189
% identity 86

NCBI Description Glycine max polyphosphoinositide binding protein Sshlp

(SSH1) mRNA, complete cds

Seq. No.

Seq. ID epx701109194.h1

44254

Method BLASTN
NCBI GI g506628
BLAST score 237
E value 1.0e-131
Match length 253
% identity 98

NCBI Description Glycine max cv. Dare photosystem II type I chlorophyll

a/b-binding protein (lhcb1*7) gene, complete cds

Seq. No. 44255

Seq. ID epx701109269.h1

Method BLASTX
NCBI GI g3914472
BLAST score 235
E value 4.0e-20
Match length 57
% identity 77

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

>gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No. 44256

Seq. ID epx701109318.hl

Method BLASTN
NCBI GI 9414665
BLAST score 169
E value 2.0e-90
Match length 228
% identity 99

NCBI Description G.max gene for coproporphyrinogen oxidase

Seq. No. 44257



```
epx701109344.h1
Seq. ID
                  BLASTN
Method
                  q506628
NCBI GI
                  194
BLAST score
                  1.0e-105
E value
Match length
                  194
                  100
% identity
                  Glycine max cv. Dare photosystem II type I chlorophyll
NCBI Description
                  a/b-binding protein (lhcb1*7) gene, complete cds
                   44258
Seq. No.
Seq. ID
                   epx701109355.h1
                   BLASTX
Method
                   g3746059
NCBI GI
                   211
BLAST score
                   2.0e-17
E value
Match length
                   66
                   59
% identity
                   (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana] >gi 4432812 gb AAD20662_ (AC006593) putative
                   cysteinyl-tRNA synthetase [Arabidopsis thaliana]
                   44259
Seq. No.
Seq. ID
                   epx701109425.h1
                   BLASTN
Method
                   g169974
NCBI GI
                   167
BLAST score
                   4.0e-89
E value
                   270
Match length
                   91
% identity
                   Glycine max vspA gene, complete cds
NCBI Description
                   44260
Seq. No.
Seq. ID
                   epx701109448.h1
                   BLASTX
Method
                   g629669
NCBI GI
BLAST score
                   166
                   7.0e-12
E value
                   53
Match length
                   51
 % identity
                   hypothetical protein - tomato
NCBI Description
 Seq. No.
                   44261
                   epx701109561.hl
 Seq. ID
                   BLASTN
Method
                   q2961299
NCBI GI
                   118
BLAST score
                   7.0e-60
E value
                   230
Match length
 % identity
                   88
                   Cicer arietinum mRNA for ribosomal protein L24
 NCBI Description
```

Seq. No. 44262

Seq. ID epx701109603.h1

Method BLASTX NCBI GI g131384 BLAST score 126



E value 2.0e-12 Match length 59 % identity 64

NCBI Description

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 81934 pir S04132

photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA

-81 to 248) [Pisum satīvum] >gi_344004 dbj_BAA02554 (D13297) precursor for 33-kDa protein of photosystem II [Pisum satīvum] >gi_226937_prf_1611461A O2 evolving

complex 33kD protein [Arachis hypogaea]

Seq. No. 44263

Seq. ID epx701109684.h1

Method BLASTX
NCBI GI g2708745
BLAST score 372
E value 4.0e-36
Match length 85
% identity 82

NCBI Description (AC003952) putative calcium-dependent ser/thr protein

kinase [Arabidopsis thaliana]

Seq. No. 44264

Seq. ID epx701109801.h1

Method BLASTX
NCBI GI g1001478
BLAST score 161
E value 3.0e-11
Match length 87
% identity 37

NCBI Description (D63999) hypothetical protein [Synechocystis sp.]

Seq. No. 44265

Seq. ID epx701109805.h1

Method BLASTX
NCBI GI g2194132
BLAST score 145
E value 2.0e-09
Match length 37
% identity 76

NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No. 44266

Seq. ID epx701109852.h1

Method BLASTX
NCBI GI g2288999
BLAST score 412
E value 9.0e-41
Match length 85
% identity 91

NCBI Description (AC002335) electron transfer flavoprotein ubiquinone

oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 44267

Seq. ID epx701109871.h1



Method BLASTN
NCBI GI g516853
BLAST score 146
E value 1.0e-76
Match length 186
% identity 32

NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No.

44268

Seq. ID epx701109964.h1

Method BLASTN
NCBI GI g1055367
BLAST score 177
E value 4.0e-95
Match length 201
% identity 97

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 44269

Seq. ID epx701110067.h1

Method BLASTX
NCBI GI g3914472
BLAST score 259
E value 7.0e-23
Match length 64
% identity 78

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

>gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669 emb CAA49693 (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No.

44270

Seq. ID epx701110138.h1

Method BLASTX
NCBI GI g2281102
BLAST score 248
E value 2.0e-21
Match length 88
% identity 64

NCBI Description (AC002333) SF16 isolog [Arabidopsis thaliana]

Seq. No.

44271

Seq. ID epx701110146.h1

Method BLASTX
NCBI GI g4531442
BLAST score 187
E value 1.0e-14
Match length 71
% identity 54

NCBI Description (AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.

44272

Seq. ID epx701110149.h1

Method BLASTN NCBI GI g1944341 BLAST score 150



```
6.0e-79
E value
Match length
                  189
                  100
% identity
                  Glycine max DNA for cysteine proteinase inhibitor, complete
NCBI Description
                  44273
Seq. No.
                  epx701110150.hl
Seq. ID
Method
                  BLASTX
                   g3297819
NCBI GI
BLAST score
                   357
                   3.0e-34
E value
                   82
Match length
                   89
% identity
                   (AL031032) protein kinase - like protein [Arabidopsis
NCBI Description
Seq. No.
                   44274
                   epx701110169.hl
Seq. ID
                   BLASTX
Method
                   g2702274
NCBI GI
BLAST score
                   173
                   4.0e-15
E value
                   71
Match length
% identity
                   (AC003033) unknown protein [Arabidopsis thaliana]
NCBI Description
                   44275
Seq. No.
                   epx701110187.hl
Seq. ID
Method
                   BLASTN
                   g217902
NCBI GI
BLAST score
                   72
                   2.0e-32
E value
                   196
Match length
% identity
                   84
                   Catharanthus roseus cyc07 mRNA, complete cds
NCBI Description
                   44276
Seq. No.
                   epx701110202.hl
Seq. ID
                   BLASTN
Method
                   g20728
NCBI GI
BLAST score
                   68
                   5.0e-30
E value
                   168
Match length
                   85
% identity
                   Pea chloroplast GAPA mRNA encoding
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A
                   (EC 1.2.1.13)
                   44277
Seq. No.
                   epx701110209.h1
Seq. ID
                   BLASTN
Method
                   g18755
NCBI GI
                   86
BLAST score
                   8.0e-41
E value
```

134

91

Match length % identity



NCBI Description Soybean SRS4 mRNA for ribulose-1,5-bisphosphate carboxylase (Rubisco) small subunit, partial cds

Seq. No. 44278

Seq. ID epx701110214.h1

Method BLASTX
NCBI GI g2827549
BLAST score 330
E value 4.0e-31
Match length 72
% identity 82

% identity 82
NCBI Description (AL021635) glycoprotein endopeptidase - like protein

[Arabidopsis thaliana]

Seq. No. 44279

Seq. ID epx701110237.h1

Method BLASTN
NCBI GI g3776024
BLAST score 58
E value 4.0e-24
Match length 122
% identity 87

NCBI Description Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH26

Seq. No. 44280

Seq. ID epx701110239.h1

Method BLASTN
NCBI GI 9710435
BLAST score 59
E value 1.0e-24
Match length 158
% identity 85

NCBI Description Glycine max low molecular weight heat shock protein Hsp22.5

(Gmhsp22.5) mRNA, complete cds

Seq. No. 44281

Seq. ID epx701110262.h1

Method BLASTN
NCBI GI g506628
BLAST score 254
E value 1.0e-141
Match length 270
% identity 99

NCBI Description Glycine max cv. Dare photosystem II type I chlorophyll

a/b-binding protein (lhcb1*7) gene, complete cds

Seq. No.

44282

Seq. ID epx701110266.h1

Method BLASTX
NCBI GI g2281083
BLAST score 121
E value 1.0e-12
Match length 88
% identity 45

NCBI Description (AC002333) polygalacturonase isolog [Arabidopsis thaliana]

Seq. No. 44283



Seq. ID epx701110277.h1

Method BLASTX
NCBI GI g3142303
BLAST score 299
E value 2.0e-27
Match length 86
% identity 66

NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug

resistance protein gb_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 44284

Seq. ID epx701110309.h1

Method BLASTX
NCBI GI g2842490
BLAST score 162
E value 2.0e-11
Match length 56
% identity 54

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 44285

Seq. ID epx701110318.h1

Method BLASTX
NCBI GI g3063691
BLAST score 341
E value 2.0e-32
Match length 82
% identity 71

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 44286

Seq. ID epx701110365.h1

Method BLASTX
NCBI GI g4210948
BLAST score 226
E value 4.0e-19
Match length 46
% identity 91

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 44287

Seq. ID epx701110414.h1

Method BLASTX
NCBI GI g3608127
BLAST score 387
E value 8.0e-38
Match length 86
% identity 80

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 44288

Seq. ID epx701110424.h1

Method BLASTX NCBI GI g4028155 BLAST score 186



```
E value
                   3.0e-14
Match length
                   76
% identity
                   46
```

(AF083221) YDR140w homolog [Fugu rubripes] NCBI Description

Seq. No. 44289

Seq. ID epx701110444.h1

Method BLASTN NCBI GI g2660767 BLAST score 94 E value 1.0e-45 Match length 186 % identity 88

Spinacia oleracea cytosolic heat shock 70 protein NCBI Description

(HSC70-3beta) gene, complete cds

Seq. No.

44290 Seq. ID epx701110453.h1

BLASTX Method NCBI GI g3063699 BLAST score 160 E value 3.0e-11 Match length 63 % identity 56

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

44291

Seq. ID euj700697903.h1

Method BLASTX NCBI GI g399213 BLAST score 176 5.0e-13 E value 75 Match length 55 % identity

ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG NCBI Description

CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato

>gi 170435 (M32604) ATP-dependent protease (CD4B)

[Lycopersicon esculentum]

Seq. No. 44292

euj700697910.h1 Seq. ID

Method BLASTX NCBI GI q1076488 BLAST score 104 E value 3.0e-09 Match length 43 % identity 79

NCBI Description glycinin A5A4B3 chain - soybean >qi 806556 emb CAA60533

(X86970) A5A4B3 subunit [Glycine soja]

Seq. No.

Seq. ID euj700697926.h1

44293

Method BLASTX NCBI GI g121276 BLAST score 458 E value 4.0e-46 Match length 94



% identity

GLYCININ G1 PRECURSOR [CONTAINS: GLYCININ A1A SUBUNIT; NCBI Description GLYCININ BX SUBUNIT] >gi 99907_pir S10851 glycinin G1 precursor - soybean >gi 255221 bbs 112930 glycinin G1

subunit [soybeans, Peptide, 495 aa] >gi_18635_emb_CAA33215_(X15121) glycinin subunit G1 [Glycine max] >gi_169973

(M36686) glycinin A-1a-B-x subunit [Glycine max]

Seq. No. 44294

Seq. ID euj700697952.h1

Method BLASTX NCBI GI g3080401 BLAST score 378 E value 9.0e-37 90 Match length 74 % identity

(AL022603) putative protein [Arabidopsis thaliana] NCBI Description

>gi_4455265_emb_CAB36801.1_ (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No. 44295

Seq. ID euj700697966.h1

Method BLASTX NCBI GI q1362615 BLAST score 155 1.0e-10 E value Match length 95 % identity 43

iswi protein - fruit fly (Drosophila melanogaster) NCBI Description

>gi 439197 (L27127) ISWI protein [Drosophila melanogaster]

Seq. No. 44296

euj700697980.h1 Seq. ID

BLASTX Method g138364 NCBI GI BLAST score 278 2.0e-33 E value

Match length 95 86 % identity

GENOME POLYPROTEIN M (CONTAINS: COAT PROTEIN VP37; COAT NCBI Description

PROTEIN VP23) >gi 75639 pir GNWXG7 genome polyprotein M bean pod mottle virus (strain Kentucky G7) >gi 210812

(M62738) coat protein [Bean pod mottle virus]

Seq. No. 44297

Seq. ID euj700698020.h1

Method BLASTX NCBI GI q3063392 BLAST score 257 E value 1.0e-22 Match length 85 % identity 64

(AB012932) Ca2+/H+ exchanger [Vigna radiata] NCBI Description

44298 Seq. No.

Seq. ID euj700698021.hl

Method BLASTX

```
q2914703
NCBI GI
                  300
BLAST score
                  7.0e-28
E value
Match length
                  60
% identity
                 (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   euj700698054.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1491710
BLAST score
                   205
E value
                   2.0e-16
                   71
Match length
% identity
                   (X96506) alpha subunit; forms heterodimer with NC2
NCBI Description
                   alpha/Dr1 [Homo sapiens]
                   44300
Seq. No.
                   euj700698057.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g126737
BLAST score
                   268
                   5.0e-26
E value
                   75
Match length
% identity
                   89
                   MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
NCBI Description
                   (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                   >gi_65939_pir__DEZMMX malate dehydrogenase
                   (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40)
                   precursor, chloroplast - maize >gi 168528 (J05130)
                   NADP-dependent malic enzyme (EC 1.\overline{1}.1.40) [Zea mays]
                   44301
Seq. No.
                   euj700698063.h1
Seq. ID
                   BLASTX
Method
                   g3746431
NCBI GI
                   333
BLAST score
                   2.0e-31
E value
Match length
                   68
 % identity
                   (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1
NCBI Description
                   [Zea mays]
 Seq. No.
                   44302
                   euj700698081.h1
 Seq. ID
                   BLASTX
 Method
                   q2506139
 NCBI GI
                   259
 BLAST score
                   4.0e-23
 E value
                   60
 Match length
                   78
 % identity
                   COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
 NCBI Description
                    (ARCHAIN) >qi 1314049 emb CAA91901_ (Z67962)
                   archain/delta-COP [Oryza sativa]
```

Seq. No. 44303

```
Seq. ID
                   euj700698093.h1
Method
                   BLASTX
                   g2605510
NCBI GI
BLAST score
                   172
                   7.0e-13
E value
Match length
                   59
% identity
                   61
                  (AB008678) alpha subunit of beta conglycinin [Glycine max]
NCBI Description
                   44304
Seq. No.
                   fC-qmf1700345191z1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q168460
BLAST score
                   428
E value
                   0.0e + 00
Match length
                   440
                   100
% identity
NCBI Description
                  Zea mays cyclophilin (CyP) mRNA, complete cds
Seq. No.
                   44305
Seq. ID
                   fC-gmf1700895992d3
Method
                  BLASTX
NCBI GI
                   g322551
BLAST score
                   267
                   2.0e-23
E value
Match length
                  71
% identity
                   69
                  nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis
NCBI Description
                   thaliana >gi_16398_emb_CAA49173_ (X69376) nucleoside
                   diphosphate kinase [Arabidopsis thaliana]
                   44306
Seq. No.
                   fC-qmf1700900218f1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18551
BLAST score
                   202
E value
                   1.0e-110
                   254
Match length
                   95
% identity
NCBI Description
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
                  protein
                   44307
Seq. No.
Seq. ID
                   fC-gmf1700902387r4
Method
                  BLASTN
NCBI GI
                  g1935018
BLAST score
                  105
E value
                   6.0e-52
Match length
                  305
% identity
                  88
NCBI Description V.faba mRNA for sucrose transporter
```

Seq. No. 44308

Seq. ID fC-qmf1700903946h1

Method BLASTX NCBI GI g1497987 BLAST score 239



```
E value
                   6.0e-20
Match length
                  67
                  75
% identity
                  (U62798) SCARECROW [Arabidopsis thaliana]
NCBI Description
                  44309
Seq. No.
                  fC-gmf1700904256h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1794171
BLAST score
                  612
E value
                  0.0e+00
Match length
                  638
% identity
                   99
NCBI Description Glycine max lipoxygenase-3 mRNA, complete cds
                   44310
Seq. No.
Seq. ID
                  fC-gmf1700904492r4
                  BLASTX
Method
                  g3152599
NCBI GI
BLAST score
                  374
E value
                  6.0e-36
                  86
Match length
% identity
                  39
                  (AC002986) Strong similarity to lupeol synthase gb U49919
NCBI Description
                  and cycloartenol synthase gb U02555 from A. thaliana (the
                  third gene with similar homology). [Arabidopsis thaliana]
Seq. No.
                   44311
Seq. ID
                   fC-gmf1700905152z1
Method
                  BLASTX
                  q4126403
NCBI GI
BLAST score
                  263
                  2.0e-46
E value
Match length
                  142
% identity
                   61
NCBI Description
                  (AB011796) flavonol synthase [Citrus unshiu]
                  44312
Seq. No.
                   fC-qmf1700906963a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1853970
BLAST score
                  463
                  2.0e-46
E value
Match length
                  124
% identity
NCBI Description
                  (D88122) CPRD46 protein [Vigna unguiculata]
Seq. No.
                  44313
```

Seq. ID fC-gmle700554424f3

Method BLASTX
NCBI GI g4544399
BLAST score 302
E value 1.0e-27
Match length 75
% identity 72

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

E value

Match length

% identity

8.0e-23 59

80



```
Seq. No.
                  44314
                  fC-gmle700554943f3
Seq. ID
Method
                  BLASTX
                  g113683
NCBI GI
BLAST score
                  138
                  1.0e-08
E value
Match length
                  67
% identity
                  39
NCBI Description ALPHA-AMYLASE ISOZYME 3E PRECURSOR (1,4-ALPHA-D-GLUCAN
                  GLUCANOHYDROLASE) >gi_100663_pir__JT0946 alpha-amylase 3E -
                  rice >gi 169773 (M59352) alpha-amylase [Oryza sativa]
Seq. No.
Seq. ID
                  fC-gmle700555621f3
Method
                  BLASTX
NCBI GI
                  g1142619
BLAST score
                  451
                  7.0e-45
E value
Match length
                  149
% identity
                  69
                  (U18348) phaseolin G-box binding protein PG1 [Phaseolus
NCBI Description
                  vulgaris]
Seq. No.
                  44316
Seq. ID
                  fC-gmle700555631d3
Method
                  BLASTX
NCBI GI
                  g4056462
BLAST score
                  325
E value
                  3.0e-30
Match length
                  72
% identity
                  83
                  (AC005990) Strong similarity to gb Y09876 aldehyde
NCBI Description
                  dehydrogenase (NAD+) from Nicotiana tabacum and a member of
                  the aldehyde dehydrogenase family PF_00171. ESTs
                  gb_F15117, gb_R83958 and gb_586262 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  44317
Seq. ID
                  fC-gmle700555748b1
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                   400
E value
                  6.0e-39
Match length
                  124
                  53
% identity
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.
                  44318
                  fC-gmle700556019b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3702328
BLAST score
                  262
```

NCBI Description (AC005397) putative cytochrome b5 [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  fC-qmle700556462d3
Method
                  BLASTX
NCBI GI
                  g4234953
BLAST score
                  176
E value
                  8.0e-13
Match length
                  54
% identity
NCBI Description
                  (AF098970) NBS-LRR-like protein cD7 [Phaseolus vulgaris]
Seq. No.
                  44320
Seq. ID
                  fC-gmle700556462f3
Method
                  BLASTX
NCBI GI
                  g2253117
BLAST score
                  186
E value
                  6.0e-14
Match length
                  57
% identity
                  (AF007098) chalcone synthase [Bromheadia finlaysoniana]
NCBI Description
                  44321
Seq. No.
                  fC-gmle700556911b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q558922
BLAST score
                  80
E value
                  6.0e-37
Match length
                  199
% identity
NCBI Description
                  Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA,
                  complete cds
Seq. No.
                  44322
                  fC-gmle700557012y1
Seq. ID
Method
                  BLASTX
                  g1703176
NCBI GI
BLAST score
                  222
E value
                  7.0e-18
Match length
                  163
% identity
                  34
                  NAD-DEPENDENT ALCOHOL DEHYDROGENASE >gi 1085620 pir S51120
NCBI Description
                  alcohol dehydrogenase (EC 1.1.1.1) - Sulfolobus sp
                  >gi_623348_emb_CAA87591_ (Z47543) alcohol dehydrogenase
                   [Sulfolobus sp.]
Seq. No.
                  44323
Seq. ID
                  fC-gmle700557012z1
Method
                  BLASTX
                  g1314712
NCBI GI
BLAST score
                  389
                  6.0e-38
E value
```

Match length 91 % identity

(U54615) calcium-dependent protein kinase [Arabidopsis NCBI Description

thaliana]

44324 Seq. No.



```
fC-qmle700559577g1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4538947
BLAST score
                   235
                   3.0e-20
E value
Match length
                   73
                   40
% identity
NCBI Description
                   (AL049483) putative mitochondrial carrier protein
                   [Arabidopsis thaliana]
Seq. No.
                   44325
                   fC-qmle700559917b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2688822
BLAST score
                   157
                   2.0e-10
E value
Match length
                   64
                   56
% identity
                   (U93272) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Prunus armeniaca]
                   44326
Seq. No.
Seq. ID
                   fC-gmle700560894z2
                   BLASTX
Method
NCBI GI
                   q510876
BLAST score
                   506
                   2.0e-51
E value
Match length
                   126
% identity
                  (X80051) NADP dependent malic enzyme [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   44327
                   fC-qmle700646043a3
Seq. ID
                   BLASTN
Method
                   g168466
NCBI GI
BLAST score
                   234
                   1.0e-129
E value
Match length
                   270
% identity
                   78
                  Corn late embryogenesis-abundant protein (EMB5) mRNA,
NCBI Description
                   complete cds
                   44328
Seq. No.
                   fC-gmle700683072b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3980254
BLAST score
                   157
E value
                   1.0e-10
Match length
                   43
% identity
                   70
```

(AJ006053) peroxisomal membrane protein [Arabidopsis NCBI Description

thaliana]

Seq. No.

44329

Seq. ID

fC-gmle700683896b1

Method

BLASTX g913445

NCBI GI



BLAST score 297 E value 7.0e-27 Match length 81 % identity 69

NCBI Description (S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv.

red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

Seq. No.

44330

Seq. ID fC-gmle700684428b1

Method BLASTX
NCBI GI g1749734
BLAST score 218
E value 8.0e-18
Match length 64
% identity 64

NCBI Description (D89263) similar to Saccharomyces cerevisiae succinate

dehydrogenase, SWISS-PROT Accession Number Q00711

[Schizosaccharomyces pombe]

Seq. No.

44331

Seq. ID fC-gmle700684751b1

Method BLASTX
NCBI GI g2257743
BLAST score 224
E value 2.0e-18
Match length 59
% identity 78

NCBI Description (U62020) lysine-sensitive aspartate kinase [Arabidopsis

thaliana]

Seq. No.

44332

Seq. ID

fC-gmle700686201b1

Method BLASTX
NCBI GI g1666096
BLAST score 174
E value 2.0e-12
Match length 41
% identity 83

NCBI Description (Y09113) dioxygenase [Marah macrocarpus]

Seq. No.

44333

Seq. ID

fC-gmle700742258a1

Method BLASTX
NCBI GI g1706822
BLAST score 288
E value 3.0e-26
Match length 84
% identity 60

NCBI Description FLAVONOL SYNTHASE (FLS) >gi 421946 pir S33510 flavonol

synthase - garden petunia >gi 311658 emb CAA80264 (Z22543)

flavonol synthase [Petunia x hybrida]

Seq. No.

44334

Seq. ID

fC-gmle700743136a1

Method NCBI GI BLASTN g169036



BLAST score 48
E value 4.0e-18
Match length 116
% identity 85

NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No. 44335

Seq. ID fC-gmle700872847y1

Method BLASTX
NCBI GI g2708741
BLAST score 826
E value 9.0e-89
Match length 190
% identity 84

NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No. 44336

Seq. ID fC-gmro7000747451f1

Method BLASTX
NCBI GI g4432846
BLAST score 148
E value 5.0e-10
Match length 42
% identity 71

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 44337

Seq. ID fC-gmro700351289h1

Method BLASTX
NCBI GI g2829885
BLAST score 378
E value 4.0e-36
Match length 96
% identity 67

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 44338

Seq. ID fC-gmro700351289i1

Method BLASTX
NCBI GI g3176662
BLAST score 717
E value 7.0e-76
Match length 230
% identity 60

NCBI Description (AC004393) Similar to mannosyl-oligosaccharide glucosidase

gb X87237 from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 44339

Seq. ID fC-gmro700561334a1

Method BLASTX
NCBI GI g2582639
BLAST score 320
E value 2.0e-29
Match length 138
% identity 53

NCBI Description (AJ002414) hnRNP-like protein [Arabidopsis thaliana]

```
44340
Seq. No.
                  fC-gmro700561429z1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4098966
BLAST score
                  40
                  6.0e-13
E value
Match length
                  84
                  87
% identity
NCBI Description Glycine max putative reistance gene analog genomic sequence
Seq. No.
                  44341
Seq. ID
                  fC-qmro700562679b1
Method
                  BLASTX
NCBI GI
                  q1905785
BLAST score
                  224
E value
                  2.0e-18
                  76
Match length
% identity
                  58
NCBI Description (Y10685) G/HBF-1 [Glycine max]
                  44342
Seq. No.
Seq. ID
                  fC-gmro700563759f2
                  BLASTX
Method
NCBI GI
                  q4539665
BLAST score
                  483
```

E value 3.0e-50 132 Match length % identity 72

(AF061282) polyprotein [Sorghum bicolor] NCBI Description

Seq. No. 44343 Seq. ID fC-gmro700566777z1 BLASTX Method g2129550 NCBI GI 570 BLAST score E value 5.0e-59 126 Match length 83 % identity

calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -NCBI Description

Arabidopsis thaliana >gi_2129554_pir__S71901

calcium-dependent protein kinase 6 - Arabidopsis thaliana

>gi 836940 (U20623) calcium-dependent protein kinase

[Arabidopsis thaliana] >gi 836944 (U20625)

calcium-dependent protein kinase [Arabidopsis thaliana] >gi 4454034 emb_CAA23031.1 (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 44344

fC-gmro700566893z1 Seq. ID

Method BLASTX NCBI GI g3183106 BLAST score 392 E value 6.0e-38 Match length 152 % identity 52

NCBI Description PROBABLE OXALYL-COA DECARBOXYLASE >gi 1788716 (AE000325)

putative enzyme [Escherichia coli]



```
44345
Seq. No.
                  fC-gmro700566983g1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q730220
                  336
BLAST score
                  2.0e-31
E value
Match length
                  169
                  42
% identity
                  OXALYL-COA DECARBOXYLASE >gi_1086099_pir__A55219 oxalyl-CoA
NCBI Description
                  decarboxylase (EC 4.1.1.8) - Oxalobacter formigenes
                  >gi 150447 (M77128) oxalyl-CoA decarboxylase [Oxalobacter
                  formigenes]
Seq. No.
                  44346
                  fC-gmro700567131y1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3719211
BLAST score
                  432
E value
                  1.0e-42
                  143
Match length
% identity
                  62
                 (U97021) UIP2 [Arabidopsis thaliana]
NCBI Description
                  44347
Seq. No.
                  fC-gmro700646337a3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4099918
BLAST score
                  43
E value
                  3.0e-15
Match length
                  75
% identity
                  89
                  Triticum aestivum pollen allergen homolog mRNA, complete
NCBI Description
                  44348
Seq. No.
                  fC-gmro700745970a1
Seq. ID
Method
                  BLASTN
                  g609224
NCBI GI
BLAST score
                  136
E value
                  2.0e-70
Match length
                  268
% identity
                  88
                  P.sativum mRNA for SAMS-2 >gi 609558 gb L36681 PEADENSYNB
NCBI Description
                  Pisum sativum S-adenosylmethionine synthase mRNA, complete
                  cds
```

Seq. No. 44349

Seq. ID fC-gmro700747348f1

Method BLASTN
NCBI GI g22274
BLAST score 129
E value 2.0e-66
Match length 280
% identity 14

NCBI Description Maize 26S - 17S rDNA spacer region from Black Mexican Sweet (BMS) suspension cells



```
Seq. No.
                   44350
Seq. ID
                   fC-gmro700747451f1
                   BLASTN
Method
NCBI GI
                   g1244652
BLAST score
                   164
E value
                   3.0e-87
Match length
                   274
% identity
                   91
                   Zea mays copia-type retroelement PREM-2 gag gene, complete
NCBI Description
                   cds
Seq. No.
                   44351
Seq. ID
                   fC-qmro700834861b2
Method
                   BLASTN
NCBI GI
                   g1143318
BLAST score
                   145
E value
                   1.0e-75
Match length
                   306
% identity
                   98
                  Glycine max biotin carboxyl carrier protein precursor
NCBI Description
                   (accB-1) mRNA, complete cds
Seq. No.
                   44352
Seq. ID
                   fC-gmro700835245e1
Method
                   BLASTN
NCBI GI
                   q3204100
BLAST score
                   64
                   8.0e-28
E value
Match length
                   148
% identity
                   86
NCBI Description Cicer arietinum mRNA for hypothetical protein, clone Can107
                   44353
Seq. No.
                   fC-gmro700843914r1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4559396
BLAST score
                   243
E value
                   1.0e-20
Match length
                   93
% identity
                   52
                  (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
                   44354
Seq. No.
Seq. ID
                   fC-gmro700844223d3
Method
                   BLASTN
                   g21954
                   33
                   4.0e-09
                   45
% identity
                   93
```

NCBI GI BLAST score E value Match length

NCBI Description Trifolium repens mRNA for non-cyanogenic beta-glucosidase

Seq. No. 44355

fC-qmro700847848a2 Seq. ID

Method BLASTN NCBI GI q1518539

```
BLAST score
                  146
                  1.0e-76
E value
Match length
                  218
% identity
                  92
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
Seq. No.
                  44356
Seq. ID
                  fC-gmro700848272f2
Method
                  BLASTX
NCBI GI
                  g1495802
BLAST score
                  431
E value
                  1.0e-42
Match length
                  111
% identity
                  69
                  (X96405) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
                  44357
Seq. No.
Seq. ID
                  fC-gmro700867540d3
Method
                  BLASTX
NCBI GI
                  g1311386
BLAST score
                  373
E value
                  9.0e-36
Match length
                  102
                  69
% identity
                  Cyanogenic Beta-Glucosidase Mol id: 1; Molecule: Cyanogenic
NCBI Description
                  Beta-Glucosidase; Chain: Null; Ec: 3.2.1.21
                  44358
Seq. No.
Seq. ID
                  fC-gmro700867615f1
Method
                  BLASTN
NCBI GI
                  q3641864
BLAST score
                  86
                  2.0e-40
E value
Match length
                  231
% identity
                  84
NCBI Description
                  Cicer arietinum mRNA for beta-galactosidase, clone
                  CanBGal-4
                  44359
Seq. No.
```

Seq. ID Method fC-gmro700868013d3

Method BLASTX
NCBI GI g3294469
BLAST score 162
E value 1.0e-11
Match length 52
% identity 58

NCBI Description (U89342) phosphoglucomutase 2 [Zea mays]

Seq. No.

44360

Seq. ID fC-gmro700875570d1

Method BLASTX
NCBI GI g4191774
BLAST score 315
E value 5.0e-29
Match length 93
% identity 65

NCBI Description (AC005917) putative beta-1,3-endoglucanase [Arabidopsis



thaliana]

Seq. No. 44361

Seq. ID fC-gmro700875617d1

Method BLASTX
NCBI GI g4127781
BLAST score 181
E value 2.0e-13
Match length 39
% identity 18

NCBI Description (AJ012588) Notchless protein [Drosophila melanogaster]

Seq. No. 44362

Seq. ID fC-gmro700877103d1

Method BLASTX
NCBI GI g1743354
BLAST score 139
E value 8.0e-09
Match length 37
% identity 70

NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No. 44363

Seq. ID fC-gmse7000752730d1

Method BLASTN
NCBI GI g2832242
BLAST score 93
E value 2.0e-45
Match length 109
% identity 12

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 44364

Seq. ID fC-gmse7000754068f1

Method BLASTN
NCBI GI g435456
BLAST score 40
E value 1.0e-13
Match length 52
% identity 94

NCBI Description Proso millet gene for aspartate aminotransferase, complete

cds

Seq. No. 44365

Seq. ID fC-gmse7000755389a1

Method BLASTX
NCBI GI g555655
BLAST score 225
E value 2.0e-18
Match length 82
% identity 61

NCBI Description (U06712) DNA-binding protein [Nicotiana tabacum]

Seq. No. 44366

Seq. ID fC-gmse7000755470d1

Method BLASTX NCBI GI g1518113



```
BLAST score
                  188
E value
                  5.0e-14
                  63
Match length
                  65
% identity
NCBI Description
                  (U66193) SLL2 [Brassica napus]
                  44367
Seq. No.
                  fC-gmse700645507a3
Seq. ID
Method
                  BLASTX
```

NCBI GI q1708025 BLAST score 434 E value 3.0e-43Match length 93 89

% identity

GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+] NCBI Description

>gi 840731 emb CAA56125 (X79677) glycerol-3-phosphate

dehydrogenase (NAD+) [Cuphea lanceolata]

Seq. No. Seq. ID fC-gmse700646592a3 Method BLASTX NCBI GI g2497904 BLAST score 159 E value 3.0e-11 49 Match length % identity 67

44368

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1667588 (U77294)

metallothionein-like protein [Oryza sativa]

>gi 2326785 emb CAA69845 (Y08529) metallothionein-like

protein [Oryza sativa] >gi 4097338 (U57638)

metallothionein-like protein [Oryza sativa] >gi 4105603

(AF048750) metallothionein [Oryza sativa]

Seq. No. 44369

Seq. ID fC-gmse700654835d1

Method BLASTN NCBI GI g515748 40 BLAST score 2.0e-13 E value Match length 128 % identity

NCBI Description Soybean chloroplast phytochrome A (phyA) gene, complete cds

44370 Seq. No.

Seq. ID fC-gmse700654835d6

Method BLASTN NCBI GI q515748 BLAST score 196 1.0e-106 E value 384 Match length % identity

NCBI Description Soybean chloroplast phytochrome A (phyA) gene, complete cds

Seq. No. 44371

fC-qmse700654980f4 Seq. ID

Method BLASTX NCBI GI g3252856



```
BLAST score
 E value
                    5.0e-16
. Match length
                    47
 % identity
                    79
                    (AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
 NCBI Description
                    tabacum]
                    44372
 Seq. No.
                    fC-gmse700656786f6
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                    g1236950
 BLAST score
                    141
 E value
                    1.0e-73
 Match length
                    184
 % identity
                    95
 NCBI Description
                   Glycine max nucleoside diphosphate kinase mRNA, complete
 Seq. No.
                    44373
 Seq. ID
                    fC-gmse700657291r2
                    BLASTN
 Method
 NCBI GI
                    g1196896
 BLAST score
                    72
                    7.0e-33
 E value
                   108
 Match length
 % identity
                    93
 NCBI Description Glycine max acidic ribosomal protein PO mRNA, complete cds
 Seq. No.
                    44374
                    fC-gmse700657837a3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4376158
 BLAST score
                    139
 E value
                    6.0e-09
 Match length
                    46
 % identity
                    63
 NCBI Description
                   (X98873) aspartate kinase [Arabidopsis thaliana]
 Seg. No.
                    44375
 Seq. ID
                    fC-gmse700658206r5
                    BLASTX
 Method
 NCBI GI
                    g1280611
 BLAST score
                    173
 E value
                    1.0e-12
                    47
 Match length
 % identity
                    64
 NCBI Description
                   (U53860) steroid reductase DET2 [Arabidopsis thaliana]
                    44376
 Seq. No.
                    fC-gmse700658613f6
 Seq. ID
```

Method BLASTN
NCBI GI g2055227
BLAST score 226
E value 1.0e-124
Match length 274
% identity 96

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. ID

Method

NCBI GI



```
44377
Seq. No.
                  fC-gmse700659714b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2661127
BLAST score
                  84
                  1.0e-39
E value
                  172
Match length
                  87
% identity
NCBI Description
                  Glycine max arginase (pAG1) mRNA, complete cds
                   44378
Seq. No.
                  fC-qmse700659714d3
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2661127
BLAST score
                  104
E value
                   2.0e-51
Match length
                   208
% identity
                   88
NCBI Description Glycine max arginase (pAG1) mRNA, complete cds
Seq. No.
                   44379
                   fC-gmse700660470r5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2194117
                  150
BLAST score
                   7.0e-10
E value
Match length
                   49
                   57
% identity
NCBI Description
                  (AC002062) Strong similarity to Arabidopsis receptor
                  protein kinase PR5K (gb_ATU48698). [Arabidopsis thaliana]
Seq. No.
                   44380
                   fC-gmse700668119k2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3928095
BLAST score
                   882
E value
                   3.0e-95
Match length
                   219
                   73
% identity
                  (AC005770) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   44381
Seq. No.
Seq. ID
                   fC-qmse700669394j2
Method
                   BLASTN
NCBI GI
                   g1330253
BLAST score
                   694
                   0.0e + 00
E value
                   694
Match length
                   100
% identity
                  Zea mays calcium-dependent protein kinase mRNA, complete
NCBI Description
                   cds
                   44382
Seq. No.
```

7086

fC-gmse700669501x2

BLASTN

g399628



BLAST score 35 E value 5.0e-10 Match length 71 % identity 89

NCBI Description Lycopersicon esculentum (DB207) meloidogyne-induced giant

cell protein mRNA, 3' end

Seq. No. 44383

Seq. ID fC-gmse700670050g3

Method BLASTN
NCBI GI g22233
BLAST score 188
E value 1.0e-102
Match length 209
% identity 97

NCBI Description Maize mRNA for catalase

Seq. No. 44384

Seq. ID fC-gmse700670315g2

Method BLASTN
NCBI GI g1046277
BLAST score 142
E value 5.0e-74
Match length 425
% identity 83

NCBI Description Phaseolus vulgaris embryo-specific acidic transcriptional

activator PvAlf mRNA, complete cds

Seq. No. 44385

Seq. ID fC-gmse700671180g1

Method BLASTX
NCBI GI g3204108
BLAST score 237
E value 1.0e-19
Match length 85
% identity 55

NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer

arietinum]

Seq. No. 44386

Seq. ID fC-gmse700671753b1

Method BLASTN
NCBI GI g1772305
BLAST score 54
E value 1.0e-21
Match length 110
% identity 87

NCBI Description Glycine max mRNA for glycinin, complete cds

Seq. No. 44387

Seq. ID fC-gmse700672004gg1

Method BLASTX
NCBI GI g2735256
BLAST score 331
E value 1.0e-30
Match length 74
% identity 82



```
NCBI Description (U89683) protein kinase [Lycopersicon esculentum]
```

Seq. No. 44388

Seq. ID fC-gmse700672157g1

Method BLASTN
NCBI GI g3342803
BLAST score 275
E value 1.0e-153
Match length 287
% identity 99

NCBI Description Zea mays strain B73 putative 6-phosphogluconate

dehydrogenase mRNA, nuclear gene encoding putative plastid

protein, partial cds

Seq. No. 44389

Seq. ID fC-gmse700672157z1

Method BLASTX
NCBI GI g3075399
BLAST score 176
E value 8.0e-13
Match length 49
% identity 73

NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No. 44390

Seq. ID fC-gmse700672216g1

Method BLASTX
NCBI GI g2281102
BLAST score 159
E value 1.0e-10
Match length 102
% identity 38

NCBI Description (AC002333) SF16 isolog [Arabidopsis thaliana]

Seq. No. 44391

Seq. ID fC-gmse700672216h1

Method BLASTX
NCBI GI g3641252
BLAST score 273
E value 6.0e-24
Match length 182
% identity 9

NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

domestical

Seq. No. 44392

Seq. ID fC-gmse700672216z1

Method BLASTX
NCBI GI g1934972
BLAST score 599
E value 3.0e-62
Match length 176
% identity 62

NCBI Description (Y08611) dihydropterin pyrophosphokinase /dihydropteroate

synthase [Pisum sativum]

Seq. No. 44393



Seq. ID fC-gmse700672271f1

Method BLASTN
NCBI GI g170009
BLAST score 92
E value 3.0e-44
Match length 224
% identity 85

NCBI Description Soybean late embryogenesis abundant (LEA) protein mRNA,

complete cds

Seq. No.

Seq. ID fC-gmse700672271y1

44394

Method BLASTX
NCBI GI g2258315
BLAST score 146
E value 5.0e-09
Match length 107
% identity 18

NCBI Description (AF004878) resistance complex protein I2C-1 [Lycopersicon

esculentum]

Seq. No. 44395

Seq. ID fC-gmse700672319g1

Method BLASTX
NCBI GI g2435511
BLAST score 569
E value 1.0e-58
Match length 132
% identity 79

NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase

alpha subunit [Arabidopsis thaliana]

Seq. No. 44396

Seq. ID fC-gmse700672582d4

Method BLASTN
NCBI GI g476213
BLAST score 77
E value 2.0e-35
Match length 233
% identity 89

NCBI Description Glycine max Century 84 p24 oleosin isoform A gene, complete

cds

Seq. No. 44397

Seq. ID fC-gmse700672582g1

Method BLASTX
NCBI GI g1199467
BLAST score 843
E value 1.0e-90
Match length 234
% identity 62

NCBI Description (D64155) possible aldehyde decarbonylase [Arabidopsis

thaliana]

Seq. No. 44398

Seq. ID fC-gmse700672649y1

Method BLASTX

```
q3805847
NCBI GI
BLAST score
                   199
                   3.0e-15
E value
Match length
                   71
% identity
                  (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44399
                   fC-gmse700672974g1
Seq. ID
Method
                  BLASTX
                  q2252472
NCBI GI
BLAST score
                   409
E value
                  7.0e-40
Match length
                  126
                   60
% identity
                 (Z97558) argininosuccinate lyase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44400
                   fC-gmse700672974z1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4220485
BLAST score
                   525
E value
                   2.0e-53
Match length
                   210
% identity
                   47
NCBI Description
                   (AC006069) putative beta-1,3-glucanase [Arabidopsis
                   thaliana]
```

44401 Seq. No.

fC-gmse700673793d3 Seq. ID

Method BLASTN NCBI GI g476215 BLAST score 60 E value 3.0e-25 Match length 163

% identity 88

Glycine max Century 84 p24 oleosin isoform B gene, complete NCBI Description

cds

44402 Seq. No.

Seq. ID fC-gmse700673793d4

Method BLASTN g476215 NCBI GI BLAST score 41 9.0e-14 E value Match length 118 % identity 82

Glycine max Century 84 p24 oleosin isoform B gene, complete NCBI Description

cds

Seq. No. 44403

fC-gmse700673793r4 Seq. ID

BLASTN Method NCBI GI q476215 BLAST score 90 E value 2.0e-43 Match length 146



% identity 90

NCBI Description Glycine max Century 84 p24 oleosin isoform B gene, complete

cds

Seq. No. 44404

Seq. ID fC-gmse700674044d3

Method BLASTN
NCBI GI g736001
BLAST score 55
E value 3.0e-22
Match length 140
% identity 84

NCBI Description G.soja (SH1) Gy5 mRNA for glycinin

Seq. No.

44405

Seq. ID fC-gmse700674044d4 Method BLASTN

NCBI GI g1772307 BLAST score 74 E value 2.0e-33 Match length 118 % identity 91

NCBI Description Glycine max mRNA for glycinin, complete cds

Seq. No.

44406

Seq. ID fC-gmse700674044d5

Method BLASTN
NCBI GI g736001
BLAST score 37
E value 1.0e-11
Match length 117
% identity 89

NCBI Description G.soja (SH1) Gy5 mRNA for glycinin

Seq. No.

44407

Seq. ID fC-gmse700674467h1

Method BLASTX
NCBI GI g4204303
BLAST score 298
E value 7.0e-27
Match length 74
% identity 73

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 44408

Seq. ID fC-gmse700675569i1

Method BLASTX
NCBI GI g1497987
BLAST score 312
E value 1.0e-28
Match length 68
% identity 84

NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]

Seq. No. 44409

Seq. ID fC-gmse700675914a3

7091



```
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  200
                  1.0e-108
E value
Match length
                  500
% identity
                  85
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  44410
Seq. No.
                  fC-gmse700675914h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  169
E value
                  6.0e-90
Match length
                  584
                  84
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
Seq. No.
                  44411
Seq. ID
                  fC-gmse700725419f1
Method
                  BLASTN
NCBI GI
                  g2244739
BLAST score
                  34
                  5.0e-10
E value
Match length
                  86
% identity
                  85
                  Cotton mRNA for endo-1,4-beta-glucanase, clone CF996,
NCBI Description
                  partial cds
Seq. No.
                  44412
                  fC-qmse700725647b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1168529
BLAST score
                  152
E value
                  5.0e-10
                  37
Match length
                   73
% identity
                  SERINE/THREONINE-PROTEIN KINASE ASK1 >gi 541890 pir
NCBI Description
                  probable serine/threonine-specific protein kinase (EC
                  2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi_166882
                   (M91548) serine/threonine kinase [Arabidopsis thaliana]
                  >gi_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]
                   44413
Seq. No.
Seq. ID
                  fC-gmse700750575a2
Method
                  BLASTX
```

Method BLASTX
NCBI GI g282881
BLAST score 145
E value 1.0e-11
Match length 53
% identity 70

NCBI Description receptor-like protein kinase precursor - Arabidopsis thaliana >gi 166846 (M84658) receptor-like protein kinase

[Arabidopsis thaliana]



```
Seq. No.
                  44414
                  fC-gmse700786268d2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3327388
BLAST score
                  178
                  2.0e-95
E value
Match length
                  432
                  6
% identity
                  Arabidopsis thaliana chromosome II BAC T12J2 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  44415
Seq. No.
Seq. ID
                  fC-gmse700830015d1
                  BLASTX
Method
NCBI GI
                  q349379
BLAST score
                  148
E value
                  2.0e-09
Match length
                  73
                  60
% identity
NCBI Description
                  (L22847) HAHB-1 [Helianthus annuus]
Seq. No.
                  44416
Seq. ID
                  fC-gmse700830206d1
Method
                  BLASTX
NCBI GI
                  g1903357
BLAST score
                  279
                  1.0e-24
E value
Match length
                  83
% identity
NCBI Description
                  (AC000104) Strong similarity to Arabidopsis 2A6
                  (gb X83096). [Arabidopsis thaliana]
                  44417
Seq. No.
                  fC-gmse700836747b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462754
BLAST score
                  175
E value
                  5.0e-16
Match length
                  130
% identity
                  36
                  (AC002292) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  44418
Seq. ID
                  fC-gmse700837723b1
                  BLASTX
Method
NCBI GI
                  g3641252
BLAST score
                  186
E value
                  2.0e-33
                  243
Match length
                  20
% identity
```

NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

domestica]

Seq. No. 44419

fC-gmse700838914b1 Seq. ID

Method BLASTX NCBI GI q2351136



BLAST score 137 E value 2.0e-13 Match length 106 % identity 36

NCBI Description (D85202) S glycoprotein [Brassica oleracea]

Seq. No. 44420

Seq. ID fC-gmse700839502b1

Method BLASTX
NCBI GI g3461835
BLAST score 114
E value 1.0e-10
Match length 53
% identity 52

NCBI Description (AC005315) putative protein kinase [Arabidopsis thaliana]

>gi 3927840 (AC005727) putative protein kinase [Arabidopsis

12 %

thaliana]

Seq. No. 44421

Seq. ID fC-gmse700843126f1

Method BLASTX
NCBI GI g2827711
BLAST score 166
E value 4.0e-12
Match length 44
% identity 70

NCBI Description (AL021684) oxoglutarate dehydrogenase - like protein

[Arabidopsis thaliana]

Seq. No. 44422

Seq. ID fC-gmse700850069f1

Method BLASTX
NCBI GI g4539330
BLAST score 179
E value 4.0e-13
Match length 98
% identity 52

NCBI Description (AL035679) putative receptor-like protein kinase (fragment)

[Arabidopsis thaliana]

Seq. No. 44423

Seq. ID fC-gmse700850850d1

Method BLASTX
NCBI GI g2245077
BLAST score 175
E value 1.0e-12
Match length 59
% identity 54

NCBI Description (Z97343) glucanase homolog [Arabidopsis thaliana]

Seq. No. 44424

Seq. ID fC-gmse800839958h1

Method BLASTX
NCBI GI g1480670
BLAST score 234
E value 8.0e-20
Match length 69



% identity 68

NCBI Description (U60267) delta 1-pyrroline-5-carboxylate synthetase

[Lycopersicon esculentum]

Seq. No. 44425

Seq. ID fC-gmst700605139a2

Method BLASTX
NCBI GI g3128225
BLAST score 357
E value 2.0e-34
Match length 81
% identity 85

NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID fC-gmst700605255a2

44426

Method BLASTX
NCBI GI g1184075
BLAST score 156
E value 1.0e-10
Match length 70
% identity 2

NCBI Description (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]

>gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon

esculentum]

Seq. No. 44427

Seq. ID fC-gmst700605481a2

Method BLASTN
NCBI GI g559535
BLAST score 123
E value 4.0e-63
Match length 173
% identity 94

NCBI Description Z.mays mRNA for metallothionein

Seq. No. 44428

Seq. ID fC-gmst700647969a3

Method BLASTX
NCBI GI g2499488
BLAST score 381
E value 3.0e-37
Match length 79
% identity 94

NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE

ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >gi 483547 emb CAA83682 (Z32849)

pyrophosphate-dependent phosphofructokinase alpha subunit

[Ricinus communis]

Seq. No. 44429

Seq. ID fC-gmst700648616a3

Method BLASTX
NCBI GI g1351107
BLAST score 146
E value 9.0e-10



Match length 48 % identity 56

NCBI Description SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE

GLUCOSYLTRANSFERASE) >gi_1361971_pir__S55253

sucrose-phosphate synthase - sugar beet

>gi_1488568_emb_CAA57500_ (X81975) sucrose-phosphate

.

synthase [Beta vulgaris]

Seq. No. 44430

Seq. ID fC-gmst700648873a3

Method BLASTX
NCBI GI g2134385
BLAST score 143
E value 2.0e-09
Match length 34
% identity 79

NCBI Description protein kinase - chicken >gi 571460 (U16656) protein kinase

[Gallus gallus]

Seq. No. 44431

Seq. ID fC-gmst700649106a3

Method BLASTN
NCBI GI g1800216
BLAST score 89
E value 1.0e-42
Match length 145
% identity 91

NCBI Description Sorghum bicolor phytochrome B (PHYB) gene, partial cds

Seq. No. 44432

Seq. ID fC-gmst700649626g1

Method BLASTX
NCBI GI g2880049
BLAST score 112
E value 1.0e-09
Match length 67
% identity 46

NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 44433

Seq. ID fC-gmst700650111a3

Method BLASTN
NCBI GI g553071
BLAST score 253
E value 1.0e-140
Match length 261
% identity 99

NCBI Description Maize catalase (Cat2) mRNA, 3' end

Seq. No. 44434

Seq. ID fC-gmst700651372d4

Method BLASTN
NCBI GI g169988
BLAST score 190
E value 1.0e-102
Match length 310
% identity 91



NCBI Description Glycine max NADP-specific isocitrate dehydrogenase (idh1) mRNA, 3' end

Seq. No. 44435

Seq. ID fC-gmst700661063a3

Method BLASTN
NCBI GI g20061
BLAST score 124
E value 2.0e-63
Match length 252
% identity 87

NCBI Description Oenothera elata subsp. hookeri mRNA for protein kinase C

inhibitor homologue

Seq. No. 44436

Seq. ID fC-gmst700665136f2

Method BLASTN
NCBI GI g170009
BLAST score 172
E value 7.0e-92
Match length 244
% identity 93

NCBI Description Soybean late embryogenesis abundant (LEA) protein mRNA,

complete cds

Seq. No. 44437

Seq. ID fC-gmst700665919a2

Method BLASTN
NCBI GI g1046277
BLAST score 38
E value 3.0e-12
Match length 89
% identity 86

NCBI Description Phaseolus vulgaris embryo-specific acidic transcriptional

activator PvAlf mRNA, complete cds

Seq. No. 44438

Seq. ID fC-gmst700888494r1

Method BLASTN
NCBI GI 9726029
BLAST score 76
E value 6.0e-35
Match length 132
% identity 89

NCBI Description Actinidia chinensis S-adenosylmethionine synthetase mRNA,

complete cds

Seq. No. 44439

Seq. ID fC-gmst700891140d3

Method BLASTX
NCBI GI g1168413
BLAST score 164
E value 6.0e-12
Match length 43
% identity 70

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE >gi 1074103 pir__C64074

fructose-bisphosphate aldolase (fba) homolog - Haemophilus



influenzae (strain Rd KW20) >gi_1573507 (U32734)
fructose-bisphosphate aldolase (fba) [Haemophilus
influenzae Rd]

Seq. No.

44440

Seq. ID Method

fde700870516.h1

Method NCBI GI BLASTX g3914472

BLAST score E value

163 5.0e-18

Match length

63

% identity NCBI Description 79
PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

>gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No.

44441

Seq. ID

fde700870585.h1

Method NCBI GI BLASTX q3249072

BLAST score

185

E value Match length 1.0e-22 81

% identity

74

NCBI Description

(AC004473) Contains similarity to hypothetical 43.1 KD

protein in NDK-GCPE intergenic region gb 493519 from E.

coli sequence gb_U02965. [Arabidopsis thaliana]

Seq. No.

44442

Seq. ID

fde700870634.h1

Method NCBI GI BLASTN g20728

BLAST score

56

E value

6.0e-23

Match length

136

% identity

85

NCBI Description

Pea chloroplast GAPA mRNA encoding

glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A

(EC 1.2.1.13)

Seq. No.

44443

Seq. ID

fde700870642.h1

Method NCBI GI BLASTX g2760323

BLAST score

159

E value

3.0e-15

Match length % identity

54

NCBI Description

(AC002130) F1N21.8 [Arabidopsis thaliana]

Seq. No.

44444

Seq. ID

fde700870684.hl

Method NCBI GI BLASTX g3142303

BLAST score E value

297 2.0e-27

7098



Match length 75 % identity 48

NCBI Description (AC002411) Strong similarity to MRP-like ABC transporter

gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus.

[Arabidopsis thaliana]

Seq. No. 44445

Seq. ID fde700870722.h1

Method BLASTN
NCBI GI g1053215
BLAST score 179
E value 3.0e-96
Match length 255
% identity 96

NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA,

nuclear gene encoding chloroplast protein, complete cds

Seq. No. 44446

Seq. ID fde700870729.h1

Method BLASTX
NCBI GI g417038
BLAST score 307
E value 2.0e-28
Match length 79
% identity 68

NCBI Description TRANSCRIPTIONAL ACTIVATOR GCN5 >gi_283135_pir__S28051

transcription factor GCN5 - yeast (Saccharomyces

cerevisiae) >gi_3736_emb_CAA48602 (X68628) GCN5 protein [Saccharomyces cerevisiae] >gi_1323458_emb_CAA97281 (Z73037) ORF YGR252w [Saccharomyces cerevisiae]

Seq. No. 44447

Seq. ID fde700870786.h1

Method BLASTX
NCBI GI g3402699
BLAST score 222
E value 1.0e-18
Match length 73
% identity 71

NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No. 44448

Seq. ID fde700870833.h1

Method BLASTN
NCBI GI g4389416
BLAST score 47
E value 1.0e-17
Match length 136
% identity 93

NCBI Description Glycine max nitrate reductase (nr2) gene, partial cds

Seq. No. 44449

Seq. ID fde700870838.h1

Method BLASTN NCBI GI g2342957

BLAST score 41



E value 6.0e-14 Match length 57

% identity 93

NCBI Description Glycine tabacina ribulose 1,5-bisphosphate

carboxylase-oxygenase large subunit (rbcL) gene,

choloroplast gene encoding chloroplast protein, partial cds

Seq. No. 44450

Seq. ID fde700870842.h1

Method BLÄSTX
NCBI GI g2618691
BLAST score 237
E value 3.0e-20
Match length 54
% identity 81

NCBI Description (AC002510) putative chloroplast envelope Ca2+-ATPase

[Arabidopsis thaliana]

Seq. No.

44451

Seq. ID fde700870843.h1

Method BLASTX
NCBI GI g3763927
BLAST score 178
E value 2.0e-13
Match length 83
% identity 57

NCBI Description (AC004450) putative carboxyphosphoenolpyruvate mutase

[Arabidopsis thaliana]

Seq. No. 44452

Seq. ID fde700870940.hl

Method BLASTN
NCBI GI g643454
BLAST score 114
E value 1.0e-57
Match length 237
% identity 87

NCBI Description Aureobasidium pullulans translation elongation factor

1-alpha (tef1) gene, complete cds

Seq. No.

44453

Seq. ID fde700870992.h1

Method BLASTX
NCBI GI g2500107
BLAST score 236
E value 2.0e-20
Match length 55
% identity 82

NCBI Description DNA REPAIR PROTEIN RAD51 HOMOLOG >gi 1143810 (U22441)

LeRAD51 [Solanum lycopersicum]

Seq. No.

44454

Seq. ID fde700871017.h1

Method BLASTN
NCBI GI g2661020
BLAST score 194
E value 1.0e-105



222 Match length % identity 97

NCBI Description Glycine max catalase (cat4) mRNA, complete cds

Seq. No.

44455

Seq. ID

fde700871024.h1

Method

BLASTX g4115563

NCBI GI BLAST score

190

E value

9.0e-15

Match length

% identity

81 51

NCBI Description

(AB013598) UDP-glucose:anthocyanin 5-0-glucosyltransferase

[Verbena x hybrida]

Seq. No.

Seq. ID

fde700871050.h1

Method NCBI GI BLASTX g3776557

44456

BLAST score

195 2.0e-15

E value Match length

68

% identity

54

NCBI Description

(AC005388) Contains similarity to gi_2924495 hypothetical

protein Rv1920 from Mycobacterium tuberculosis genome

gb_AL022020. [Arabidopsis thaliana]

Seq. No.

Seq. ID

44457 fde700871051.hl

Method

BLASTX

NCBI GI

g3367578

BLAST score

284

E value

1.0e-25

Match length

73

% identity

NCBI Description

(AL031135) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No.

44458

Seq. ID

fde700871174.h1

Method

BLASTN

NCBI GI

g3021356

BLAST score

56

E value

6.0e-23

Match length

68 96

% identity

NCBI Description Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,

clone GEPI48

Seq. No.

44459

Seq. ID

fde700871196.hl

Method NCBI GI BLASTN

q1150683

BLAST score

52

E value Match length 1.0e-20

% identity

210 82

7101



```
NCBI Description V.radiata atpB, rbcL and trnK genes
```

Seq. No. 44460 fde700871314.h1 Seq. ID Method BLASTX NCBI GI q1170646 BLAST score 146 E value 1.0e-09

Match length 71 % identity 39

NCBI Description SERINE/THREONINE-PROTEIN KINASE RIM15

> >gi 1084696 pir S56221 hypothetical protein YFL033c yeast (Saccharomyces cerevisiae) >gi_836721_dbj_BAA09206_ (D50617) YFL033C [Saccharomyces cerevisiae] >gi 2213667

(U83459) Rim15p [Saccharomyces cerevisiae] >gi 3250892 emb CAA04486 (AJ001030) putative

serine/threonine protein kinase [Saccharomyces cerevisiae]

Seq. No. 44461

Seq. ID fde700871345.hl

Method BLASTX NCBI GI q1620920 BLAST score 128 E value 5.0e-10 Match length 64 % identity 59

NCBI Description (Y08886) 23kD protein of oxygen evolving system of

photosystem II [Brassica juncea]

Seq. No. 44462

Method

Seq. ID fde700871367.h1

BLASTN

NCBI GI g2924257 BLAST score 69 E value 1.0e-30 Match length 181

% identity 85

NCBI Description Tobacco chloroplast genome DNA

Seq. No. 44463

Seq. ID fde700871395.h1

Method BLASTX NCBI GI q4468810 BLAST score 171 1.0e-12 E value Match length 66 % identity 45

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 44464

Seq. ID fde700871443.h1

Method BLASTX NCBI GI g282929 BLAST score 176 E value 4.0e-13 Match length 81 % identity 48

7102

NCBI Description

44470

fde700871633.hl

Seq. No.

Seq. ID



```
NCBI Description carbonate dehydratase (EC 4.2.1.1) - garden pea
Seq. No.
                   44465
Seq. ID
                  fde700871472.h1
Method
                  BLASTX
NCBI GI
                  g2191151
BLAST score
                  140
E value
                  6.0e-09
                  78
Match length
% identify
                  35
NCBI Description
                  (AF007269) contains similarity to membrane associated
                  salt-inducible protein [Arabidopsis thaliana]
Seq. No.
                  44466
                  fde700871478.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2853087
BLAST score
                  382
E value
                  2.0e-37
Match length
                  80
% identity
                  90
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]
Seq. No.
                  44467
Seq. ID
                  fde700871487.h1
Method
                  BLASTX
NCBI GI
                  q3928543
BLAST score
                  153
E value
                  2.0e-10
Match length
                  78
% identity
                  38
NCBI Description
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
                  thaliana]
Seq. No.
                  44468
Seq. ID
                  fde700871534.h1
Method
                  BLASTN
NCBI GI
                  g166379
BLAST score
                  91
E value
                  8.0e-44
Match length
                  209
% identity
                  70
NCBI Description
                 Alfalfa glucose-regulated endoplasmic reticular protein
                  mRNA, complete cds
Seq. No.
                  44469
Seq. ID
                  fde700871536.h1
Method
                  BLASTX
NCBI GI
                  g2781347
BLAST score
                  177
E value
                  2.0e-13
Match length
                  74
% identity
                  53
```

(AC003113) F2401.3 [Arabidopsis thaliana]



Method BLASTN
NCBI GI g1150683
BLAST score 65
E value 3.0e-28
Match length 227
% identity 81

NCBI Description V.radiata atpB, rbcL and trnK genes

Seq. No.

44471

44472

Seq. ID

fde700871767.hl

Method BLASTN
NCBI GI g3281845
BLAST score 41
E value 5.0e-14

Match length 65 % identity 91

NCBI Description Arabidopsis thaliana mRNA for LATE ELONGATED HYPOCOTYL MYB

transcription factor

Seq. No.

Seq. ID fde700871818.h1

Method BLASTX
NCBI GI g3643611
BLAST score 218
E value 3.0e-18
Match length 66
% identity 58

NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No. 44473

Seq. ID fde700871869.h1

Method BLASTX
NCBI GI g225267
BLAST score 250
E value 8.0e-22

Match length 80 % identity 56

NCBI Description ORF 1244 [Nicotiana tabacum]

Seq. No. 44474

Seq. ID fde700871894.h1

Method BLASTX
NCBI GI g2245004
BLAST score 177
E value 4.0e-14
Match length 64
% identity 55

NCBI Description (Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

Seq. No.

Seq. ID fde700871895.h1

44475

Method BLASTX
NCBI GI g3746071
BLAST score 238
E value 1.0e-20
Match length 81



% identity

NCBI Description (AC005311) putative GTP-binding protein [Arabidopsis

Seq. No. 44476

fde700871910.hl Seq. ID

Method BLASTN NCBI GI g343022 BLAST score 50 E value 2.0e-19 Match length 62 95 % identity

Pea chloroplast photosystem II gene encoding the D2 and NCBI Description

44kd chlorophyll a-binding proteins, complete cds

Seq. No. 44477

fde700871938.h1 Seq. ID

Method BLASTN NCBI GI q4406529 BLAST score 60 E value 2.0e-25 Match length 144

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 44478

% identity

Seq. ID fde700871950.h1

85

Method BLASTN NCBI GI g3059094 BLAST score 72 E value 2.0e-32 Match length 168

% identity 86

NCBI Description Glycine max mRNA for magnesium chelatase subunit

Seq. No. 44479

Seq. ID fde700872054.hl

Method BLASTX NCBI GI g134615 263 BLAST score E value 2.0e-23 Match length 64 73 % identity

NCBI Description SUPEROXIDE DISMUTASE (CU-ZN) >gi 101875 pir A36591

superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - Neurospora crassa >gi_168909 (M58687) Cu/Zn-superoxide dismutase

[Neurospora crassa]

Seq. No. 44480

fde700872167.h1 Seq. ID

Method BLASTX NCBI GI g3021283 BLAST score 157 E value 2.0e-24 Match length 76 % identity 80



(AL022347) serine/threonine kinase - like protein NCBI Description [Arabidopsis thaliana]

Seq. No. 44481

Seq. ID fde700872206.h1

Method BLASTX NCBI GI g267055 BLAST score 264 E value 1.0e-23 Match length 73 68

% identity NCBI Description SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)

>gi_66572_pir__YUMU sucrose synthase (EC 2.4.1.13) -Arabidopsis thaliana >gi 16526 emb CAA43303 (X60987)

sucrose synthase [Arabidopsis thaliana]

Seq. No. 44482

Seq. ID fde700872458.h1

Method BLASTX NCBI GI g1293099 BLAST score 161 E value 2.0e-11 Match length 80 % identity 42

NCBI Description (U53884) aimless RasGEF [Dictyostelium discoideum]

Seq. No. 44483

Seq. ID fde700872481.h1

Method BLASTX NCBI GI g2435517 BLAST score 204 E value 2.0e-16 Match length 74

49 % identity

(AF024504) contains similarity to peptidase family A1 NCBI Description

[Arabidopsis thaliana]

Seq. No. 44484

fde700872665.h1 Seq. ID

Method BLASTX NCBI GI g3451068 BLAST score 263 E value 2.0e-23 Match length 77 % identity 74

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 44485

% identity

Seq. ID fde700872703.h1

68

Method BLASTX NCBI GI q1168411 BLAST score 199 E value 9.0e-16 Match length 69

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR



```
Seq. No.
                   44486
                   fde700872707.hl
Seq. ID
Method
                  BLASTX
                  g2673910
NCBI GI
                   183
BLAST score
                   5.0e-14
E value
                  82
Match length
% identity
                   49
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
                   44487
Seq. No.
Seq. ID
                   fde700872718.h1
Method
                  BLASTX
NCBI GI
                  g3540180
BLAST score
                   182
                   5.0e-14
E value
Match length
                   48
                   69
% identity
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   44488
Seq. ID
                   fde700872776.h1
Method
                  BLASTX
NCBI GI
                   g3334667
BLAST score
                  169
E value
                   2.0e-12
                  82
Match length
% identity
                   43
NCBI Description (Y10493) putative cytochrome P450 [Glycine max]
                   44489
Seq. No.
Seq. ID
                   fde700872802.hl
Method
                   BLASTX
NCBI GI
                   q3395432
BLAST score
                   229
E value
                   2.0e-19
Match length
                  55
% identity
                  71
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                   44490
Seq. No.
Seq. ID
                   fde700872896.h1
Method
                  BLASTN
NCBI GI
                  g3985934
BLAST score
                   42
E value
                  1.0e-14
Match length
                   86
% identity
                   87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJE7, complete sequence [Arabidopsis thaliana]
```

Seq. No. 44491

Seq. ID fde700872921.h1

BLASTX Method NCBI GI g2959767 BLAST score 342 1.0e-32 E value

```
82
Match length
% identity
                   78
NCBI Description
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
Seq. No.
                  44492
                  fde700872947.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3550551
BLAST score
                  39
E value
                  9.0e-13
Match length
                  59
% identity
                  92
NCBI Description Pisum sativum hsfA gene, exons 1 to 2, partial
Seq. No.
                   44493
Seq. ID
                  fde700872950.h1
Method
                  BLASTN
NCBI GI
                  g429117
BLAST score
                  98
E value
                  5.0e-48
Match length
                  206
% identity
                  87
NCBI Description P.cinnamomi GRP78/BiP gene
Seq. No.
                  44494
Seq. ID
                  fde700872964.h1
Method
                  BLASTN
NCBI GI
                  g169157
BLAST score
                  100
E value
                  4.0e-49
Match length
                  188
% identity
                  88
NCBI Description
                  Pisum sativum serine hydroxymethyltransferase mRNA,
                  complete cds
                  44495
Seq. No.
                  fde700872978.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2677828
BLAST score
                  128
E value
                  6.0e-17
Match length
                  79
% identity
                  47
NCBI Description
                  (U93166) cysteine protease [Prunus armeniaca]
```

Seq. No. 44496

Seq. ID fde700872990.h1

Method BLASTX
NCBI GI 94490314
BLAST score 299
E value 9.0e-28
Match length 67
% identity 76

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

```
Seq. No.
                   44497
Seq. ID
                   fde700872996.h1
Method
                   BLASTX
NCBI GI
                   g1708191
BLAST score
                   270
E value
                   4.0e-24
Match length
                   63
% identity
                   76
NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose
                   carrier protein [Ricinus communis]
Seq. No.
                   44498
Seq. ID
                   fde700873018.h1
Method
                   BLASTX
NCBI GI
                   g4415937
BLAST score
                   191
E value
                   8.0e-15
Match length
                   89
% identity
                   47
NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   44499
Seq. ID
                   fde700873042.h1
Method
                   BLASTX
NCBI GI
                   g441457
BLAST score
                   355
E value
                   4.0e-34
Match length
                   83
% identity
                   78
NCBI Description
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
                   esculentum]
Seq. No.
                   44500
Seq. ID
                   fde700873047.h1
Method
                  BLASTX
NCBI GI
                   g1168970
BLAST score
                  232
E value
                  1.0e-19
Match length
                  80
% identity
                  57
```

NCBI Description MINOR ALLERGEN CLA H 5 (CLA H V) >gi_1086046_pir__\$43116

minor allergen - Cladosporium herberum

>gi_467629_emb CAA55068_ (X78224) minor allergen

[Cladosporium herbarum]

Seq. No. 44501

Seq. ID fde700873131.h1

Method BLASTN g18644 NCBI GI BLAST score 199 E value 1.0e-108 Match length 250 % identity 95

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No.

44502

Seq. ID fde700873158.h1

Match length

% identity

60

47



```
Method
                   BLASTX
NCBI GI
                   g3355486
BLAST score
                   220
E value
                   3.0e-18
Match length
                   66
% identity
                   70
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.
                   44503
Seq. ID
                   fde700873180.h1
Method
                   BLASTX
NCBI GI
                   g4115383
BLAST score
                   239
E value
                   1.0e-20
Match length
                   78
% identity
                   58
NCBI Description
                  (AC005967) receptor-like protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   44504
Seq. ID
                   fde700873216.h1
Method
                   BLASTX
NCBI GI
                   q4314378
BLAST score
                   284
E value
                   9.0e-26
Match length
                   87
% identity
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.
                   44505
Seq. ID
                   fde700873259.h1
Method
                  BLASTX
NCBI GI
                   q3402749
BLAST score
                  228
E value
                   3.0e-19
Match length
                  81
% identity
NCBI Description
                  (AL031187) putative protein [Arabidopsis thaliana]
Seq. No.
                  44506
Seq. ID
                  fde700873267.h1
Method
                  BLASTN
NCBI GI
                  g2970050
BLAST score
                  97
E value
                  2.0e-47
Match length
                  109
% identity
                  97
NCBI Description Vigna radiata mRNA for ARG10, complete cds
Seq. No.
                  44507
Seq. ID
                  fde700873359.h1
Method
                  BLASTX
NCBI GI
                  g2213599
BLAST score
                  149
                  5.0e-10
E value
```

```
NCBI Description
                  (AC000348) T7N9.19 [Arabidopsis thaliana]
Seq. No.
                   44508
Seq. ID
                  fde700873362.h1
Method
                  BLASTN
NCBI GI
                  q20755
BLAST score
                  38
E value
                  4.0e-12
Match length
                  50
% identity
                  94
NCBI Description P.sativum mRNA rab for ras-related GTP-binding protein
Seq. No.
                  44509
Seq. ID
                  fde700873375.h1
Method
                  BLASTX
NCBI GI
                  q82083
BLAST score
                  394
E value
                  9.0e-39
Match length
                  80
% identity
                  96
NCBI Description
                  phosphopyruvate hydratase (EC 4.2.1.11) - tomato (fragment)
                  >gi_1161573_emb_CAA41116 (X58109) enolase [Lycopersicon
                  esculentum]
Seq. No.
                  44510
Seq. ID
                  fde700873392.h1
Method
                  BLASTN
NCBI GI
                  g167265
BLAST score
                  74
E value
                  1.0e-33
Match length
                  126
% identity
                  90
NCBI Description
                  Mesembryanthemum crystallinum phosphoribulokinase mRNA,
```

complete CDS

Seq. No. 44511

Seq. ID fde700873445.h1

Method BLASTX NCBI GI g1495366 BLAST score 148 E value 8.0e-10 Match length 83 % identity 37

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

44512 Seq. No.

Seq. ID fde700873476.h1

Method BLASTX NCBI GI g2244867 BLAST score 252 E value 5.0e-22 Match length 85 % identity 53

NCBI Description (Z97337) hydroxymitrile lyase [Arabidopsis thaliana]

Seq. No. 44513

fde700873491.h1 Seq. ID

BLAST score

E value

174

5.0e-13



```
Method
                   BLASTX
NCBI GI
                   g3721856
BLAST score
                   196
E value
                   4.0e-32
Match length
                   82
% identity
                   71
NCBI Description
                  (AB014057) beta-Amyrin Synthase [Panax ginseng]
Seq. No.
                   44514
Seq. ID
                   fde700873510.h1
Method
                   BLASTX
NCBI GI
                   g3688350
BLAST score
                   165
E value
                   7.0e-12
Match length
                   71
% identity
                   49
                  (AL030996) dJ1189B24.4 (novel PUTATIVE protein similar to
NCBI Description
                   hypothetical proteins S. pombe C22F3.14C and C. elegans
                   C16A3.8) [Homo sapiens]
Seq. No.
                   44515
Seq. ID
                   fde700873511.h1
Method
                  BLASTX
NCBI GI
                  g2352084
BLAST score
                  155
E value
                  1.0e-10
Match length
                  77
% identity
                  54
NCBI Description
                  (U96613) serine/threonine kinase [Arabidopsis thaliana]
Seq. No.
                  44516
Seq. ID
                  fde700873531.h1
Method
                  BLASTN
NCBI GI
                  g456567
BLAST score
                  40
E value
                  2.0e-13
Match length
                  68
% identity
                  90
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
                  44517
Seq. No.
Seq. ID
                  fde700873585.h1
Method
                  BLASTX
NCBI GI
                  q3402485
BLAST score
                  149
E value
                  4.0e-10
Match length
                  45
% identity
                  56
NCBI Description
                  (AB014888) MRJ [Homo sapiens]
                  44518
Seq. No.
Seq. ID
                  fde700873592.h1
Method
                  BLASTX
NCBI GI
                  g4566435
```



```
Match length
                   71
% identity
NCBI Description
                  (AF087672) eRFS [Mus musculus]
Seq. No.
                   44519
Seq. ID
                   fde700873650.h1
Method
                  BLASTX
NCBI GI
                  g2244905
```

BLAST score 208 E value 6.0e-17 Match length 79 % identity 51

NCBI Description (Z97339) indole-3-acetate beta-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 44520 fde700873670.h1 Seq. ID

Method BLASTX NCBI GI q631001 BLAST score 272 E value 2.0e-24 Match length 78 % identity 63

NCBI Description alpha-N-acetylgalactosaminidase - chicken >gi_435037

(L18754) alpha-N-acetylgalactosaminidase [Gallus gallus]

Seq. No. 44521 Seq. ID fde700873672.h1

Method BLASTX NCBI GI g4467151 BLAST score 197 E value 1.0e-15 Match length 79

% identity 52

(AL035540) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

44522 Seq. ID fde700873706.h1

Method BLASTX NCBI GI g4006869 BLAST score 201 E value 1.0e-17 Match length 84 % identity 57

NCBI Description (Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No.

Seq. ID fde700873716.h1

44523

Method BLASTX NCBI GI g1749542 BLAST score 263 E value 3.0e-23 Match length 86 % identity 60

NCBI Description (D89167) similar to Saccharomyces cerevisiae

5-methyltetrahydropteroyltriglutamate-homocysteine s-methyltransferase, SWISS-PROT Accession Number P05694



[Schizosaccharomyces pombe]

Seq. No. 44524 Seq. ID

fde700873723.h1

Method BLASTN NCBI GI g20740 BLAST score 80 E value 3.0e-37 Match length 200 % identity 85

NCBI Description Pisum sativum mRNA for P protein, a part of glycine

cleavage complex

Seq. No. 44525

Seq. ID fde700873726.h1

Method BLASTX NCBI GI q4337196 BLAST score 177 E value 3.0e-13 Match length 87 % identity 48

NCBI Description (AC006403) putative serine/threonine receptor kinase

[Arabidopsis thaliana]

Seq. No. 44526

Seq. ID fde700873749.h1

Method BLASTN NCBI GI g11565 BLAST score 77 E value 2.0e-35 Match length 81 % identity 99

NCBI Description Soybean chloroplast psb A gene coding for photosystem II

thylakoid membrane protein

Seq. No. 44527

Seq. ID fde700873763.h1

Method BLASTN NCBI GI g1619904 BLAST score 86 E value 8.0e-41 Match length 117 % identity

NCBI Description Glycine max thiol protease isoform A mRNA, partial cds

Seq. No. 44528

fde700873776.h1 Seq. ID

Method BLASTN NCBI GI g1055367 BLAST score 253 E value 1.0e-140 Match length 253 % identity 100

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 44529



Seq. ID fde700873787.h1

Method BLASTN NCBI GI g2739003

BLAST score 88 E value 5.0e-42 Match length 172 % identity 92

NCBI Description Glycine max cytochrome P450 monooxygenase CYP82C1p

(CYP82C1) mRNA, complete cds

Seq. No.

44530

Seq. ID fde700873796.h1

Method BLASTN
NCBI GI 9725331
BLAST score 48
E value 4.0e-18
Match length 48
% identity 100

NCBI Description Glycine max mitochondrion polymorphic marker DNA sequence

Seq. No.

44531

Seq. ID fde700873802.h1

Method BLASTX
NCBI GI g2281086
BLAST score 219
E value 4.0e-18
Match length 84
% identity 51

NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog

[Arabidopsis thaliana]

Seq. No. 44532

Seq. ID fde700873808.h1

Method BLASTX
NCBI GI g3805850
BLAST score 188
E value 1.0e-14
Match length 39
% identity 87

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 44533

Seq. ID fde700873824.h1

Method BLASTX
NCBI GI g2760325
BLAST score 127
E value 3.0e-10
Match length 59
% identity 66

NCBI Description (AC002130) F1N21.10 [Arabidopsis thaliana]

Seq. No. 44534

Seq. ID fde700873877.h1

Method BLASTX
NCBI GI g4249386
BLAST score 260
E value 3.0e-23



Match length 75 % identity 69

NCBI Description (AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 44535

Seq. ID fde700873879.h1

Method BLASTN
NCBI GI g3341716
BLAST score 34
E value 8.0e-10
Match length 82
% identity 85

NCBI Description Arabidopsis thaliana ACC oxidase (ACO2) mRNA, complete cds

Seq. No.

Seq. ID fde700873962.h1

44536

Method BLASTX
NCBI GI g1351772
BLAST score 315
E value 2.0e-29
Match length 81
% identity 74

NCBI Description HYPOTHETICAL 51.9 KD PROTEIN YCF45 (ORF455)

>gi 1185186 emb CAA91669 (Z67753) ORF455, homologous to

Porphyra ORF565 [Odontella sinensis]

Seq. No. 44537

Seq. ID fde700873977.h1

Method BLASTX
NCBI GI g2252840
BLAST score 180
E value 1.0e-13
Match length 57
% identity 56

NCBI Description (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No. 44538

Seq. ID fde700874065.h1

Method BLASTX
NCBI GI g3063392
BLAST score 230
E value 2.0e-19
Match length 70
% identity 63

NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No. 44539

Seq. ID fde700874082.h1

Method BLASTX
NCBI GI g118494
BLAST score 280
E value 2.0e-25
Match length 83
% identity 65

7116



NCBI Description ALDEHYDE DEHYDROGENASE, CYTOSOLIC (CLASS 1) (ALHDII) (ALDH-E1) >gi 89113 pir S02302 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 1, cytosolic - horse

Seq. No. 44540

Seq. ID fde700874107.h1

Method BLASTX
NCBI GI g1170922
BLAST score 223
E value 1.0e-18
Match length 76
% identity 54

NCBI Description AMMONIUM TRANSPORTER MEP2 >gi_1084510_pir__S51089 ammonium

transport protein MEP2 - yeast (Saccharomyces cerevisiae) >gi_619514_emb_CAA58587_ (X83608) ammonium transporter [Saccharomyces cerevisiae] >gi_854496_emb_CAA86884_ (Z46843) NH3 permease [Saccharomyces cerevisiae] >gi_1302091 emb_CAA96025 (Z71418) ORF_YNL142w

[Saccharomyces cerevisiae]

Seq. No. 44541

Seq. ID fde700874178.h1

Method BLASTN
NCBI GI g166763
BLAST score 59
E value 9.0e-25
Match length 143
% identity 85

NCBI Description A.thaliana heat shock protein HSP70-2 gene, exons 1 and 2

(partial)

Seq. No. 44542

Seq. ID fde700874203.h1

Method BLASTX
NCBI GI g99737
BLAST score 195
E value 3.0e-17
Match length 69
% identity 71

NCBI Description NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -

Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No. 44543

Seq. ID fde700874426.h1

Method BLASTX
NCBI GI g3395426
BLAST score 252
E value 4.0e-22
Match length 67
% identity 67

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 44544

Seq. ID fde700874452.h1

Method BLASTN NCBI GI g1055367



BLAST score 153 E value 8.0e-81 Match length 233 % identity 92

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 44545

Seq. ID fde700874587.h1

Method BLASTX
NCBI GI g2252843
BLAST score 128
E value 6.0e-12
Match length 80
% identity 52

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 44546

Seq. ID fde700874610.h1

Method BLASTX
NCBI GI g4490704
BLAST score 173
E value 1.0e-12
Match length 87
% identity 56

NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No. 44547

Seq. ID fde700874646.h1

Method BLASTX
NCBI GI g2146731
BLAST score 114
E value 2.0e-14
Match length 79

% identity 35
NCBI Description FK506-binding protein - Arabido

NCBI Description FK506-binding protein - Arabidopsis thaliana >gi_1354207

(U49453) rof1 [Arabidopsis thaliana]

Seq. No.

Seq. ID fde700874651.h1

44548

Method BLASTX
NCBI GI g2623301
BLAST score 167
E value 5.0e-12
Match length 43
% identity 65

NCBI Description (AC002409) putative kinase [Arabidopsis thaliana]

Seq. No. 44549

Seq. ID fde700874688.h1

Method BLASTN
NCBI GI g2661020
BLAST score 253
E value 1.0e-140
Match length 253
% identity 100

NCBI Description Glycine max catalase (cat4) mRNA, complete cds



```
44550
Seq. No.
Seq. ID
                  fde700874727.h1
                  BLASTN
Method
NCBI GI
                  q170071
BLAST score
                  192
                  1.0e-104
E value
                  247
Match length
                  95
% identity
NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds
                  44551
Seq. No.
                  fde700874739.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3334320
BLAST score
                  268
E value
                  7.0e-24
                  72
Match length
                  69
% identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                  44552
                  fde700874751.h1
Seq. ID
Method
                  BLASTX
                  g99982
NCBI GI
BLAST score
                  305
E value
                  3.0e-28
                  81
Match length
                  69
% identity
NCBI Description isoflavone reductase - alfalfa >gi 19620 emb CAA41106
                  (X58078) isoflavone reductase [Medicago sativa]
                  44553
Seq. No.
                  fde700874752.h1
Seq. ID
Method
                  BLASTN
                  q343022
NCBI GI
BLAST score
                  50
                  3.0e-19
E value
                  58
Match length
                  97
% identity
NCBI Description Pea chloroplast photosystem II gene encoding the D2 and
                  44kd chlorophyll a-binding proteins, complete cds
Seq. No.
                   44554
Seq. ID
                   fde700874763.h1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g399014
BLAST score 153
E value 1.0e-10
Match length 46
% identity 59
NCBI Description ADP,ATP

ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_99444_pir_A41677 ADP, ATP carrier protein - Chlorella kessleri >gi_516597 (M76669) ATP/ADP translocator [Chlorella kessleri]



```
Seq. No.
                   44555
                   fde700874769.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4538965
BLAST score
                   166
                   6.0e-12
E value
Match length
                   55
                   49
% identity
                  (AL049488) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44556
                   fde700874779.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245115
BLAST score
                   141
E value
                   5.0e-09
Match length
                   82
% identity
NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]
                   44557
Seq. No.
Seq. ID
                   fde700874790.h1
                   BLASTX
Method
NCBI GI
                   g629641
BLAST score
                   120
                   1.0e-09
E value
Match length
                   64
                   62
% identity
                   PsHSC71.0 protein - garden pea >gi 1076530_pir__S53500
NCBI Description
                   HSC71.0 protein - garden pea >gi_473217 emb_CAA83548
                   (Z32537) PsHSC71.0 [Pisum sativum]
Seq. No.
                   44558
                   fde700874805.h1
Seq. ID
                   BLASTN
Method
                   g169036
NCBI GI
BLAST score
                   42
                   2.0e-14
E value
Match length
                   74
                   89
% identity
NCBI Description Pisum sativum L. aldolase gene, 3' end cds
                   44559
Seq. No.
                   fde700874871.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g462739
BLAST score
                   229
                   2.0e-19
E value
Match length
                   83
% identity
                   57
NCBI Description NPL4 PROTEIN >gi 422119 pir S34340 NPL4 protein - yeast
                   (Saccharomyces cerevisiae) >gi_312610_emb_CAA51026_
                    (X72224) NPL4 [Saccharomyces cerevisiae]
                   >gi_402608_emb_CAA52450_ (X74437) open reading frame
YBR12.31 [Saccharomyces cerevisiae]
```

[Saccharomyces cerevisiae]

>gi_536514_emb_CAA85131_ (Z36039) ORF YBR170c

Match length

NCBI Description

% identity

53 62

```
44560
Seq. No.
                  fde700874878.h1
Seq. ID
                  BLASTN
Method
                  g20880
NCBI GI
                  157
BLAST score
                  4.0e-83
E value
Match length
                  224
% identity
                  93
                  Pea mRNA for plastid ribosomal protein CL9
NCBI Description
                   44561
Seq. No.
                   fde700875063.h1
Seq. ID
Method
                  BLASTX
                  g399015
NCBI GI
                  251
BLAST score
                   4.0e-22
E value
Match length
                   54
% identity
                   55
                  ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT)
                   >gi 218145 dbj BAA02161_ (D12637) ATP/ADP translocator
                   [Oryza sativa]
Seq. No.
                   44562
                   fde700875117.h1
Seq. ID
                   BLASTN
Method
                   q169952
NCBI GI
BLAST score
                   139
E value
                   1.0e-72
                   143
Match length
                   99
% identity
NCBI Description Glycine max ferritin mRNA, complete cds
Seq. No.
                   44563
Seq. ID
                   fde700875206.h1
                   BLASTX
Method
NCBI GI
                   g4415918
BLAST score
                   149
                   2.0e-11
E value
                   85
Match length
                   24
% identity
NCBI Description (AC006282) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   44564
                   fde700875247.h1
Seq. ID
                   BLASTX
Method
                   q1076580
NCBI GI
BLAST score
                   204
E value
                   2.0e-16
```

alcohol dehydrogenase homolog ADH3b - tomato

>gi_913446_bbs_160508 (S75487) alcohol dehydrogenase ADH {EC 1.1.1. $\overline{1}$ } [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 390 aa] [Lycopersicon esculentum]



Seq. No. 44565

Seq. ID fde700875264.h1

Method BLASTN
NCBI GI g516853
BLAST score 163
E value 1.0e-86
Match length 215
% identity 27

NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No.

Seq. ID fde700875281.h1

44566

Method BLASTN
NCBI GI g984307
BLAST score 196
E value 1.0e-106
Match length 250
% identity 93

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No. 44567

Seq. ID fde700875316.h1

Method BLASTX
NCBI GI g3881117
BLAST score 153
E value 2.0e-10
Match length 46
% identity 59

NCBI Description (AL032649) cDNA EST yk293f3.3 comes from this gene

[Caenorhabditis elegans]

Seq. No. 44568

Seq. ID fde700875330.hl

Method BLASTX
NCBI GI g2244749
BLAST score 256
E value 2.0e-22
Match length 55
% identity 91

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 44569

Seq. ID fde700875375.h1

Method BLASTN
NCBI GI g210811
BLAST score 173
E value 9.0e-93
Match length 233
% identity 94

NCBI Description Bean pod mottle virus coat protein gene, complete cds,

complete middle component (M) RNA

Seq. No. 44570



```
fde700875376.hl
Seq. ID
                  BLASTN
Method
                  g1619324
NCBI GI
                  70
BLAST score
                  3.0e-31
E value
Match length
                  123
% identity
                  90
NCBI Description P.sativum mRNA for ADP-glucose pyrophosphorylase
                  44571
Seq. No.
                  fde700875387.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2924257
BLAST score
                  74
                  1.0e-33
E value
                  240
Match length
                  90
% identity
NCBI Description Tobacco chloroplast genome DNA
                  44572
Seq. No.
                  fde700875401.h1
Seq. ID
                  BLASTX
Method
                  q4106395
NCBI GI
                  375
BLAST score
                  2.0e-36
E value
                  80
Match length
                  85
% identity
NCBI Description (AF073744) raffinose synthase [Cucumis sativus]
                  44573
Seq. No.
Seq. ID
                  fde700875432.h1
                  BLASTX
Method
NCBI GI
                  g3560264
                  142
BLAST score
E value
                  3.0e-09
                  73
Match length
                  45
% identity
NCBI Description (AL031535) soll family protein [Schizosaccharomyces pombe]
                  44574
Seq. No.
                  fde700875465.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2970654
BLAST score
                  195
                  2.0e-15
E value
                  43
Match length
% identity
                  (AF052058) ferritin subunit cowpea2 precursor [Vigna
NCBI Description
                  unguiculata]
                   44575
Seq. No.
Seq. ID
                   fde700875469.h1
Method
                  BLASTX
```

NCBI GI g2262158 BLAST score 285 E value 5.0e-2677 Match length



% identity 66

NCBI Description (AC002329) putative mitochondrial phosphate translocator

protein [Arabidopsis thaliana]

Seq. No. 44576

Seq. ID fde700875478.h1

Method BLASTX
NCBI GI g3123310
BLAST score 155
E value 9.0e-11
Match length 69
% identity 43

NCBI Description PUTATIVE FLAVOPROTEIN C26F1.14C

Seq. No.

44577

Seq. ID fde700875481.h1

Method BLASTX
NCBI GI g1723894
BLAST score 165
E value 6.0e-12
Match length 76
% identity 51

NCBI Description HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC

REGION >gi_2131584_pir__S64106 hypothetical protein YGL099w

- yeast (Saccharomyces cerevisiae)

>gi_1322637_emb_CAA96805_ (Z72621) ORF YGL099w

[Saccharomyces cerevisiae]

Seq. No. 44578

Seq. ID fde700875533.h1

Method BLASTX
NCBI GI g3738301
BLAST score 277
E value 6.0e-25
Match length 83
% identity 59

NCBI Description (AC005309) putative zinc-finger protein [Arabidopsis thaliana] >gi_4249397 (AC006072) putative zinc-finger

protein (B-box zinc finger domain) [Arabidopsis thaliana]

Seq. No. 44579

Seq. ID fde700875555.h1

Method BLASTX
NCBI GI g4455151
BLAST score 233
E value 8.0e-20
Match length 83
% identity 53

NCBI Description (AL022603) putative serine/threonine kinase (fragment)

[Arabidopsis thaliana]

Seq. No. 44580

Seq. ID fde700875570.h1

Method BLASTX
NCBI GI g4371296
BLAST score 183
E value 6.0e-14



Match length % identity

(AC006260) putative receptor protein kinase [Arabidopsis NCBI Description

44581

Seq. No.

fde700875622.h1 Seq. ID

BLASTX Method NCBI GI g2262116 BLAST score 153 2.0e-10 E value Match length 76 38

% identity (AC002343) cellulose synthase isolog [Arabidopsis thaliana] NCBI Description

44582 Seq. No.

Seq. ID fde700875638.h1

BLASTX Method NCBI GI q3360502 334 BLAST score 1.0e-31 E value 84 Match length 76 % identity

(AF061279) heat shock protein [Plectonema boryanum] NCBI Description

44583 Seq. No.

Seq. ID fde700875685.h1

Method BLASTX NCBI GI g1076291 BLAST score 380 5.0e-37 E value Match length 82

87 % identity

amino acid transporter AAT1 - Arabidopsis thaliana NCBI Description

>gi 2911069 emb CAA17531 (AL021960) amino acid transport

protein AAT1 [Arabidopsis thaliana]

44584 Seq. No.

fde700875734.h1 Seq. ID

BLASTX Method q456013 NCBI GI BLAST score 143 E value 3.0e-09 Match length 68 24 % identity

(L28174) disulfide-like protein [Acanthamoeba castellanii] NCBI Description

>gi_1092589_prf 2024291A protein disulfide isomerase-like

protein [Acanthamoeba castellanii]

44585 Seq. No.

fde700875744.h1 Seq. ID

Method BLASTN NCBI GI g4240030 BLAST score 42

E value 1.0e-14 Match length 74 % identity 89



NCBI Description Pisum sativum mRNA for DNA binding zinc finger protein (Pspzf), partial cds

Seq. No. 44586

Seq. ID fde700875780.h1

Method BLASTX
NCBI GI g1235752
BLAST score 250
E value 6.0e-23
Match length 80
% identity 28

NCBI Description (D63916) protein phosphotase 2A 65kD regulatory sububit (A

subunit) [Schizosaccharomyces pombe]

Seq. No. 44587

Seq. ID fde700875793.hl

Method BLASTX
NCBI GI g3763932
BLAST score 149
E value 3.0e-10
Match length 58
% identity 59

NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No. 44588

Seq. ID fde700875867.hl

Method BLASTX
NCBI GI g2655098
BLAST score 218
E value 3.0e-28
Match length 85
% identity 75

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 44589

Seq. ID fde700875910.h1

Method BLASTX
NCBI GI 94455366
BLAST score 311
E value 5.0e-29
Match length 82
% identity 70

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 44590

Seq. ID fde700875975.hl

Method BLASTX
NCBI GI g132989
BLAST score 320
E value 4.0e-30
Match length 75
% identity 77

NCBI Description 60S RIBOSOMAL PROTEIN L5 >gi_345694_pir__JC1308 ribosomal

protein L5 - chicken >gi_62983_emb_CAA40335_ (X57016)

ribosomal protein L5 [Gallus gallus]

>gi_391647_dbj_BAA01581_ (D10737) ribosomal protein L5

[Gallus gallus]



57

sp.]

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770

% identity

```
44591
Seq. No.
                  fde700876071.hl
Seq. ID
                  BLASTN
Method
                  g4406529
NCBI GI
                  91
BLAST score
                  8.0e-44
E value
Match length
                  134
% identity
                  93
                  Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
NCBI Description
                  encoding chloroplast protein, complete cds
                  44592
Seq. No.
                  fde700876081.h1
Seq. ID
                  BLASTN
Method
                  g4406529
NCBI GI
                  97
BLAST score
                  2.0e-47
E value
Match length
                  180
% identity
                  89
                  Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
NCBI Description
                   encoding chloroplast protein, complete cds
                   44593
Seq. No.
                   fde700876095.hl
Seq. ID
                  BLASTX
Method
                   g3914052
NCBI GI
                   177
BLAST score
                   5.0e-28
E value
Match length
                   81
                   78
% identity
NCBI Description DNA MISMATCH REPAIR PROTEIN MSH6 >gi 2104549 (AF001535)
                   AGAA.3 [Arabidopsis thaliana]
                   44594
Seq. No.
                   fde700876138.hl
Seq. ID
                   BLASTX
Method
                   g2119802
NCBI GI
BLAST score
                   119
                   1.0e-10
E value
                   79
Match length
                   49
% identity
NCBI Description probable membrane protein YDL247w - yeast (Saccharomyces
                   cerevisiae) >gi_1431422_emb_CAA98827_ (Z74295) ORF YDL247w
                   [Saccharomyces cerevisiae]
                   44595
Seq. No.
                   fde700876185.hl
Seq. ID
                   BLASTX
Method
                   g3025189
NCBI GI
                   161
BLAST score
                   1.0e-17
E value
                   77
Match length
```

>gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis



```
44596
Seq. No.
Seq. ID
                  fde700876192.h1
Method
                  BLASTX
NCBI GI
                  g4336747
BLAST score
                  194
E value
                  8.0e-25
                  78
Match length
% identity
                  76
                  (AF104924) unconventional myosin heavy chain [Zea mays]
NCBI Description
                  44597
Seq. No.
                  fde700876239.h1
Seq. ID
                  BLASTX
Method
                  g1006835
NCBI GI
BLAST score
                  186
E value
                  6.0e-24
Match length
                  83
% identity
                  (U35111) rubisco activase precursor [Nicotiana tabacum]
NCBI Description
                   44598
Seq. No.
                   fde700876279.h1
Seq. ID
                  BLASTN
Method
                  g1504102
NCBI GI
                   60
BLAST score
E value
                   3.0e-25
                  108
Match length
                   70
% identity
NCBI Description N.crassa mRNA for erp38 gene
                   44599
Seq. No.
                   fde700876304.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g256142
BLAST score
                   250
E value
                   1.0e-138
Match length
                   254
% identity
                   100
                   cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                   Prize, mRNA, 1450 nt]
Seq. No.
                   44600
                   fde700876329.h1
Seq. ID
                   BLASTX
Method
                   g4056482
NCBI GI
                   146
BLAST score
E value
                   1.0e-09
                   72
Match length
% identity
                   44
                  (ACO05896) putative ABC transporter [Arabidopsis thaliana]
NCBI Description
                   44601
Seq. No.
                   fde700876330.h1
Seq. ID
```

NCBI GI g2058281 BLAST score 36

Method

BLASTN

7128



```
E value
                   6.0e-11
Match length
                   88
% identity
```

A.thaliana mRNA for AtRanBP1a protein NCBI Description

Seq. No.

44602 Seq. ID

fde700876390.h1 BLASTX Method g3540198 NCBI GI

BLAST score 153 E value 2.0e-10 58 Match length 55 % identity

(AC004260) Unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

44603

Seq. ID fde700876513.h1 Method BLASTX q4204288 NCBI GI

233 BLAST score 8.0e-20 E value Match length 80 % identity 54

(AC003027) lcl prt seq No definition line found NCBI Description

[Arabidopsis thaliana]

Seq. No. 44604

Seq. ID fde700876515.h1

Method BLASTX NCBI GI q2244929 BLAST score 194 E value 3.0e-15 Match length 77

% identity 53

NCBI Description (Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No. 44605

fde700876538.h1 Seq. ID

Method BLASTX NCBI GI g4138647 BLAST score 284 E value 8.0e-26 Match length 80 % identity 60

(AJ011939) peroxidase [Trifolium repens] NCBI Description

Seq. No. 44606

Seq. ID fde700876545.hl

Method BLASTX g2924785 NCBI GI BLAST score 188 E value 1.0e-14 Match length 79 7 % identity

(AC002334) similar to disease resistance protein NCBI Description

[Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  fde700876591.h1
                  BLASTN
Method
NCBI GI
                  g4521246
BLAST score
                  122
E value
                  3.0e-62
Match length
                  194
                  91
% identity
                  Aspergillus oryzae tef gene for translation elongation
NCBI Description
                  factor 1 alpha, complete cds
Seq. No.
                  44608
Seq. ID
                  fde700876630.h1
                  BLASTX
Method
                  g2341033
NCBI GI
BLAST score
                  327
E value
                  8.0e-31
Match length
                  84
                  75
% identity
                  (AC000104) Similar to Babesia aldo-keto reductase
NCBI Description
                   (gb M93122). [Arabidopsis thaliana]
Seq. No.
                  44609
Seq. ID
                  fde700876667.h1
                  BLASTN
Method
                  g1498343
NCBI GI
BLAST score
                  76
E value
                  7.0e-35
                  76
Match length
                  100
% identity
NCBI Description Glycine max actin (Soy115) gene, partial cds
Seq. No.
                   44610
Seq. ID
                   fde700876832.h1
                  BLASTN
Method
NCBI GI
                  q256142
BLAST score
                   87
E value
                   2.0e-41
                   95
Match length
% identity
                  cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                   Prize, mRNA, 1450 nt]
Seq. No.
                   44611
                   fde700876843.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4406529
BLAST score
                   113
E value
                   6.0e-57
```

Match length 244 % identity 87

Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene NCBI Description

encoding chloroplast protein, complete cds

44612 Seq. No.

fde700876889.h1 Seq. ID

BLASTX Method



NCBI GI g2827546
BLAST score 221
E value 2.0e-18
Match length 78
% identity 51

NCBI Description (AL021635) cytochrome P450 like protein [Arabidopsis

thaliana]

Seq. No.

44613

Seq. ID fde700876904.h1

Method BLASTX
NCBI GI g3122671
BLAST score 200
E value 6.0e-16
Match length 53
% identity 64

NCBI Description HYPOTHETICAL RAE1-LIKE PROTEIN >gi_2129676_pir__S71241 probable export protein - Arabidopsis thaliana >gi_1297188

(U53501) Theoretical protein with similarity to Swiss-Prot

Accession Number P41838 poly A+ RNA export protein

[Arabidopsis thaliana]

Seq. No.

44614

Seq. ID fde700876908.hl

Method BLASTX
NCBI GI g4469008
BLAST score 158
E value 9.0e-14
Match length 66
% identity 49

NCBI Description (AL035602) UDP rhamnose--anthocyanidin-3-glucoside

rhamnosyltransferase-like protein [Arabidopsis thaliana]

Seq. No. 44615

Seq. ID fde700876924.h1

Method BLASTX
NCBI GI g3176072
BLAST score 443
E value 2.0e-44
Match length 83
% identity 92

NCBI Description (AJ002485) protein phosphatase 1, catalytic beta subunit

[Medicago sativa]

Seq. No.

Seq. ID fde700876948.h1

44616

Method BLASTX
NCBI GI g121026
BLAST score 243
E value 1.0e-24
Match length 75
% identity 58

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN >gi_99395_pir__S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi_18145_emb_CAA37638_ (X53574) putative protein has homology to G protein beta subunit [Chlamydomonas



reinhardtii]

```
Seq. No.
                  44617
Seq. ID
                  fde700877166.h1
                  BLASTX
Method
NCBI GI
                  g172764
BLAST score
                  313
                  4.0e-29
E value
Match length
                  86
                  72
% identity
NCBI Description (M83755) STH1 protein [Saccharomyces cerevisiae]
                  44618
Seq. No.
Seq. ID
                  fde700877168.h1
                  BLASTN
Method
                  g2760167
NCBI GI
BLAST score
                  32
                  1.0e-08
E value
Match length
                  64
% identity
                  88
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCO15, complete sequence [Arabidopsis thaliana]
                  44619
Seq. No.
Seq. ID
                  fde700877175.h1
                  BLASTX
Method
                  g2499623
NCBI GI
BLAST score
                  161
                  3.0e-11
E value
                  87
Match length
% identity
                  45
                  PROBABLE SERINE/THREONINE-PROTEIN KINASE YOL100W
NCBI Description
                  >gi 1078290 pir S51899 probable protein kinase HRC1081 (EC
                  2.7.1.-) - yeast (Saccharomyces cerevisiae)
                  >gi 663254 emb CAA88162 (Z48149) probable protein kinase
                  [Saccharomyces cerevisiae] >gi 1419952 emb CAA99113_
                  (Z74842) ORF YOL100w [Saccharomyces cerevisiae]
                  44620
Seq. No.
Seq. ID
                  fde700877288.h1
Method
                  BLASTX
NCBI GI
                  g2651310
BLAST score
                  145
E value
                  7.0e-16
Match length
                  66
                  58
% identity
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
                  44621
Seq. No.
                  fde700877293.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3928149
                  56
BLAST score
                  6.0e-23
E value
```

175

84

Match length

% identity



```
NCBI Description Cicer arietinum mRNA for hypothetical protein
                   44622
Seq. No.
                   fde700877295.h1
Seq. ID
                   BLASTX
Method
                   g2583130
NCBI GI
BLAST score
                   108
E value
                   6.0e-11
                   79
Match length
                   49
% identity
                   (AC002387) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
                   44623
Seq. No.
                   fjg700968354.hl
Seq. ID
                   BLASTX
Method
                   g3249081
NCBI GI
BLAST score
                   253
                   3.0e-22
E value
                   77
Match length
                   9
% identity
                   (AC004473) Strong similarity to AROGP2 gene gb_1762634 from
NCBI Description
                   Lycopersicon esculentum. [Arabidopsis thaliana]
Seq. No.
                   44624
                   fjg700968381.h1
Seq. ID
                   BLASTX
Method
                   g1149569
NCBI GI
                   238
BLAST score
                   2.0e-20
E value
                   75
Match length
                   59
% identity
                  (Z50851) HD-zip [Arabidopsis thaliana]
NCBI Description
                   44625
Seq. No.
Seq. ID
                   fjq700968421.h1
                   BLASTN
Method
NCBI GI
                   g945086
                   52
BLAST score
                   1.0e-20
E value
Match length
                   64
% identity
NCBI Description Glycine max transcription factor TFIIB mRNA, complete cds
Seq. No.
                   44626
                   fjg700968454.h1
Seq. ID
                   BLASTX
Method
                   q2632254
NCBI GI
```

Method BLASTX
NCBI GI g2632254
BLAST score 163
E value 1.0e-11
Match length 44
% identity 73

NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 44627

Seq. ID fua701036926.h1

Method BLASTN



```
g2208907
NCBI GI
                  37
BLAST score
                  2.0e-11
E value
                  53
Match length
                  92
% identity
                  Catharanthus roseus mRNA for phosphate transporter,
NCBI Description
                  complete cds
                  44628
Seq. No.
Seq. ID
                  fua701036963.h1
                  BLASTN
Method
NCBI GI
                  g169978
                  86
BLAST score
                  9.0e-41
E value
                  101
Match length
% identity
                  Soybean (G.max) hydroproline-rich protein mRNA, partial cds
NCBI Description
                   44629
Seq. No.
                   fua701037008.h1
Seq. ID
                  BLASTX
Method
                  g4539403
NCBI GI
BLAST score
                  117
                   2.0e-14
E value
                  73
Match length
                   61
% identity
                  (AL049524) putative protein [Arabidopsis thaliana]
NCBI Description
                   44630
Seq. No.
Seq. ID
                   fua701037035.hl
Method
                   BLASTX
NCBI GI
                   q2316016
BLAST score
                   167
E value
                   5.0e-12
                   90
Match length
                   39
% identity
                  (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
NCBI Description
                   44631
Seq. No.
                   fua701037053.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4467154
BLAST score
                   337
E value
                   6.0e-32
                   85
Match length
                   78
% identity
                   (AL035540) putative thaumatin-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   44632
Seq. No.
Seq. ID
                   fua701037083.h1
Method
                   BLASTX
```

NCBI GI q2267567 BLAST score 175 E value 5.0e-13 50 Match length % identity 72



(AF009003) glycine-rich RNA binding protein 1 [Pelargonium NCBI Description x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding

protein 2 [Pelargonium x hortorum]

44633 Seq. No.

Seq. ID fua701037125.h1

BLASTX Method a2618689 NCBI GI 304 BLAST score 4.0e-28 E value 81 Match length

74 % identity

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID fua701037220.h1

44634

Method BLASTN NCBI GI q927504 105 BLAST score 4.0e-52 E value 197 Match length 88

% identity NCBI Description P.sativum mRNA for fructose-1, 6-biphosphate aldolase

(clone aldcyt2)

44635 Seq. No.

Seq. ID fua701037229.hl

BLASTX Method g2130080 NCBI GI BLAST score 404 9.0e-40 E value 93 Match length 82

% identity

Nramp1 protein - rice >gi_1470320_bbs_177441 (S81897) NCBI Description

OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane

protein [Oryza sativa]

Seq. No. 44636

Seq. ID fua701037245.h1

Method BLASTX NCBI GI q2062169 BLAST score 286 6.0e-26 E value 92 Match length % identity

(ACO01645) ABC transporter (PDR5-like) isolog [Arabidopsis NCBI Description

thaliana]

44637 Seq. No.

fua701037323.h1 Seq. ID

Method BLASTX q3080398 NCBI GI 318 BLAST score 1.0e-29 E value 89 Match length



% identity (AL022603) putative protein [Arabidopsis thaliana] NCBI Description 44638 Seq. No. Seq. ID fua701037329.h1 Method BLASTX q3091216 NCBI GI BLAST score 164 1.0e-11 E value Match length 84 % identity NCBI Description (AF060192) putative resistance protein [Glycine max] 44639 Seq. No. Seq. ID fua701037334.h1 BLASTX Method NCBI GI g3005576 BLAST score 279 E value 3.0e-25 91 Match length 57 % identity (AF047718) putative high affinity nitrate transporter; NCBI Description GmNRT2 [Glycine max] 44640 Seq. No. Seq. ID fua701037351.h1 BLASTX Method NCBI GI g3983665 BLAST score 167 5.0e-12 E value Match length 53 58 % identity NCBI Description (AB011271) importin-beta2 [Oryza sativa] 44641 Seq. No. fua701037381.h1 Seq. ID BLASTN Method NCBI GI g829118 BLAST score 53 2.0e-21 E value Match length 121 86 % identity NCBI Description P.vulgaris gene for cyclophilin Seq. No. 44642

fua701037576.hl Seq. ID

BLASTX Method q3169065 NCBI GI BLAST score 153 6.0e-13 E value 68 Match length 56 % identity

NCBI Description (AL023704) putative translocation elongation factor-Tu

family [Schizosaccharomyces pombe]

Seq. No. 44643

fua701037740.h1 Seq. ID



Method BLASTN
NCBI GI g644492
BLAST score 92
E value 2.0e-44
Match length 231
% identity 87

NCBI Description Corn elongation factor lalpha gene, complete cds

Seq. No.

44644

Seq. ID fua701037750.h1

Method BLASTX
NCBI GI g1707878
BLAST score 332
E value 2.0e-31
Match length 77
% identity 81

NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T

PROTEIN) >gi 2129976_pir__S59948 aminomethyltransferase (EC

2.1.2.10) precursor - potato >gi 438254 emb CAA81081_

(Z25862) T-protein [Solanum tuberosum]

Seq. No. 44645

Seq. ID fua701037764.h1

Method BLASTX
NCBI GI g2642154
BLAST score 303
E value 6.0e-28
Match length 83
% identity 72

NCBI Description (AC003000) unknown protein [Arabidopsis thaliana] >qi 3790595 (AF079186) RING-H2 finger protein RHC2a

[Arabidopsis thaliana]

Seq. No. 44646

Seq. ID fua701037775.h1

Method BLASTN
NCBI GI g3687405
BLAST score 49
E value 1.0e-18
Match length 114

% identity 92

NCBI Description Lycopersicon esculentum mRNA for hypothetical protein

Seq. No. 44647

Seq. ID fua701037781.h1

Method BLASTX
NCBI GI g4508068
BLAST score 141
E value 6.0e-09
Match length 40
% identity 72

NCBI Description (AC005882) 3063 [Arabidopsis thaliana]

Seq. No. 44648

Seq. ID fua701037849.h1

Method BLASTX NCBI GI g3395431



BLAST score 383 E value 3.0e-37 Match length 92 % identity 73

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.

44649

Seq. ID fua701037857.h1

Method BLASTX
NCBI GI g1663648
BLAST score 226
E value 5.0e-19
Match length 64
% identity 69

NCBI Description (U75321) chromaffin granule ATPase II homolog [Mus

musculus]

Seq. No.

44650

Seq. ID fua701037889.h1

Method BLASTN
NCBI GI g256142
BLAST score 253
E value 1.0e-140
Match length 257
% identity 100

NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var

Prize, mRNA, 1450 nt]

Seq. No.

Seq. ID fua701037934.h1

Method BLASTN
NCBI GI g18764
BLAST score 187
E value 1.0e-101
Match length 259
% identity 93

NCBI Description G.max tefS1 gene for elongation factor EF-la

Seq. No.

44652

44651

Seq. ID fua701037949.h1

Method BLASTX
NCBI GI g4063743
BLAST score 235
E value 6.0e-20
Match length 94
% identity 50

NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.

44653

Seq. ID fua701038027.h1

Method BLASTN
NCBI GI g169956
BLAST score 98
E value 6.0e-48
Match length 98
% identity 100

NCBI Description Glycine max G-box binding factor (GBF1) mRNA, complete cds



```
44654
Seq. No.
Seq. ID
                  fua701038148.h1
                  BLASTX
Method
NCBI GI
                  g3395443
BLAST score
                  157
                   9.0e-11
E value
Match length
                  35
% identity
                   (AC004683) putative ammonium transporter, 3' partial
NCBI Description
                   [Arabidopsis thaliana]
                   44655
Seq. No.
Seq. ID
                   fua701038175.hl
                   BLASTX
Method
NCBI GI
                  g1168470
BLAST score
                  240
                   2.0e-20
E value
                   76
Match length
                   59
% identity
NCBI Description
                  PROTEIN KINASE APK1A >gi 282877 pir S28615 protein kinase,
                   tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                   Arabidopsis thaliana >gi 217829 dbj BAA02092 (D12522)
                   protein tyrosine-serine-threonine kinase [Arabidopsis
                   thaliana]
                   44656
Seq. No.
                   fua701038234.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3329368
BLAST score
                   251
                   8.0e-22
E value
Match length
                   73
                   63
% identity
                  (AF031244) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44657
                   fua701038235.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3269296
BLAST score
                   364
E value
                   5.0e-35
Match length
                   95
% identity
                   69
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   44658
Seq. No.
                   fua701038359.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3242077
BLAST score
                   175
E value
                   3.0e-13
```

Seq. No. 44659

44 75

Match length

NCBI Description

% identity

(AJ003119) protein phosphatase 2C [Arabidopsis thaliana]



Seq. ID fua701038437.h1

Method BLASTN
NCBI GI g849135
BLAST score 103
E value 5.0e-51
Match length 143
% identity 94

NCBI Description Vigna radiata vacuolar H+-ATPase subunit A mRNA, complete

cds

Seq. No. 44660

Seq. ID fua701038508.h1

Method BLASTX
NCBI GI g3819099
BLAST score 280
E value 3.0e-25
Match length 92
% identity 53

NCBI Description (AJ009825) copper amine oxidase [Cicer arietinum]

Seq. No.

44661

Seq. ID fua701038530.h1

Method BLASTX
NCBI GI g4185139
BLAST score 350
E value 2.0e-33
Match length 88
% identity 72

NCBI Description (AC005724) putative diacylglycerol kinase [Arabidopsis

thaliana]

44662

Seq. No.

Seq. ID fua701038620.h1

Method BLASTX
NCBI GI g1504008
BLAST score 165
E value 8.0e-12
Match length 83
% identity 46

NCBI Description (D86967) Containing ATP/GTP-binding site motif A(P-loop):

Similar to C.elegans protein(P1:CEC47E128); Similar to Mouse

alpha-mannosidase(P1:B54407) [Homo sapiens]

Seq. No. 44663

Seq. ID fua701038640.h1

Method BLASTX
NCBI GI 94309969
BLAST score 331
E value 3.0e-31
Match length 83
% identity 66

NCBI Description (AC002983) putative phosphoglyceride transfer protein

[Arabidopsis thaliana]

Seq. No. 44664

Seq. ID fua701038652.h1

Method BLASTN



g2264317 NCBI GI BLAST score 47 E value 1.0e-17 Match length 135 % identity 84 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MUG13, complete sequence [Arabidopsis thaliana] Seq. No. 44665 Seq. ID fua701038712.hl Method BLASTN NCBI GI q2369713 BLAST score 65 E value 3.0e-28 Match length 217 % identity 89 NCBI Description Beta vulgaris cDNA for elongation factor 44666 Seq. No. Seq. ID fua701038715.hl Method BLASTX NCBI GI q4454484 BLAST score 294 5.0e-27 E value Match length 76 75 % identity (AC006234) putative diacylglycerol kinase [Arabidopsis NCBI Description thaliana] Seq. No. 44667 Seq. ID fua701038721.hl Method BLASTX NCBI GI q3033395 BLAST score 141 E value 4.0e-09 Match length 58 % identity 52 (AC004238) putative zinc-finger protein [Arabidopsis NCBI Description thaliana] Seq. No. 44668 fua701038725.h1 Seq. ID Method BLASTX NCBI GI g2746086 BLAST score 301 7.0e-28 E value Match length 78 % identity 72 (AF025292) putative high-affinity potassium transporter NCBI Description [Hordeum vulgare]

44669 Seq. No.

fua701038736.h1 Seq. ID

Method BLASTX g3176686 NCBI GI BLAST score 141 E value 4.0e-09



Match length 41 % identity 73

NCBI Description (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 44670

Seq. ID fua701038755.h1

Method BLASTX
NCBI GI g2853078
BLAST score 155
E value 9.0e-11
Match length 76
% identity 38

NCBI Description (AL021768) TMV resistance protein N-like [Arabidopsis

thaliana]

Seq. No. 44671

Seq. ID fua701038821.h1

Method BLASTX
NCBI GI g2465923
BLAST score 256
E value 1.0e-22
Match length 68
% identity 63

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 44672

Seq. ID fua701038843.h1

Method BLASTN
NCBI GI g3175989
BLAST score 76
E value 6.0e-35
Match length 128
% identity 90

NCBI Description Cicer arietinum mRNA for GDP dissociation inhibitor (gdi)

Seq. No. 44673

Seq. ID fua701038858.h1

Method BLASTN
NCBI GI g4490734
BLAST score 32
E value 1.0e-08
Match length 48
% identity 92

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)

Seq. No. 44674

Seq. ID fua701038912.h1

Method BLASTX
NCBI GI g2244990
BLAST score 264
E value 2.0e-23
Match length 67
% identity 81

(Z97340) similarity to LIM homeobox protein -NCBI Description Caenorhabditis [Arabidopsis thaliana] 44675 Seq. No. Seq. ID fua701038929.h1 Method BLASTX q4204095 NCBI GI 165 BLAST score 4.0e-15 E value Match length 84 56 % identity (AF030260) CYP94A1 [Vicia sativa] NCBI Description 44676 Seq. No. fua701038941.h1 Seq. ID Method BLASTX NCBI GI g1785621 BLAST score 304 E value 4.0e-28 85 Match length 72 % identity (Z84202) AtPK2324 [Arabidopsis thaliana] >gi 2465927 NCBI Description (AF024650) receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi 4249408 (AC006072) putative serine/threonine protein kinase [Arabidopsis thaliana] 44677 Seq. No. Seq. ID fua701038946.hl BLASTX Method NCBI GI g2827699 BLAST score 170 E value 2.0e-12 Match length 73 % identity NCBI Description (AL021684) predicted protein [Arabidopsis thaliana] 44678 Seq. No. Seq. ID fua701038984.hl BLASTX Method NCBI GI g2062169 BLAST score 160 E value 3.0e-11

Match length 36 % identity

(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis NCBI Description

thaliana]

Seq. No. 44679

fua701038985.h1 Seq. ID

Method BLASTX NCBI GI g3850584 BLAST score 183 E value 3.0e-18 Match length 64 % identity 78

(AC005278) ESTs gb_H37641 and gb_AA651422 come from this NCBI Description

gene. [Arabidopsis thaliana]



Seq. No. 44680
Seq. ID fua701039028.h1

Method BLASTX
NCBI GI g1402888

NCBI GI G1402888
BLAST score 150
E value 5.0e-10
Match length 79
% identity 41

NCBI Description (X98130) unknown [Arabidopsis thaliana]

Seq. No. 44681

Seq. ID fua701039095.h1

Method BLASTX
NCBI GI g3033386
BLAST score 148
E value 7.0e-10
Match length 66
% identity 42

NCBI Description (AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No. 44682

Seq. ID fua701039138.h1

Method BLASTX
NCBI GI g3785989
BLAST score 154
E value 2.0e-10
Match length 86
% identity 42

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 44683

Seq. ID fua701039150.h1

Method BLASTX
NCBI GI g2052510
BLAST score 390
E value 4.0e-38
Match length 89
% identity 76

NCBI Description (U95758) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

Seq. No. 44684

Seq. ID fua701039157.h1

Method BLASTN
NCBI GI g16508
BLAST score 64
E value 1.0e-27
Match length 140
% identity 86

NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene

sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana

S-adenosylmethionine synthetase gene, complete cds

Seq. No. 44685

Seq. ID fua701039179.h1

Method BLASTN



```
g3482999
NCBI GI
BLAST score
                  32
                  1.0e-08
E value
Match length
                  36
                  60
% identity
NCBI Description
                  Human DNA sequence from clone 211A9 on chromosome 22q12.1
                  Contains EST, STS, GSS, CpG island, complete sequence [Homo
                  sapiens]
                  44686
Seq. No.
Seq. ID
                  fua701039215.h1
                  BLASTX
Method
                  g2462929
NCBI GI
                  138
BLAST score
                  1.0e-17
E value
Match length
                  82
                  51
% identity
NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]
                  44687
Seq. No.
                  fua701039327.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4335714
BLAST score
                  150
                  4.0e-10
E value
                  37
Match length
% identity
                  (AC006248) putative glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  44688
Seq. No.
Seq. ID
                  fua701039335.h1
Method
                  BLASTX
NCBI GI
                  q2129635
BLAST score
                  238
E value
                  2.0e-20
Match length
                  76
% identity
                  light repressible receptor protein kinase - Arabidopsis
NCBI Description
                   thaliana >gi 1321686 emb CAA66376 (X97774) light
                   repressible receptor protein kinase [Arabidopsis thaliana]
Seq. No.
                   44689
                   fua701039356.hl
Seq. ID
Method
                  BLASTN
                  q1944574
NCBI GI
BLAST score
                  33
E value
                  3.0e-09
Match length
                  73
```

% identity 86

NCBI Description L.esculentum mRNA for pectinesterase

Seq. No. 44690

fua701039358.h1 Seq. ID

BLASTN Method g609224 NCBI GI BLAST score 60



E value 2.0e-25 Match length 136 % identity 86

NCBI Description P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB Pisum sativum S-adenosylmethionine synthase mRNA, complete

cds

Seq. No. 44691

Seq. ID fua701039373.h1

Method BLASTN
NCBI GI g1781039
BLAST score 106
E value 9.0e-53
Match length 222
% identity 87

NCBI Description M.sativa mRNA for delta-1-pyrroline-5-carboxylate synthase,

P5CS-2

Seq. No.

44692

44693

Seq. ID fua701039375.h1

Method BLASTN
NCBI GI g3378649
BLAST score 65
E value 3.0e-28
Match length 133
% identity 87

NCBI Description M.sativa mRNA translated from abscisic activated gene

Seq. No.

Seq. ID fua701039388.h1

Method BLASTX
NCBI GI 94220445
BLAST score 145
E value 1.0e-09
Match length 78
% identity 5

NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible

protein homolog from Arabidopsis thaliana BAC gb_AC003673.

[Arabidopsis thaliana]

Seq. No. 44694

Seg. ID fua701039412.hl

Method BLASTX
NCBI GI g2244949
BLAST score 161
E value 2.0e-11
Match length 59
% identity 56

NCBI Description (Z97339) similarity to ORF - Lilium longiflorum

[Arabidopsis thaliana]

Seq. No. 44695

Seq. ID fua701039530.hl

Method BLASTX
NCBI GI g3451078
BLAST score 177
E value 2.0e-13



Match length 48 % identity 67

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 44696

Seq. ID fua701039542.h1

Method BLASTX
NCBI GI g3269301
BLAST score 312
E value 6.0e-29
Match length 92
% identity 61

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 44697

Seq. ID fua701039551.h1

Method BLASTX
NCBI GI g2979562
BLAST score 342
E value 2.0e-32
Match length 96
% identity 39

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana] >gi 3386623 (AC004665) unknown protein [Arabidopsis

thaliana]

Seq. No. 44698

Seq. ID fua701039608.h1

Method BLASTX
NCBI GI g3819099
BLAST score 150
E value 6.0e-14
Match length 44
% identity 80

NCBI Description (AJ009825) copper amine oxidase [Cicer arietinum]

Seq. No. 44699

Seq. ID fua701039792.h1

Method BLASTX
NCBI GI g2347193
BLAST score 167
E value 5.0e-12
Match length 87
% identity 43

NCBI Description (AC002338) unknown protein [Arabidopsis thaliana]

Seq. No. 44700

Seq. ID fua701039913.h1

Method BLASTX
NCBI GI g3482978
BLAST score 194
E value 4.0e-15
Match length 54
% identity 72

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 44701



```
fua701039935.hl
Seq. ID
                  BLASTX
Method
                  q4454480
NCBI GI
                  210
BLAST score
E value
                  5.0e-17
Match length
                  47
% identity
                  77
                  (AC006234) putative (1-4)-beta-mannan endohydrolase
NCBI Description
                   [Arabidopsis thaliana]
                  44702
Seq. No.
Seq. ID
                  fua701040015.h1
                  BLASTX
Method
                  g4191791
NCBI GI
BLAST score
                  150
E value
                  5.0e-10
Match length
                  44
                   61
% identity
                  (AC005917) putative sf21 {Helianthus annuus} protein
NCBI Description
                   [Arabidopsis thaliana]
                   44703
Seq. No.
                   fua701040089.h1
Seq. ID
                   BLASTN
Method
                   q530086
NCBI GI
                   91
BLAST score
E value
                   1.0e-43
Match length
                   261
% identity
                   91
                  Glycine max aminoalcoholphosphotransferase (AAPT1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   44704
Seq. ID
                   fua701040184.h1
Method
                   BLASTN
NCBI GI
                   g986968
BLAST score
                   61
E value
                   7.0e-26
                   81
Match length
% identity
NCBI Description Glycine max TGACG-motif binding protein (STGA1) mRNA,
                   complete cds
                   44705
Seq. No.
                   fua701040206.h1
Seq. ID
Method
                   BLASTX
                   q1616628
NCBI GI
BLAST score
                   172
E value
                   2.0e-12
Match length
                   67
% identity
NCBI Description (X80472) sts15 [Solanum tuberosum]
                   44706
Seq. No.
                   fua701040238.hl
Seq. ID
```

BLASTX

q3540207

Method

NCBI GI



```
BLAST score
                  2.0e-35
E value
                  95
Match length
                  82
% identity
                  (AC004260) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  44707
Seq. No.
                  fua701040251.hl
Seq. ID
                  BLASTN
Method
                  q16508
                  84
```

NCBI GI g16508 BLAST score 84 E value 2.0e-39 Match length 200 % identity 85

NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene

sam-1 >gi_166871_gb M55077_ATHSAM A.thaliana

S-adenosylmethionine synthetase gene, complete cds

 Seq. No.
 44708

 Seq. ID
 fua701040252.h1

 Method
 BLASTX

 NCBI GI
 g4218991

 BLAST score
 153

 E value
 3.0e-10

Match length 76 % identity 41

NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

 Seq. No.
 44709

 Seq. ID
 fua701040302.h1

 Method
 BLASTN

 NCBI GI
 g3927822

NCBI GI g392782
BLAST score 41
E value 6.0e-14
Match length 69
% identity 90

NCBI Description Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 44710

Seq. ID fua701040344.h1

Method BLASTN
NCBI GI g1223925
BLAST score 199
E value 1.0e-108
Match length 259
% identity 94

NCBI Description Vigna radiata carboxypeptidase II mRNA, partial cds

Seq. No. 44711

Seq. ID fua701040356.h1

Method BLASTN
NCBI GI g3819163
BLAST score 202
E value 1.0e-110
Match length 253
% identity 97



```
NCBI Description
                 Glycine max cctd gene
                  44712
Seq. No.
                  fua701040530.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4249388
                  227
BLAST score
                  5.0e-19
E value
                  88
Match length
                  53
% identity
                  (AC005966) Similar to gb AF025438 Opa-interacting protein
NCBI Description
                   (OIP2) from Homo sapiens. [Arabidopsis thaliana]
                   44713
Seq. No.
                   fua701040538.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3075399
BLAST score
                  250
                   9.0e-22
E value
                   68
Match length
                   74
% identity
                  (AC004484) SF16-like protein [Arabidopsis thaliana]
NCBI Description
                   44714
Seq. No.
                   fua701040550.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4263710
                   195
BLAST score
                   3.0e-15
E value
Match length
                   44
% identity
                   89
                  (AC006223) putative pur-alpha transcriptional activator
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   44715
                   fua701040565.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1170504
BLAST score
                   336
                   7.0e-32
E value
Match length
                   87
                   79
% identity
                   EUKARYOTIC INITIATION FACTOR (ISO) 4F SUBUNIT P82
NCBI Description
                   (IEIF-(ISO)4F P82) >gi 452440 (M95747) initiation factor
                   (iso)4f p82 subunit [Triticum aestivum]
                   44716
Seq. No.
                   fua701040606.hl
Seq. ID
                   BLASTX
Method
                   g2921338
NCBI GI
```

Method BLASTX
NCBI GI g2921338
BLAST score 136
E value 4.0e-11
Match length 50
% identity 64

NCBI Description (AF034133) MYB-like DNA-binding domain protein [Gossypium

hirsutum]



Seq. No. 44717 fua701040618.h1 Seq. ID Method BLASTX NCBI GI q2315983 BLAST score 262 E value 4.0e-23 Match length 89 54 % identity (U82087) calmodulin-like domain protein kinase [Tortula NCBI Description ruralis] 44718 Seq. No. Seq. ID fua701040658.h1 Method BLASTX

NCBI GI g2344895 BLAST score 228 E value 3.0e-19 85

Match length % identity

(AC002388) cytochrome P450 isolog [Arabidopsis thaliana] NCBI Description

Seq. No. 44719

fua701040661.h1 Seq. ID

Method BLASTN NCBI GI g4324966 BLAST score 98 E value 6.0e-48 Match length 138 93 % identity

NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No. 44720

fua701040677.h1 Seq. ID

BLASTX Method g3445397 NCBI GI BLAST score 259 E value 7.0e-23 Match length 83 % identity 51

(AJ010166) S-domain receptor-like protein kinase [Zea mays] NCBI Description

Seq. No. 44721

fua701040719.h1 Seq. ID

BLASTN Method g2317899 NCBI GI 179 BLAST score 2.0e-96 E value 187 Match length % identity 99

NCBI Description Glycine max Sali3-2 mRNA, complete cds

Seq. No. 44722

fua701040769.h1 Seq. ID

BLASTX Method g2367431 NCBI GI BLAST score 187 E value 1.0e-14



```
Match length
% identity
                  (AF000403) putative cytochrome P450 [Lotus japonicus]
NCBI Description
                  44723
Seq. No.
Seq. ID
                  fua701040858.hl
                  BLASTN
Method
NCBI GI
                  q2218149
BLAST score
                  99
                  1.0e-48
E value
                  189
Match length
                  94
% identity
                  Vigna unguiculata type IIIa membrane protein cp-wap11 mRNA,
NCBI Description
                  complete cds
                  44724
Seq. No.
Seq. ID
                  fua701040889.h1
                  BLASTX
Method
NCBI GI
                  g2062171
                  202
BLAST score
                   2.0e-16
E value
                   65
Match length
                   60
% identity
                   (AC001645) DNA binding protein (CDC27SH) isolog
NCBI Description
                   [Arabidopsis thaliana]
                   44725
Seq. No.
Seq. ID
                   fua701040908.h1
                   BLASTX
Method
NCBI GI
                   q71066
                   293
BLAST score
                   9.0e-27
E value
                   81
Match length
                   67
% identity
                   ribosomal protein XL1a - African clawed frog
NCBI Description
                   >gi_224828_prf__1202260A ribosomal protein L1a [Xenopus
                   laevis]
                   44726
Seq. No.
                   fua701040918.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3399678
BLAST score
                   40
E value
                   3.0e-13
                   156
Match length
                   81
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,
                   complete sequence [Arabidopsis thaliana]
```

44727 Seq. No. Seq. ID fua701040946.h1 Method BLASTX

NCBI GI g2465923 BLAST score 255 3.0e-24E value 83 Match length 69 % identity





```
(AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                  44728
Seq. No.
Seq. ID
                  fua701040976.hl
Method
                  BLASTN
                  g170073
NCBI GI
                  169
BLAST score
                  2.0e-90
E value
                  219
Match length
                  95
% identity
NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds
                  44729
Seq. No.
                  fua701040991.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201541
BLAST score
                  185
                  4.0e-14
E value
                  45
Match length
                   69
% identity
NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]
                   44730
Seq. No.
                   fua701041002.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4210504
                   299
BLAST score
                   2.0e-27
E value
Match length
                   95
% identity
                   63
                  (AC002392) putative cadmium-transporting ATPase
NCBI Description
                   [Arabidopsis thaliana]
                   44731
Seq. No.
Seq. ID
                   fua701041026.h1
Method
                   BLASTX
NCBI GI
                   q3549667
BLAST score
                   411
                   1.0e-40
E value
Match length
                   93
% identity
NCBI Description
                  (AL031394) Arabidopsis dynamin-like protein ADL2
                   [Arabidopsis thaliana]
                   44732
Seq. No.
                   fua701041037.hl
Seq. ID
Method
                   BLASTX
                   g3953471
NCBI GI
BLAST score
                   170
                   2.0e-12
E value
                   50
Match length
```

(AC002328) F2202.16 [Arabidopsis thaliana] NCBI Description

% identity

Seq. No.

fua701041056.hl Seq. ID

44733



```
BLASTX
Method
NCBI GI
                  g2245138
BLAST score
                  225
                  9.0e-19
E value
Match length
                  57
% identity
                  79
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  44734
Seq. No.
Seq. ID
                  fua701041071.h1
Method
                  BLASTN
                  g1399566
NCBI GI
BLAST score
                  48
                   4.0e-18
E value
                  76
Match length
% identity
                   91
                  Nigella damascena nuclear 26S ribosomal RNA gene, partial
NCBI Description
                  sequence
                   44735
Seq. No.
                   fua701041114.h1
Seq. ID
Method
                  BLASTX
                  g3158476
NCBI GI
                  268
BLAST score
                   6.0e-24
E value
Match length
                   63
                   84
% identity
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
                   44736
Seq. No.
Seq. ID
                   fua701041119.h1
                   BLASTX
Method
NCBI GI
                   q3036805
BLAST score
                   198
E value
                   1.0e-15
Match length
                   58
% identity
                   66
NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]
                   44737
Seq. No.
Seq. ID
                   fua701041157.hl
Method
                   BLASTX
NCBI GI
                   q4467125
BLAST score
                   147
E value
                   8.0e-10
Match length
                   56
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44738
                   fua701041162.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2104536
```

% identity 62

174 6.0e-13

61

BLAST score

E value Match length



```
(AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  44739
Seq. ID
                  fua701041182.hl
Method
                  BLASTX
NCBI GI
                  q3688173
BLAST score
                  218
E value
                  4.0e-18
Match length
                  76
% identity
                  59
                 (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                  44740
Seq. No.
Seq. ID
                  fua701041189.h1
Method
                  BLASTX
NCBI GI
                  g4510377
BLAST score
                  136
                 1.0e-08
E value
Match length
                  68
% identity
NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]
                  44741
Seq. No.
                  fua701041194.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3047104
BLAST score
                  289
E value
                  2.0e-26
Match length
                  77
% identity
                  73
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
                  44742
Seq. No.
                  fua701041235.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3641845
BLAST score
                  218
E value
                  5.0e-31
Match length
                  79
% identity
                  85
                  (AJ223358) stelar K+ outward rectifying channel
NCBI Description
                   [Arabidopsis thaliana]
                  44743
Seq. No.
                  fua701041286.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1708424
                  132
BLAST score
```

E value 3.0e-18 Match length 65 % identity 78

NCBI Description ISOFLAVONE REDUCTASE HOMOLOG >gi 1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]

44744 Seq. No.

Seq. ID fua701041446.hl



```
BLASTN
Method
                  g684941
NCBI GI
                  97
BLAST score
                  2.0e-47
E value
Match length
                  168
% identity
                   90
                  Medicago sativa S-adenosyl-L-methionine:trans-caffeoyl-CoA
NCBI Description
                   3-O-methyltransferase (CCOMT) mRNA, complete cds
                   44745
Seq. No.
Seq. ID
                   fua701041458.hl
                  BLASTN
Method
                   g170048
NCBI GI
                   248
BLAST score
                   1.0e-137
E value
                   264
Match length
% identity
                  Glycine max SbPRP1 gene encoding a proline-rich protein,
NCBI Description
                   complete cds
                   44746
Seq. No.
Seq. ID
                   fua701041472.h1
                   BLASTX
Method
                   g4538964
NCBI GI
                   282
BLAST score
E value
                   2.0e-25
Match length
                   55
                   89
% identity
                  (ALO49488) NAM/NAP like protein [Arabidopsis thaliana]
NCBI Description
                   44747
Seq. No.
Seq. ID
                   fua701041506.hl
Method
                   BLASTX
NCBI GI
                   q4572674
BLAST score
                   188
E value
                   1.0e-25
Match length
                   65
% identity
                   88
                   (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
                   44748
Seq. No.
                   fua701041509.hl
Seq. ID
Method
                   BLASTN
                   q1808591
NCBI GI
                   123
BLAST score
                   8.0e-63
E value
                   175
Match length
                   93
% identity
NCBI Description C.arietinum mRNA for SAM-synthetase
                   44749
Seq. No.
                   fua701041603.h1
```

Seq. ID

BLASTX Method g1495804 NCBI GI 239 BLAST score 2.0e-28 E value 91 Match length



% identity (X96406) 13-lipoxygenase [Solanum tuberosum] NCBI Description Seq. No. 44750 Seq. ID fua701041622.h1 Method BLASTN NCBI GI q2905771 BLAST score 140 5.0e-73 E value Match length 156

Glycine max glyceraldehyde-3 phosphate dehydrogenase NCBI Description (GAPDH) mRNA, partial cds

Seq. No. 44751

Seq. ID fua701041659.h1

97

Method BLASTX NCBI GI g2623296 .BLAST score 254 3.0e-22 E value Match length 84 % identity 63

(AC002409) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

% identity

Seq. ID fua701041693.h1

44752

Method BLASTX NCBI GI q3757524 BLAST score 214 E value 1.0e-17 Match length 60 % identity 67

(AC005167) tetracycline transporter-like protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 44753

fua701041709.h1 Seq. ID

BLASTN Method g2687437 NCBI GI BLAST score 37 E value 2.0e-11 Match length 37 100 % identity

Jepsonia parryi large subunit 26S ribosomal RNA gene, NCBI Description

partial sequence

Seq. No.

fua701041711.h1 Seq. ID

44754

Method BLASTX NCBI GI g2244904 BLAST score 277 E value 6.0e-25 Match length 88 66 % identity

(Z97339) similar to hypothetical protein C02F5.7 - Caenorha NCBI Description

[Arabidopsis thaliana]



Seq. No. 44755 Seq. ID

fua701041809.h1

Method BLASTN g2687432 NCBI GI 45 BLAST score 3.0e-16

E value 45 Match length 100 % identity

Plumbago auriculata large subunit 26S ribosomal RNA gene, NCBI Description

partial sequence

44756 Seq. No.

fua701041902.h1 Seq. ID

Method BLASTX g2275219 NCBI GI 328 BLAST score 7.0e-31 E value 92 Match length 67 % identity

(AC002337) unknown protein [Arabidopsis thaliana] NCBI Description

44757 Seq. No.

fua701041932.h1 Seq. ID

BLASTX Method NCBI GI g2281115 331 BLAST score 3.0e-31 E value 92 Match length 71 % identity

(AC002330) putative cullin-like 1 protein [Arabidopsis NCBI Description

thaliana]

44758 Seq. No.

fua701041948.h1 Seq. ID

Method BLASTX NCBI GI g2980793 BLAST score 290 E value 2.0e-26 Match length 77 73

% identity

(AL022197) putative protein [Arabidopsis thaliana] NCBI Description

44759 Seq. No.

fua701041955.h1 Seq. ID

Method BLASTX NCBI GI g2147966 338 BLAST score E value 4.0e-32 Match length 87 % identity 74

probable 1-acyl-sn-glycerol-3-phosphate acyltransferase -NCBI Description

Limnanthes douglasii >gi_1067138_emb_CAA88620_ (Z48730) 1-acyl-sn-glycerol-3-phosphate acyltransferase (putative)

[Limnanthes douglasii]

Seq. No. 44760

Seq. ID fua701042034.h1



```
Method
                  BLASTX
NCBI GI
                  g2388569
BLAST score
                  272
E value
                  2.0e-24
Match length
                  82
% identity
                  61
                  (AC000098) Similar to hypothetical protein PID_e327464
NCBI Description
                  (gb Z97338). [Arabidopsis thaliana]
                  44761
Seq. No.
Seq. ID
                  fua701042107.hl
                  BLASTX
Method
                  g1781322
NCBI GI
BLAST score
                  153
                  2.0e-10
E value
Match length
                  63
% identity
                  52
NCBI Description (Y10462) peroxidase [Spinacia oleracea]
                  44762
Seq. No.
Seq. ID
                  fua701042140.h1
Method
                  BLASTX
                  q3924596
NCBI GI
                  259
BLAST score
                  8.0e-23
E value
                  85
Match length
% identity
                  61
                  (AF069442) putative phospho-ser/thr phosphatase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  44763
Seq. ID
                  fua701042169.hl
Method
                  BLASTX
NCBI GI
                  q4455252
BLAST score
                  269
                  5.0e-24
E value
Match length
                  71
% identity
                  (AL035523) respiratory burst oxidase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   44764
Seq. No.
Seq. ID
                   fua701042173.hl
Method
                  BLASTX
                  g2914710
NCBI GI
BLAST score
                  289
                  2.0e-26
E value
Match length
                  84
% identity
                  (AC003974) putative beta-D-galactosidase [Arabidopsis
NCBI Description
```

thaliana]

Seq. No. 44765

fua701042179.h1 Seq. ID

BLASTX Method g4063747 NCBI GI BLAST score 234



```
6.0e-20
E value
Match length
                   61
% identity
                   (AC005851) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  44766
Seq. ID
                  fua701042218.hl
                  BLASTX
Method
                  q3080420
NCBI GI
                  194
BLAST score
E value
                   4.0e-15
                  76
Match length
                   57
% identity
                   (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                   44767
Seq. No.
Seq. ID
                   fua701042220.h1
Method
                  BLASTX
NCBI GI
                   g1514643
BLAST score
                   338
E value
                   5.0e-32
Match length
                   90
                   66
% identity
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                   44768
Seq. No.
                   fua701042296.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4006829
BLAST score
                   277
                   3.0e-25
E value
Match length
                   75
% identity
                  (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   44769
Seq. No.
Seq. ID
                   fua701042322.h1
Method
                   BLASTX
NCBI GI
                   q1049407
BLAST score
                   180
E value
                   1.0e-13
Match length
                   79
% identity
                   46
                   (U39655) Similar to long-chain-fatty-acid coA ligase.
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                   44770
Seq. ID
                   fua701042539.h1
Method
                   BLASTX
NCBI GI
                   g3426048
BLAST score
                   160
```

E value 3.0e-11 Match length 32 % identity 91

(AC005168) putative hydroxymethylglutaryl-CoA lyase NCBI Description

precursor [Arabidopsis thaliana]



```
Seq. No.
                  44771
Seq. ID
                  fua701042553.h1
Method
                  BLASTX
NCBI GI
                  g3242789
BLAST score
                  137
                  3.0e-17
E value
Match length
                  56
% identity
                  (AF055357) respiratory burst oxidase protein D [Arabidopsis
NCBI Description
                  thaliana]
                  44772
Seq. No.
Seq. ID
                  fua701042662.h1
                  BLASTX
Method
NCBI GI
                  g629783
BLAST score
                  130
E value
                  3.0e-12
Match length
                  42
                  76
% identity
NCBI Description ES43 protein - barley >gi 1345528 emb CAA54682 (X77575)
                  ES43 [Hordeum vulgare]
                  44773
Seq. No.
Seq. ID
                  fua701042675.h1
                  BLASTX
Method
NCBI GI
                  g3080411
                  275
BLAST score
                  1.0e-24
E value
Match length
                  76
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                  44774
Seq. No.
Seq. ID
                  fua701042696.h1
Method
                  BLASTX
NCBI GI
                  g2894606
BLAST score
                  190
E value
                  1.0e-14
Match length
                  56
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                  44775
Seq. No.
                  fua701042715.hl
Seq. ID
Method
                  BLASTX
                  g2129703
NCBI GI
BLAST score
                  335
E value
                  9.0e-32
Match length
                  82
                  73
% identity
                  receptor kinase - Arabidopsis thaliana
NCBI Description
                  >gi 2129704 pir S71184 receptor kinase - Arabidopsis
```

[Arabidopsis thaliana]

thaliana >gi 166692 (M80238) receptor kinase [Arabidopsis

thaliana] >gi 445123 prf 1908429A receptor kinase



```
44776
Seq. No.
                   fua701042716.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3510264
BLAST score
                   202
                   4.0e-16
E value
Match length
                   76
% identity
                   51
                   (AC005310) hypothetical protein, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
                   44777
Seq. No.
                   fua701042733.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2252839
BLAST score
                   296
                   3.0e-27
E value
Match length
                   84
% identity
                   73
                   (AF013293) Similar to receptor-like protein kinase precusor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   44778
                   fua701042735.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1669599
BLAST score
                   222
E value
                   2.0e-18
Match length
                   83
                   53
% identity
NCBI Description
                  (D88746) AR791 [Arabidopsis thaliana]
                   44779
Seq. No.
                   fua701042751.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2304954
BLAST score
                   251
E value
                   1.0e-139
Match length
                   251
                   100
% identity
NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds
Seq. No.
                   44780
                   fua701042775.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245099
BLAST score
                   180
E value
                   1.0e-13
Match length
                   81
% identity
                   44
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   44781
```

Seq. ID fua701042784.h1

Method BLASTX NCBI GI g4263722 BLAST score 225



```
E value
                  7.0e-19
Match length
                  57
                  79
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  44782
                  fua701042993.hl
Seq. ID
                  BLASTX
Method
                  q4538897
NCBI GI
                  137
BLAST score
E value
                  9.0e-09
                  53
Match length
% identity
                  47
                  (AL049482) AX110P-like protein [Arabidopsis thaliana]
NCBI Description
                  44783
Seq. No.
                  fua701043049.h1
Seq. ID
Method
                  BLASTN
                  q473216
NCBI GI
                  55
BLAST score
                  2.0e-22
E value
Match length
                  107
                  88
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
                   44784
Seq. No.
Seq. ID
                   fua701043051.hl
                  BLASTN
Method
NCBI GI
                  g3334660
BLAST score
                   64
E value
                   8.0e-28
Match length
                   160
% identity
                   85
                  G.max mRNA for putative cytochrome P450, clone CP3
NCBI Description
                   44785
Seq. No.
Seq. ID
                   fua701043064.h1
                  BLASTN
Method
                   g862930
NCBI GI
BLAST score
                   36
                   4.0e-11
E value
Match length
                   52
% identity
                   92
                  Medicago sativa acidic glucanase mRNA, complete cds
NCBI Description
                   44786
Seq. No.
                   fua701043087.h1
Seq. ID
                   BLASTX
Method
                   g3377848
NCBI GI
                   177
BLAST score
```

2.0e-13 E value Match length 57 58 % identity

(AF076274) contains similarity to reverse transcriptases NCBI Description (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]

Seq. No. 44787



```
fua701043177.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q516853
                   102
BLAST score
E value
                   2.0e-50
Match length
                   161
                   39
% identity
                   Soybean SUBI-2 gene for ubiquitin, complete cds
NCBI Description
                   44788
Seq. No.
Seq. ID
                   fua701043180.h1
                   BLASTX
Method
                   g4580531
NCBI GI
                   237
BLAST score
                   2.0e-20
E value
Match length
                   77
% identity
                   (AF036309) scarecrow-like 14 [Arabidopsis thaliana]
NCBI Description
                   44789
Seq. No.
                   fua701043204.hl
Seq. ID
Method
                   BLASTN
                   q3873174
NCBI GI
BLAST score
                   33
                   3.0e-09
E value
                   57
Match length
% identity
                   89
                   Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   44790
Seq. No.
Seq. ID
                   fua701043234.h1
Method
                   BLASTX
                   q3805956
NCBI GI
BLAST score
                   236
                   3.0e-20
E value
Match length
                   76
% identity
                   61
                   (Y13769) laccase [Populus balsamifera subsp. trichocarpa]
NCBI Description
Seq. No.
                   44791
                   fua701043247.hl
Seq. ID
Method
                   BLASTN
                   g303900
NCBI GI
                   55
BLAST score
                   2.0e-22
E value
                   106
Match length
% identity
                   47
                   Soybean gene for ubiquitin, complete cds
NCBI Description
                   44792
Seq. No.
                   fua701043259.h1
 Seq. ID
                   BLASTX
Method
                   g2494144
NCBI GI
                   291
BLAST score
```

7164

1.0e-26

78

E value

Match length



% identity (AC002329) predicted leucine-rich protein [Arabidopsis NCBI Description thaliana]

Seq. No. 44793

fua701043270.h1 Seq. ID

Method BLASTX NCBI GI g1617268 BLAST score 186 2.0e-14 E value Match length 54 % identity 67

(Z72153) acyl CoA synthetase [Brassica napus] NCBI Description

Seq. No.

44794

Seq. ID fua701043275.hl Method BLASTX

NCBI GI q4335751 BLAST score 274 E value 1.0e-24 Match length 76 % identity 66

(AC006284) putative methyltransferase [Arabidopsis NCBI Description

thaliana]

Seq. No. 44795

fua701043307.h1 Seq. ID

Method BLASTX NCBI GI g2894599 BLAST score 193 5.0e-15 E value Match length 42 % identity 76

(AL021889) putative protein [Arabidopsis thaliana] NCBI Description

44796 Seq. No.

fua701043367.h1 Seq. ID

BLASTX Method NCBI GI g4567319 BLAST score 279 4.0e-25 E value Match length 84 % identity 68

(AC005956) putative copper amine oxidase [Arabidopsis NCBI Description

thaliana]

Seq. No.

44797

44798

fua701043408.hl Seq. ID

Method BLASTX NCBI GI g4510406 124 BLAST score E value 6.0e-15 76 Match length 56 % identity

(AC006587) putative protein kinase [Arabidopsis thaliana] NCBI Description

Seq. No.



Seq. ID fua701043424.h1

Method BLASTX
NCBI GI g3063699
BLAST score 124
E value 1.0e-14
Match length 81
% identity 46

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 44799

Seg. ID fua701043439.h1

Method BLASTN
NCBI GI g2149954
BLAST score 95
E value 3.0e-46
Match length 202
% identity 87

NCBI Description Phaseolus vulgaris putative aquaporin-1 (Mip-1) mRNA,

complete cds

Seq. No. 44800

Seq. ID fua701043466.h1

Method BLASTX
NCBI GI g3335341
BLAST score 136
E value 3.0e-12
Match length 56
% identity 71

NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No. 44801

Seq. ID fua701043559.h1

Method BLASTX
NCBI GI g4314365
BLAST score 198
E value 1.0e-15
Match length 69
% identity 57

NCBI Description (AC006340) putative copia-like retrotransposon Hopscotch

[Arabidopsis thaliana]

Seq. No. 44802

Seq. ID fua701043610.h1

Method BLASTX
NCBI GI g3063459
BLAST score 266
E value 1.0e-23
Match length 86
% identity 66

NCBI Description (AC003981) F22013.21 [Arabidopsis thaliana]

Seq. No. 44803

Seq. ID fua701043651.h1

Method BLASTX
NCBI GI g1654140
BLAST score 311
E value 6.0e-29



```
Match length
% identity
                  (U37840) lipoxygenase [Lycopersicon esculentum]
NCBI Description
                  44804
Seq. No.
                  fua701043682.hl
Seq. ID
                  BLASTX
Method
                  a4309731
NCBI GI
                  180
BLAST score
                  1.0e-21
E value
Match length
                  76
% identity
                   66
                  (AC006439) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   44805
Seq. No.
Seq. ID
                   fua701043688.hl
Method
                   BLASTX
NCBI GI
                   q4185511
BLAST score
                   257
                   1.0e-22
E value
                   58
Match length
                   86
% identity
                   (AF102822) actin depolymerizing factor 4 [Arabidopsis
NCBI Description
                   thaliana]
                   44806
Seq. No.
Seq. ID
                   fua701043695.h1
                   BLASTX
Method
                   g4567315
NCBI GI
BLAST score
                   307
                   2.0e-28
E value
Match length
                   65
% identity
                  (AC005956) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   44807
Seq. No.
Seq. ID
                   gbt700547960.h1
Method
                   BLASTX
NCBI GI
                   g3402754
BLAST score
                   297
E value
                   3.0e-27
Match length
                   72
% identity
                   76
                  (AL031187) putative protein [Arabidopsis thaliana]
NCBI Description
                   44808
Seq. No.
                   qbt700547985.h1
Seq. ID
Method
                   BLASTN
                   g170073
NCBI GI
BLAST score
                   187
                   1.0e-101
E value
Match length
                   233
```

NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds

% identity

Seq. No.

Seq. ID gbt700547988.h1

96

44809



Method BLASTN
NCBI GI g3510347
BLAST score 37
E value 1.0e-11
Match length 126
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No. 44810

Seq. ID gbt700548008.hl

Method BLASTX
NCBI GI g3327870
BLAST score 198
E value 1.0e-15
Match length 90
% identity 47

NCBI Description (AB012913) COP1-Interacting ProteinI 7 (CIP7) [Arabidopsis

thaliana]

Seq. No. 44811

Seq. ID gbt700548022.h1

Method BLASTX
NCBI GI g2392771
BLAST score 130
E value 2.0e-12
Match length 70
% identity 61

NCBI Description (AC002534) putative kinesin-like protein [Arabidopsis

thaliana]

Seq. No. 44812

Seq. ID gbt700548023.h1

Method BLASTX
NCBI GI g4336747
BLAST score 192
E value 1.0e-26
Match length 76
% identity 77

NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]

Seq. No. 44813

Seq. ID gbt700548085.h1

Method BLASTN
NCBI GI g2245377
BLAST score 52
E value 2.0e-20
Match length 140
% identity 85

NCBI Description Arabidopsis thaliana auxin response factor 1 (ARF1) mRNA,

complete cds

Seq. No. 44814

Seq. ID gsf700698322.h1

Method BLASTX
NCBI GI g2495359
BLAST score 242



```
1.0e-20
E value
Match length
                  46
                  100
% identity
                  HEAT SHOCK PROTEIN HSS1 >gi 881932 (U26597) HSS1 [Puccinia
NCBI Description
                  graminis f. sp. tritici]
                  44815
Seq. No.
Seq. ID
                  qsf700698332.h1
                  BLASTX
Method
                  q1345971
NCBI GI
BLAST score
                  163
                  2.0e-11
E value
                  27
Match length
                  100
% identity
                  OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_541947_pir__JQ2339 omega-3 fatty acid desaturase (EC
                  1.1\overline{4.99.-} GMD - soybean >gi 408792 (L22965) omega-3 fatty
                  acid desaturase [Glycine soja]
                   44816
Seq. No.
                  qsf700698349.h1
Seq. ID
Method
                  BLASTX
                  g2062169
NCBI GI
                   254
BLAST score
                   5.0e-30
E value
                   96
Match length
                   69
% identity
                   (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                   thaliana]
                   44817
Seq. No.
Seq. ID
                   qsf700698492.h1
Method
                   BLASTX
NCBI GI
                   q4097880
BLAST score
                   477
                   2.0e-48
E value
Match length
                   93
% identity
                   97
                  (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
Seq. No.
                   44818
Seq. ID
                   qsv701043716.h1
Method
                   BLASTX
                   q1352316
NCBI GI
                   188
BLAST score
                   2.0e-14
E value
Match length
                   39
% identity
                   95
                   DR1 PROTEIN HOMOLOG >gi_633026_dbj_BAA07288_ (D38110) Dr1
NCBI Description
```

Seq. No. 44819

Seq. ID gsv701043939.h1

Method BLASTN
NCBI GI g3334755
BLAST score 47
E value 8.0e-18

[Arabidopsis thaliana]



Match length % identity 85

Medicago sativa mRNA for putative arginine/serine-rich NCBI Description

splicing factor

Seq. No. 44820

Seq. ID gsv701044018.hl

Method BLASTN NCBI GI q167072 BLAST score 106 E value 9.0e-53 Match length 206 % identity 88

NCBI Description Barley ubiquitin (mub1) gene, complete cds

Seq. No. 44821

Seq. ID gsv701044037.hl

Method BLASTX NCBI GI q2828293 BLAST score 183 E value 5.0e-14 Match length 81 % identity

(AL021687) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 44822

Seq. ID gsv701044060.h1

Method BLASTX NCBI GI g3386621 BLAST score 186 3.0e-14 E value Match length 45 78

% identity

(AC004665) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 44823

gsv701044063.h1 Seq. ID

Method BLASTX NCBI GI q4263789 BLAST score 284 9.0e-26 E value Match length 83 % identity 67

(AC006068) putative monooxygenase [Arabidopsis thaliana] NCBI Description

44824 Seq. No.

gsv701044122.hl Seq. ID

Method BLASTN NCBI GI g4432811 BLAST score 40 E value 2.0e-13 Match length 52 94 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F16D14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 44825



```
gsv701044144.h1
Seq. ID
Method
                  BLASTX
                  g3377803
NCBI GI
BLAST score
                  300
                  1.0e-27
E value
                  78
Match length
                  83
% identity
                  (AF075597) Similar to (p)ppGpp synthetase; T2H3.9
NCBI Description
                   [Arabidopsis thaliana]
                  44826
Seq. No.
                  gsv701044206.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2618689
BLAST score
                  374
E value
                  5.0e-43
Match length
                  101
% identity
                  88
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  44827
                  gsv701044233.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2828186
BLAST score
                  71
E value
                  9.0e-32
Match length
                  171
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18I23, complete sequence [Arabidopsis thaliana]
Seq. No.
                  44828
                  gsv701044255.h1
Seq. ID
Method
                  BLASTN
                  g20898
NCBI GI
BLAST score
                  44
                  6.0e-16
E value
Match length
                  44
                  100
% identity
NCBI Description
                  Pea U5 snRNA (clone pPSU5.4)
                  44829
Seq. No.
                  gsv701044271.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462756
BLAST score
                  287
                  5.0e-26
E value
                  95
Match length
                  42
% identity
NCBI Description
                  (AC002292) putative receptor kinase [Arabidopsis thaliana]
Seq. No.
                  44830
                  gsv701044273.h1
Seq. ID
Method
                  BLASTN
```

BLAST score 53 E value 5.0e-21

NCBI GI

g710349

7171



Match length 161 % identity 83

NCBI Description Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA,

complete cds

Seq. No. 44831

Seq. ID gsv701044283.hl

Method BLASTN
NCBI GI g170053
BLAST score 116
E value 1.0e-58
Match length 192
% identity 90

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 44832

Seq. ID gsv701044304.h1

Method BLASTX
NCBI GI g3913008
BLAST score 344
E value 9.0e-33
Match length 78
% identity 83

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>qi 3021338 emb CAA06308 (AJ005041) cytosolic

fructose-1,6-bisphosphate aldolase [Cicer arietinum]

Seq. No. 44833

Seq. ID gsv701044337.h1

Method BLASTN
NCBI GI g170071
BLAST score 261
E value 1.0e-145
Match length 265
% identity 100

NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds

Seq. No. 44834

Seq. ID gsv701044357.h1

Method BLASTN
NCBI GI g3193311
BLAST score 39
E value 8.0e-13
Match length 167
% identity 81

NCBI Description Arabidopsis thaliana BAC F6N15

Seq. No. 44835

Seq. ID gsv701044363.hl

Method BLASTN
NCBI GI g2656026
BLAST score 41
E value 6.0e-14
Match length 125
% identity 83

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDF20



```
44836
Seq. No.
                  gsv701044371.hl
Seq. ID
Method
                  BLASTN
                  g2736287
NCBI GI
                  37
BLAST score
                  1.0e-11
E value
                  49
Match length
                  94
% identity
                  Camptotheca acuminata isopentenyl diphosphate isomerase II
NCBI Description
                   (IPI2) mRNA, complete cds
                  44837
Seq. No.
                  gsv701044377.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1103318
BLAST score
                  144
                  2.0e-09
E value
                  69
Match length
                   43
% identity
                   (X78818) casein kinase I [Arabidopsis thaliana]
NCBI Description
                  >gi_2244791_emb_CAB10213.1_ (Z97336) casein kinase I
                   [Arabidopsis thaliana]
                   44838
Seq. No.
                   gsv701044391.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953458
BLAST score
                   416
                   3.0e-41
E value
                   82
Match length
                   93
% identity
                  (AC002328) F20N2.3 [Arabidopsis thaliana]
NCBI Description
                   44839
Seq. No.
                   gsv701044403.h1
Seq. ID
Method
                   BLASTX
                   g4006888
NCBI GI
BLAST score
                   163
                   1.0e-11
E value
                   67
Match length
% identity
                   48
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44840
                   gsv701044437.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2935416
BLAST score
                   180
E value
                   1.0e-13
Match length
                   43
% identity
                   79
                  (AF047896) isoflavone reductase homolog [Betula pendula]
NCBI Description
```

Seq. No. 44841

Seq. ID gsv701044439.h1

Method BLASTX

```
q3925363
NCBI GI
                  312
BLAST score
                  5.0e-29
E value
                  86
Match length
% identity
                   (AF067961) homeodomain protein [Malus domestica]
NCBI Description
                   44842
Seq. No.
Seq. ID
                   gsv701044440.hl
                   BLASTX
Method
NCBI GI
                   q4539459
                   153
BLAST score
                   2.0e-10
E value
                   58
Match length
% identity
                   (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                   44843
Seq. No.
Seq. ID
                   qsv701044469.hl
                   BLASTN
Method
                   q4056429
NCBI GI
BLAST score
                   67
                   2.0e-29
E value
                   107
Match length
                   91
% identity
                   Arabidopsis thaliana chromosome 1 BAC F508 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   44844
Seq. No.
Seq. ID
                   qsv701044558.hl
                   BLASTX
Method
NCBI GI
                   q4325343
BLAST score
                   192
                   3.0e-15
E value
                   41
Match length
% identity
                   90
                   (AF128393) contains similarity to homeobox domains (Pfam:
NCBI Description
                   PF00046, Score, 36.5, E=6.9e-08, N=1) [Arabidopsis thaliana]
                   44845
Seq. No.
                   gsv701044578.h1
 Seq. ID
Method
                   BLASTX
                   q2865433
NCBI GI
                   148
BLAST score
                   5.0e-10
E value
                   30
Match length
 % identity
                   83
                   (AF039374) chromomethylase [Arabidopsis suecica]
 NCBI Description
```

Seq. No. 44846

Seq. ID gsv701044677.h1

Method BLASTX
NCBI GI 94530126
BLAST score 294
E value 6.0e-27
Match length 86
% identity 62



NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No. 44847

Seq. ID gsv701044689.h1

Method BLASTX
NCBI GI g2708741
BLAST score 279
E value 2.0e-25
Match length 62
% identity 84

NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No. 44848

Seq. ID gsv701044837.h1

Method BLASTN
NCBI GI g3869072
BLAST score 45
E value 2.0e-16
Match length 109
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJB24, complete sequence [Arabidopsis thaliana]

Seq. No. 44849

Seq. ID gsv701044839.hl

Method BLASTN
NCBI GI g217902
BLAST score 72
E value 2.0e-32
Match length 196
% identity 84

NCBI Description Catharanthus roseus cyc07 mRNA, complete cds

Seq. No.

Seq. ID gsv701044857.h1

44850

Method BLASTX
NCBI GI g1168189
BLAST score 229
E value 1.0e-19
Match length 60
% identity 78

NCBI Description 14-3-3-LIKE PROTEIN A (VFA-1433A) >gi_1076542_pir__S52899

14-3-3 brain protein homolog - fava bean

>gi 695765 emb CAA88415 (Z48504) 14-3-3 brain protein

homolog [Vicia faba]

Seq. No. 44851

Seq. ID gsv701044871.h1

Method BLASTX
NCBI GI 94432839
BLAST score 248
E value 8.0e-22
Match length 80
% identity 64

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]



```
44852
Seq. No.
                  gsv701044903.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2462746
BLAST score
                  180
                  2.0e-28
E value
Match length
                  77
                  79
% identity
                   (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   44853
Seq. No.
                   gsv701044920.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4154092
BLAST score
                   180
                   9.0e-14
E value
Match length
                   45
% identity
                   69
                   (Z98533) putative cell division cycle protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   44854
Seq. No.
                   gsv701044924.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3821793
BLAST score
                   214
E value
                   1.0e-19
Match length
                   55
% identity
                   82
                  (Y11526) casein kinase II alpha subunit [Zea mays]
NCBI Description
                   44855
Seq. No.
                   gsv701044950.h1
Seq. ID
Method
                   BLASTN
                   g1196896
NCBI GI
                   184
BLAST score
                   3.0e-99
E value
Match length
                   191
                   99
% identity
NCBI Description Glycine max acidic ribosomal protein PO mRNA, complete cds
                   44856
Seq. No.
                   gsv701044954.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3228517
                   157
BLAST score
                   2.0e-23
E value
                   86
Match length
                   65
% identity
                  (AF007788) ETTIN [Arabidopsis thaliana]
NCBI Description
                   44857
```

qsv701044955.h1 Seq. ID

BLASTN Method NCBI GI g2905771 136 BLAST score

Seq. No.



E value 1.0e-70 Match length 155 % identity 97

NCBI Description Glycine max glyceraldehyde-3 phosphate dehydrogenase

(GAPDH) mRNA, partial cds

Seq. No. 44858

Seq. ID gsv701044964.h1

Method BLASTN
NCBI GI g288187
BLAST score 176
E value 2.0e-94
Match length 223
% identity 95

NCBI Description V.unguiculata cysteine proteinase inhibitor mRNA

Seq. No. 44859

Seq. ID gsv701045023.h1

Method BLASTX
NCBI GI g3924596
BLAST score 206
E value 8.0e-17
Match length 52
% identity 75

NCBI Description (AF069442) putative phospho-ser/thr phosphatase

[Arabidopsis thaliana]

Seq. No. 44860

Seq. ID gsv701045025.h1

Method BLASTX
NCBI GI g1171978
BLAST score 208
E value 5.0e-17
Match length 52
% identity 26

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)

(PABP 2) >gi_304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)

...

poly(A)-binding protein [Arabidopsis thaliana]

Seq. No. 44861

Seq. ID gsv701045026.h1

Method BLASTX
NCBI GI g4139230
BLAST score 140
E value 4.0e-09
Match length 51
% identity 59

NCBI Description (AF109243) mismatch repair protein [Arabidopsis thaliana]

Seq. No. 44862

Seq. ID gsv701045070.h1

Method BLASTN
NCBI GI g2052028
BLAST score 258
E value 1.0e-143
Match length 274

7177

```
% identity
                  G.max mRNA for glutathione transferase
NCBI Description
Seq. No.
                  44863
Seq. ID
                  gsv701045076.h1
Method
                  BLASTX
                  q1432056
NCBI GI
                  172
BLAST score
                  8.0e-13
E value
                  46
Match length
% identity
                  (U56834) WRKY3 [Petroselinum crispum]
NCBI Description
                  44864
Seq. No.
                  gsv701045143.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1076344
BLAST score
                   172
                   3.0e-14
E value
                   61
Match length
                   60
% identity
                  kinase-associated protein phosphatase precursor -
NCBI Description
                  Arabidopsis thaliana
                   44865
Seq. No.
Seq. ID
                   gsv701045150.hl
Method
                   BLASTN
                   g3132697
NCBI GI
                   37
BLAST score
E value
                   1.0e-11
                   73
Match length
                   88
% identity
NCBI Description
```

Pisum sativum SAR DNA-binding protein (SARBP-2) mRNA, complete cds

44866 Seq. No. Seq. ID gsv701045203.h1 Method BLASTX g2245086 NCBI GI BLAST score 160

E value 2.0e-11 Match length 46 % identity 70

(Z97343) hypothetical protein [Arabidopsis thaliana] NCBI Description

44867 Seq. No.

gsv701045218.h1 Seq. ID

Method BLASTX g1732517 NCBI GI 283 BLAST score 7.0e-26 E value 64 Match length % identity 83

(U62745) putative cytoskeletal protein [Arabidopsis NCBI Description

thaliana]

44868 Seq. No.



```
qsv701045228.h1
Seq. ID
                   BLASTN
Method
                   g1053048
NCBI GI
BLAST score
                   65
                   2.0e-28
E value
                   143
Match length
                   98
% identity
                  Glycine max histone H3 gene, partial cds, clone S3
NCBI Description
Seq. No.
                   44869
                   gsv701045367.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                   g16508
BLAST score
                   116
                   1.0e-58
E value
```

164 Match length 93 % identity

A.thaliana DNA for S-adenosylmethionine synthetase gene NCBI Description

sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana

S-adenosylmethionine synthetase gene, complete cds

44870 Seq. No. Seq. ID gsv701045422.h1 BLASTXMethod g729335 NCBI GI

176 BLAST score 5.0e-13 E value 70 Match length 51 % identity

SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN NCBI Description

PRECURSOR (IP) >gi 508849 (L27705) succinate dehydrogenase

iron-protein subunit [Drosophila melanogaster]

44871 Seq. No.

qsv701045437.h1 Seq. ID

BLASTX Method NCBI GI q1856971 BLAST score 235 E value 5.0e-20 Match length 49 % identity 90

NCBI Description (D26058) This gene is specifically expressed at the S phase

during the cell cycle in the synchronous culture of

periwinkle cells. [Catharanthus roseus]

Seq. No. 44872

gsv701045489.h1 Seq. ID

Method BLASTN g2920665 NCBI GI BLAST score 148 8.0e-78 E value Match length 184 % identity 95

Glycine max 2,4-D inducible glutathione S-transferase NCBI Description

(GSTa) mRNA, complete cds

Seq. No. 44873



```
gsv701045513.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512707
                  234
BLAST score
E value
                  5.0e-20
Match length
                  76
% identity
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   44874
Seq. ID
                  qsv701045522.h1
                  BLASTX
Method
                   g3421384
NCBI GI
                   288
BLAST score
                   2.0e-26
E value
Match length
                   70
% identity
                   79
                   (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
NCBI Description
                   [Arabidopsis thaliana]
                   44875
Seq. No.
Seq. ID
                   gsv701045571.hl
                   BLASTN
Method
                   g169954
NCBI GI
                   80
BLAST score
                   3.0e-37
E value
Match length
                   80
                   100
% identity
                  Glycine max iron superoxide dismutase (FeSOD) mRNA,
NCBI Description
                   complete cds
                   44876
Seq. No.
                   gsv701045577.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4519199
BLAST score
                   202
E value
                   2.0e-16
Match length
                   64
                   62
% identity
                   (AB024050) MYC-RP [Perilla frutescens]
NCBI Description
                   44877
Seq. No.
                   gsv701045641.h1
Seq. ID
                   BLASTN
Method
                   q3510337
NCBI GI
                   45
BLAST score
                   2.0e-16
E value
Match length
                   133
                   83
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19E20, complete sequence [Arabidopsis thaliana]
                   44878
Seq. No.
                   gsv701045706.h1
Seq. ID
```

7180

BLASTN

54

g2687432

Method

NCBI GI BLAST score



E value Match length 100 % identity Plumbago auriculata large subunit 26S ribosomal RNA gene, NCBI Description partial sequence 44879 Seq. No. Seq. ID gsv701045737.h1 Method BLASTX q4185599 NCBI GI BLAST score 153 E value 2.0e-10 Match length 80 % identity 42 NCBI Description (AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora] Seq. No. 44880 Seq. ID gsv701045758.h1 Method BLASTX NCBI GI g3599491 BLAST score 271 E value 3.0e-24Match length 64 % identity NCBI Description (AF085149) putative aminotransferase [Capsicum chinense] Seq. No. 44881 gsv701045760.h1 Seq. ID Method BLASTX NCBI GI q4539345 BLAST score 189 E value 1.0e-14 Match length 55 % identity NCBI Description (AL035539) hypothetical protein [Arabidopsis thaliana] Seq. No. 44882 gsv701045946.h1 Seq. ID Method BLASTX g3080396 NCBI GI BLAST score 224 E value 1.0e-18 Match length 57 % identity NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 44883

Seq. ID gsv701045988.h1

Method BLASTX NCBI GI g3023432 BLAST score 193 4.0e-15 E value Match length 69 % identity 62

NCBI Description CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA

3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT)





>gi_1785477_dbj_BAA19102_ (AB000408) caffeoyl-CoA
3-O-methyltransferase [Populus kitakamiensis]

```
Seq. No.
                   44884
Seq. ID
                   gsv701046033.hl
Method
                  BLASTX
NCBI GI
                   q1805654
BLAST score
                   199
E value
                   9.0e-16
Match length
                   89
% identity
                   45
                   (X99972) calmodulin-stimulated calcium-ATPase [Brassica
NCBI Description
                   oleracea]
Seq. No.
                   44885
Seq. ID
                   gsv701046210.h1
Method
                   BLASTX
NCBI GI
                   q99737
BLAST score
                   184
                   3.0e-14
E value
Match length
                   39
% identity
                   85
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                   Arabidopsis thaliana >gi 16189 emb CAA46815 (X66017)
                   NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
Seq. No.
                   44886
Seq. ID
                   gsv701046215.h1
Method
                   BLASTX
NCBI GI
                   g2832616
BLAST score
                   139
E value
                   5.0e-09
Match length
                   65
% identity
                   45
                   (AL021711) heat shock transcription factor - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   44887
Seq. No.
                   gsv701046263.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2760829
BLAST score
                   42
                   1.0e-14
E value
Match length
                   102
% identity
                   85
                   Arabidopsis thaliana chromosome II BAC F18A8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   44888
                   gsv701046277.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3264762
BLAST score
                   73
                   4.0e-33
E value
Match length
                   141
```

NCBI Description Prunus armeniaca 40S ribosomal protein S4 (RPS4) mRNA,

88

% identity



complete cds

Seq. No. 44889

Seq. ID gsv701046292.h1

Method BLASTX
NCBI GI g477094
BLAST score 332
E value 1.0e-31
Match length 67
% identity 94

NCBI Description STE11 protein kinase homolog NPK1 - common tobacco

Seq. No. 44890

Seq. ID gsv701046387.h1

Method BLASTN
NCBI GI g871769
BLAST score 33
E value 3.0e-09
Match length 108
% identity 21

NCBI Description V.unguiculata mRNA for glycin-rich protein

Seq. No. 44891

Seq. ID gsv701046403.h1

Method BLASTN
NCBI GI g2606080
BLAST score 65
E value 3.0e-28
Match length 173
% identity 84

NCBI Description Glycine max sucrose synthase (SS) mRNA, complete cds

Seq. No. 44892

Seq. ID gsv701046466.h1

Method BLASTN
NCBI GI g463251
BLAST score 64
E value 1.0e-27
Match length 120
% identity 88

NCBI Description M.sativa (Nagyszenasi) mRNA for ribosomal protein RL5

Seq. No. 44893

Seq. ID gsv701046511.h1

Method BLASTX
NCBI GI g2529668
BLAST score 139
E value 1.0e-08
Match length 49
% identity 59

NCBI Description (AC002535) putative photolyase/blue-light receptor

[Arabidopsis thaliana] >gi_3319288 (AF053366)

photolyase/blue light photoreceptor PHR2 [Arabidopsis

thaliana

Seq. No. 44894

Seq. ID gsv701046564.h1



Method BLASTX
NCBI GI g3241945
BLAST score 206
E value 9.0e-17
Match length 57
% identity 61

NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]

Seq. No. 44895

Seq. ID gsv701046622.h1

Method BLASTX
NCBI GI g3024019
BLAST score 210
E value 3.0e-17
Match length 51
% identity 78

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_2225879_dbj_BAA20876_ (AB004823) eukaryotic initiation
factor 5A2 [Solanum tuberosum] >gi_2225887_dbj_BAA20880_
(AB004827) eukaryotic initiation factor 5A1 [Solanum

tuberosum]

Seq. No. 44896

Seq. ID gsv701046636.h1

Method BLASTX
NCBI GI g4544402
BLAST score 192
E value 5.0e-15
Match length 83
% identity 26

NCBI Description (AC007047) putative leucine rich repeat protein

[Arabidopsis thaliana]

Seq. No. 44897

Seq. ID gsv701046638.h1

Method BLASTX
NCBI GI g3298555
BLAST score 169
E value 3.0e-12
Match length 47
% identity 62

NCBI Description (AC004681) putative homeobox protein, 3' partial

[Arabidopsis thaliana]

Seq. No. 44898

Seq. ID gsv701046646.h1

Method BLASTN
NCBI GI g2304954
BLAST score 243
E value 1.0e-134
Match length 251
% identity 99

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No. 44899

Seq. ID gsv701046654.h1

Method BLASTX

NCBI GI

BLAST score

g968901

53



```
q4417266
NCBI GI
BLAST score
                  153
                  2.0e-10
E value
                  49
Match length
% identity
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]
                  44900
Seq. No.
                  gsv701046665.h1
Seq. ID
                  BLASTX
Method
                  g1173055
NCBI GI
BLAST score
                  229
                  3.0e-19
E value
                  53
Match length
                  89
% identity
                  60S RIBOSOMAL PROTEIN L11 (L5) >gi 541961 pir S42497
NCBI Description
                  ribosomal protein L11.e - alfalfa >gi 1076504 pir S51819
                  RL5 ribosomal protein - alfalfa >gi 463252 emb CAA55090
                  (X78284) RL5 ribosomal protein [Medicago sativa]
                  44901
Seq. No.
                  gsv701046725.hl
Seq. ID
                  BLASTX
Method
                  q2760830
NCBI GI
                  178
BLAST score
                  3.0e-13
E value
                  93
Match length
                  32
% identity
NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana]
                  44902
Seq. No.
                  gsv701046727.h1
Seq. ID
                  BLASTX
Method
                  q4415925
NCBI GI
                  134
BLAST score
                  9.0e-15
E value
                  53
Match length
% identity
NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis
                  thaliana]
Seq. No.
                   44903
Seq. ID
                   qsv701046730.h1
                  BLASTX
Method
                   q1813329
NCBI GI
BLAST score
                   144
                   3.0e-09
E value
Match length
                   83
% identity
NCBI Description (AB000637) HMG-1 [Canavalia gladiata]
Seq. No.
                   44904
Seq. ID
                   gsv701046765.hl
Method
                   BLASTN
```



E value 4.0e-21
Match length 171
% identity 87
NCBI Description Rice mR

NCBI Description Rice mRNA for ribosomal protein S8, complete cds

Seq. No. Seq. ID

44905 qsv701046782.h1

Method BLASTX
NCBI GI g3252807
BLAST score 162
E value 2.0e-20

E value 2.0e-20 Match length 79 % identity 68

NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.

44906

Seq. ID

gsv701046812.h1

Method BLASTX
NCBI GI g3193292
BLAST score 245
E value 2.0e-21
Match length 69
% identity 74

NCBI Description (AF069298) similar to ATPases associated with various

cellular activites (Pfam: AAA.hmm, score: 230.91)

[Arabidopsis thaliana]

Seq. No.

44907

Seq. ID

Seq. ID

gsv701046820.h1

Method BLASTX
NCBI GI g3790587
BLAST score 177
E value 2.0e-13
Match length 71
% identity 58

NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis

thaliana]

44908

Seq. No.

gsv701046895.h1

Method BLASTN
NCBI GI g16508
BLAST score 136
E value 1.0e-70
Match length 224
% identity 90

NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene

 $sam-1 > gi_166871_gb_M55077_ATHSAM A.thaliana$

S-adenosylmethionine synthetase gene, complete cds

Seq. No.

44909

Seq. ID

gsv701046951.h1

Method BLASTN
NCBI GI g431269
BLAST score 43
E value 4.0e-15
Match length 95



% identity Arabidopsis thaliana ubiquitin conjugating enzyme (UBC5) NCBI Description gene, complete cds Seq. No. 44910 Seq. ID qsv701046954.hl BLASTN Method q1360083 NCBI GI BLAST score 44 1.0e-15 E value 84 Match length 88 % identity NCBI Description N.tabacum mRNA for zinc finger protein, BBF2aO 44911 Seq. No. Seq. ID gsv701046970.h1 Method BLASTX NCBI GI g3786006 BLAST score 361 9.0e-35 E value 89 Match length 76 % identity (AC005499) hypothetical protein [Arabidopsis thaliana] NCBI Description 44912 Seq. No. qsv701047020.hl Seq. ID BLASTX Method g2507229 NCBI GI 215 BLAST score 1.0e-17 E value Match length 63 % identity 55 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) NCBI Description (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN) >gi_423247_pir__A46579 estrogen receptor-binding cyclophilin - bovine >gi_393300 dbj_BAA03159 (D14074) cyclophilin [Bos taurus] 44913 Seq. No. qsv701047068.h1 Seq. ID Method BLASTN NCBI GI q169980 BLAST score 50 E value 3.0e-19 Match length 50 % identity 100 NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds Seq. No. 44914 gsv701047073.h1 Seq. ID

Method BLASTX NCBI GI g4574324 BLAST score 188 1.0e-14 E value 84 Match length 54 % identity

7187



NCBI Description (AF119225) caffeic acid ortho-methyltransferase [Pinus radiata]

Seq. No. 44915

Seq. ID gsv701047095.h1

Method BLASTN
NCBI GI g456713
BLAST score 112
E value 1.0e-56
Match length 132
% identity 96

NCBI Description Glycine max gene for ubiquitin, complete cds

Seq. No. 44916

Seq. ID gsv701047324.h1

Method BLASTX
NCBI GI g2500930
BLAST score 386
E value 1.0e-37
Match length 89
% identity 81

NCBI Description BETA-FRUCTOFURANOSIDASE PRECURSOR (SUCROSE-6-PHOSPHATE

HYDROLASE) (INVERTASE) >gi 1160488 emb CAA59677 (X85327)

beta-fructofuranosidase [Pisum sativum]

Seq. No. 44917

Seq. ID gsv701047330.h1

Method BLASTX
NCBI GI g3024444
BLAST score 287
E value 4.0e-26
Match length 88
% identity 60

NCBI Description SERINE/THREONINE-PROTEIN KINASE PRP4 HOMOLOG >gi 1399462

(U48736) serine/threonine-protein kinase PRP4h [Homo sapiens] >gi_4506125_ref_NP_003904.1_pPRP4_ UNKNOWN

Seq. No. 44918

Seq. ID gsv701047409.hl

Method BLASTN
NCBI GI g4464184
BLAST score 48
E value 2.0e-18
Match length 115
% identity 90

NCBI Description Phaseolus vulgaris lipoxygenase mRNA, complete cds

Seq. No. 44919

Seq. ID gsv701047420.h1

Method BLASTX
NCBI GI g1743354
BLAST score 196
E value 2.0e-15
Match length 47
% identity 74

NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]



```
Seq. No.
                   44920
Seq. ID
                   gsv701047426.h1
Method
                   BLASTX
NCBI GI
                   g4262149
BLAST score
                   351
E value
                   1.0e-33
Match length
                   74
% identity
                   84
NCBI Description
                   (AC005275) putative xyloglucan endotransglycosylase
                   [Arabidopsis thaliana]
Seq. No.
                   44921
Seq. ID
                   gsv701047432.h1
Method
                   BLASTX
NCBI GI
                   g4455364
BLAST score
                   290
E value
                   2.0e-26
Match length
                   73
% identity
                   71
NCBI Description
                   (AL035524) senescence-associated protein-like [Arabidopsis
                   thaliana]
Seq. No.
                   44922
Seq. ID
                   gsv701047433.h1
Method
                   BLASTN
NCBI GI
                   g3327043
BLAST score
                  276
E value
                   1.0e-154
Match length
                   276
% identity
                   100
NCBI Description Homo sapiens mRNA for KIAA0615 protein, complete cds
Seq. No.
                   44923
Seq. ID
                   gsv701047495.h1
Method
                  BLASTX
NCBI GI
                   g3176686
BLAST score
                   181
E value
                   6.0e-14
Match length
                   60
% identity
                   55
                   (AC003671) Similar to high affinity potassium transporter,
NCBI Description
                   HAK1 protein gb_U22945 from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
Seq. No.
                  44924
Seq. ID
                  gsv701047562.h1
Method
                  BLASTN
                  g414833
```

NCBI GI BLAST score 77 E value 1.0e-35 Match length 138 % identity

NCBI Description Glycine max (Rab7p) mRNA, complete cds

Seq. No.

Seq. ID gsv701047608.h1

Method BLASTN



```
NCBI GI
                   q1236950
BLAST score
                   44
E value
                   7.0e-16
Match length
                   52
                   96
% identity
NCBI Description
                  Glycine max nucleoside diphosphate kinase mRNA, complete
                   cds
Seq. No.
                   44926
Seq. ID
                   gsv701047614.h1
Method
                   BLASTN
NCBI GI
                   g1518539
BLAST score
                   134
E value
                   1.0e-69
Match length
                   134
% identity
                   100
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
Seq. No.
                   44927
Seq. ID
                   gsv701047762.h1
Method
                   BLASTX
NCBI GI
                   g4539437
BLAST score
                   208
E value
                   8.0e-17
Match length
                   87
% identity
                   51
NCBI Description (AL049523) putative protein [Arabidopsis thaliana]
Seq. No.
                   44928
Seq. ID
                   gsv701047779.h1
Method
                  BLASTX
NCBI GI
                   g4454051
BLAST score
                   319
E value
                  8.0e-30
Match length
                  67
% identity
                  88
NCBI Description
                  (AL035394) putative polygalacturonase [Arabidopsis
                  thaliana]
Seq. No.
                  44929
                  gsv701047782.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2649831
BLAST score
                  156
E value
                  1.0e-10
Match length
                  85
% identity
                  36
NCBI Description
                  (AE001051) conserved hypothetical protein [Archaeoglobus
                  fulgidus]
Seq. No.
                  44930
Seq. ID
```

gsv701047812.h1

Method BLASTX NCBI GI g1076344 BLAST score 256 E value 2.0e-25 Match length 85

% identity 66

NCBI Description kinase-associated protein phosphatase precursor -

Arabidopsis thaliana

Seq. No. 44931

Seq. ID gsv701047886.h1

Method BLASTX
NCBI GI g2959781
BLAST score 377
E value 2.0e-39
Match length 81

% identity 94
NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No. 44932

Seq. ID gsv701047890.h1

Method BLASTX
NCBI GI g132939
BLAST score 117
E value 6.0e-10
Match length 50
% identity 51

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal

protein L3 (ARP1) - Arabidopsis thaliana >gi 166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No. 44933

Seq. ID gsv701047893.h1

Method BLASTX
NCBI GI g3335375
BLAST score 328
E value 1.0e-31
Match length 81
% identity 85

NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.

44934

Seq. ID gsv701047965.h1 Method BLASTX

NCBI GI g4322421 BLAST score 232 E value 1.0e-19 Match length 85 % identity 47

NCBI Description (AF085230) cadmium resistance factor 1 [Arabidopsis

thaliana]

Seq. No. 44935

Seq. ID gsv701047984.h1

Method BLASTX
NCBI GI g2196466
BLAST score 284
E value 9.0e-26
Match length 86
% identity 60

NCBI Description (Y13673) TATA binding protein-associated factor

[Arabidopsis thaliana]



```
Seq. No.
                   44936
Seq. ID
                   gsv701047989.h1
Method
                   BLASTX
NCBI GI
                   g3402687
                   132
BLAST score
E value
                   2.0e-10
Match length
                   66
% identity
                   56
NCBI Description
                  (AC004697) unknown protein [Arabidopsis thaliana]
Seq. No.
                   44937
Seq. ID
                   gsv701048002.h1
Method
                  BLASTX
NCBI GI
                  g4115915
BLAST score
                  178
E value
                  1.0e-13
Match length
                   42
% identity
                  69
NCBI Description
                  (AF118222) contains similarity to Helix pomatia br-1
                  protein (GB: X96994) [Arabidopsis thaliana]
Seq. No.
                  44938
Seq. ID
                  gsv701048082.h1
Method
                  BLASTX
NCBI GI
                  q4263522
BLAST score
                  203
E value
                  3.0e-16
Match length
                  90
% identity
                  9
NCBI Description
                  (AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  44939
Seq. ID
                  gsv701048092.h1
Method
                  BLASTN
NCBI GI
                  g945038
BLAST score
                  146
E value
                  1.0e-76
Match length
                  192
% identity
                  99
NCBI Description
                  Glycine max phosphatidylinositol-specific phospholipase C
                  mRNA, complete cds
Seq. No.
                  44940
Seq. ID
                  gsv701048094.h1
Method
                  BLASTN
NCBI GI
                  g1518539
BLAST score
                  210
E value
                  1.0e-115
Match length
                  210
% identity
                  100
NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds
```

Seq. No. 44941

Seq. ID gsv701048128.h1

Method BLASTX NCBI GI g4467359



BLAST score 117 E value 2.0e-12 Match length 58 % identity 67

NCBI Description (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis

thaliana]

Seq. No. 44942

Seq. ID gsv701048129.h1

Method BLASTX
NCBI GI g3337367
BLAST score 156
E value 5.0e-11
Match length 64
% identity 42

NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 44943

Seq. ID gsv701048159.h1

Method BLASTN
NCBI GI g18644
BLAST score 133
E value 7.0e-69
Match length 177
% identity 94

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 44944

Seq. ID gsv701048237.h1

Method BLASTX
NCBI GI g3164142
BLAST score 183
E value 5.0e-14
Match length 80
% identity 47

NCBI Description (D78606) cytochrome P450 monooxygenase [Arabidopsis

thaliana]

Seq. No. 44945

Seq. ID gsv701048324.h1

Method BLASTN
NCBI GI g4510323
BLAST score 63
E value 4.0e-27

Match length 155 % identity 85

NCBI Description Arabidopsis thaliana BAC T7B11 from chromosome IV near 10

cM, complete sequence

Seq. No. 44946

Seq. ID gsv701048372.h1

Method BLASTN
NCBI GI g3386593
BLAST score 41
E value 6.0e-14
Match length 57
% identity 93



NCBI Description Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 44947

Seq. ID gsv701048449.h1

Method BLASTX
NCBI GI g3293551
BLAST score 146
E value 1.0e-09
Match length 67
% identity 42

NCBI Description (AF072697) SHYC [Mus musculus]

Seq. No. 44948

Seq. ID gsv701048469.h1

Method BLASTN
NCBI GI g945086
BLAST score 85
E value 2.0e-40
Match length 101
% identity 96

NCBI Description Glycine max transcription factor TFIIB mRNA, complete cds

Seq. No. 44949

Seq. ID gsv701048489.h1

Method BLASTX
NCBI GI g2104446
BLAST score 151
E value 3.0e-10

Match length 86 % identity 42

NCBI Description (Z95396) WD-repeat protein [Schizosaccharomyces pombe]

Seq. No. 44950

Seq. ID gsv701048507.h1

Method BLASTX
NCBI GI g4512663
BLAST score 137
E value 1.0e-08
Match length 74

% identity 15

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

>gi_4544470_gb_AAD22377.1_AC006580_9 (AC006580)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 44951

Seq. ID gsv701048510.h1

Method BLASTX
NCBI GI 94309681
BLAST score 180
E value 1.0e-13
Match length 79
% identity 52

NCBI Description (AC006930) R33423_1 [Homo sapiens]

Seq. No. 44952

Seq. ID gsv701048583.h1

7194



```
Method
                   BLASTN
NCBI GI
                   q3819163
BLAST score
                   127
E value
                   1.0e-65
Match length
                   139
% identity
                   98
NCBI Description Glycine max cctd gene
Seq. No.
                   44953
Seq. ID
                   gsv701048661.h1
Method
                   BLASTX
NCBI GI
                   g4138912
BLAST score
                   285
E value
                   6.0e-26
Match length
                  83
                   67
% identity
NCBI Description
                  (AF059487) expansin precursor [Lycopersicon esculentum]
Seq. No.
                   44954
Seq. ID
                   gsv701048705.hl
Method
                  BLASTX
NCBI GI
                  g2578823
BLAST score
                   263
E value
                  3.0e-23
Match length
                  87
% identity
                   68
NCBI Description
                  (AB000835) similar to YGR200c [Arabidopsis thaliana]
Seq. No.
                   44955
                  gsv701048763.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2341024
BLAST score
                  191
E value
                  8.0e-15
Match length
                  57
% identity
                  56
NCBI Description (AC000104) F19P19.1 [Arabidopsis thaliana]
Seq. No.
                  44956
Seq. ID
                  gsv701048883.h1
Method
                  BLASTX
NCBI GI
                  q2623248
BLAST score
                  158
E value
                  6.0e-11
Match length
                  89
% identity
                  44
NCBI Description
                  (AF030882) SU1 isoamylase [Zea mays]
Seq. No.
                  44957
Seq. ID
                  gsv701048972.hl
Method
                  BLASTN
```

NCBI GI q2735775 BLAST score 58 E value 2.0e-24 Match length 74 % identity 95

NCBI Description Marah macrocarpus 18S ribosomal RNA gene, complete sequence



```
Seq. No.
                   44958
Seq. ID
                   gsv701049003.h1
Method
                   BLASTX
NCBI GI
                   q710626
BLAST score
                   228
E value
                   3.0e-19
Match length
                   48
% identity
                   83
NCBI Description
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
Seq. No.
                   44959
Seq. ID
                   gsv701049025.h1
Method
                   BLASTX
NCBI GI
                   g2244785
BLAST score
                   158
E value
                   3.0e-11
Match length
                   43
% identity
                   74
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   44960
Seq. ID
                   gsv701049062.h1
Method
                   BLASTX
NCBI GI
                   g2959781
BLAST score
                   241
E value
                   6.0e-21
Match length
                   48
% identity
                   90
NCBI Description
                  (AJ223508) Zwille protein [Arabidopsis thaliana]
Seq. No.
                   44961
Seq. ID
                   gsv701049067.h1
Method
                   BLASTX
NCBI GI
                   g4455232
BLAST score
                   242
E value
                   5.0e-21
Match length
                   45
% identity
                   89
NCBI Description
                  (AL035523) putative protein [Arabidopsis thaliana]
Seq. No.
                   44962
Seq. ID
                   gsv701049131.h1
Method
                  BLASTX
NCBI GI
                   g3413511
                  183
E value
                  7.0e-14
Match length
                  44
                  73
```

BLAST score

% identity

NCBI Description (AJ000265) glucose-6-phosphate isomerase [Spinacia

oleracea]

Seq. No.

44963 Seq. ID

gsv701049142.h1



```
Method
                   BLASTX
NCBI GI
                   q2129471
BLAST score
                   357
E value
                   3.0e-34
Match length
                   91
% identity
                   73
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
                   precursor - Scotch pine >gi 1100223 (L32560)
                   glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
Seq. No.
                   44964
Seq. ID
                   gsv701049243.h1
Method
                   BLASTX
NCBI GI
                   g1732517
BLAST score
                   160
E value
                   2.0e-11
Match length
                   58
% identity
                   57
NCBI Description
                   (U62745) putative cytoskeletal protein [Arabidopsis
                   44965
Seq. No.
Seq. ID
                  gsv701049252.h1
Method
                  BLASTX
NCBI GI
                  q4455331
BLAST score
                  215
E value
                  1.0e-17
Match length
                   63
% identity
                  59
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  44966
Seq. ID
                  gsv701049266.h1
Method
                  BLASTX
NCBI GI
                  g2982301
BLAST score
                  222
E value
                  2.0e-18
Match length
                  58
% identity
                  72
NCBI Description
                  (AF051235) YGL010w-like protein [Picea mariana]
Seq. No.
                  44967
Seq. ID
                  gsv701049306.h1
Method
                  BLASTX
                  g1346396
                  154
```

NCBI GI BLAST score E value 2.0e-10 Match length 72 % identity 44

PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR NCBI Description

>gi_100913_pir__S10930 probable receptor protein kinase (EC 2.7.1.-) precursor - maize >gi 22432_emb CAA36611 (X52384)

precursor protein (AA -26 to 791) [Zea mays]

>gi_22436_emb_CAA47962 (X67733) receptor-like protein kinase [Zea mays] >gi_226927 prf 1611404A receptor protein

kinase [Zea mays]



```
Seq. No.
                   44968
Seq. ID
                   gsv701049432.h1
Method
                   BLASTX
NCBI GI
                   q2760830
BLAST score
                   178
E value
                   2.0e-14
Match length
                   77
% identity
                   55
                  (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   44969
Seq. ID
                   qsv701049509.h1
Method
                   BLASTX
NCBI GI
                   g2244975
BLAST score
                   308
E value
                   8.0e-29
Match length
                   66
% identity
                   92
NCBI Description
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
                   44970
Seq. No.
Seq. ID
                   gsv701049529.h1
Method
                   BLASTX
NCBI GI
                   g3953466
BLAST score
                   332
E value
                   2.0e-31
Match length
                   81
% identity
                   81
NCBI Description
                  (AC002328) F20N2.11 [Arabidopsis thaliana]
Seq. No.
                   44971
Seq. ID
                   gsv701049530.h1
Method
                   BLASTX
NCBI GI
                   q3337352
BLAST score
                   290
                   8.0e-28
E value
Match length
                   87
% identity
                   77
                   (AC004481) putative chromatin structural protein Supt5hp
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   44972
Seq. ID
                   gsv701049538.h1
Method
                  BLASTN
NCBI GI
                   q2687725
BLAST score
                   118
E value
                   4.0e-60
Match length
                  158
% identity
                   94
                  Glycine max mRNA for putative 2-hydroxydihydrodaidzein
NCBI Description
```

Seq. No. 44973

Seq. ID gsv701049563.h1

reductase

Method BLASTX NCBI GI g2129677



BLAST score 143 E value 4.0e-10 Match length 72 % identity 46

NCBI Description probablel N-acetyltransferase hookless 1 - Arabidopsis thaliana >gi_1277090 (U50399) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi_1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis

thaliana] >gi_4468983_emb_CAB38297_ (AL035605) probable N-acetyltransferase hookless 1 [Arabidopsis thaliana]

Seq. No. 44974

Seq. ID gsv701049575.h1

Method BLASTX
NCBI GI g974782
BLAST score 193
E value 3.0e-15
Match length 41
% identity 93

NCBI Description (Z49150) cobalamine-independent methionine synthase

[Solenostemon scutellarioides]

Seq. No. 44975

Seq. ID gsv701049592.h1

Method BLASTX
NCBI GI 94510400
BLAST score 340
E value 2.0e-32
Match length 72
% identity 81

NCBI Description (AC006587) putative vacuolar-type H(+)-ATPase [Arabidopsis

thaliana]

Seq. No. 44976

Seq. ID gsv701049654.hl

Method BLASTX
NCBI GI g3850587
BLAST score 359
E value 2.0e-34
Match length 88
% identity 83

NCBI Description (AC005278) Strong similarity to gi_2244780 hypothetical

protein from Arabidopsis thaliana chromosome 4 contig

gb_Z97335. [Arabidopsis thaliana]

Seq. No. 44977

Seq. ID gsv701049686.h1

Method BLASTX
NCBI GI g3004548
BLAST score 158
E value 6.0e-11
Match length 74
% identity 42

NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]

>gi_4185151 (AC005724) putative methyltransferase

[Arabidopsis thaliana]



```
Seq. No.
                   44978
Seq. ID
                   gsv701049716.h1
Method
                   BLASTX
NCBI GI
                   q4006848
BLAST score
                   154
E value
                   9.0e-11
Match length
                   66
% identity
                   50
NCBI Description
                  (AJ131433) selenocysteine methyltransferase [Astragalus
                  bisulcatus]
                   44979
Seq. No.
                   gsv701049730.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1871185
                   292
BLAST score
E value
                   6.0e-27
Match length
                   63
% identity
                  78
NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]
Seq. No.
                   44980
Seq. ID
                  gsv701049805.hl
Method
                  BLASTN
NCBI GI
                  g439616
BLAST score
                  38
E value
                   4.0e-12
Match length
                   63
% identity
                  78
NCBI Description Soybean G protein alpha subunit mRNA, complete cds
                  44981
Seq. No.
                  gsv701049813.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4325369
BLAST score
                  293
E value
                  1.0e-26
Match length
                  88
% identity
                  52
NCBI Description
                  (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
                  44982
Seq. No.
Seq. ID
                  gsv701049852.h1
Method
                  BLASTX
NCBI GI
                  q475257
BLAST score
                  248
E value
                  2.0e-21
Match length
                  53
% identity
                  91
NCBI Description
                  (M95065) similar to ribosomal protein L19 [Zea mays]
Seq. No.
                  44983
```

Seq. ID gsv701049876.h1

Method BLASTX
NCBI GI g4539345
BLAST score 266
E value 1.0e-23



Match length 89 % identity 64

NCBI Description (AL035539) hypothetical protein [Arabidopsis thaliana]

Seq. No. 44984

Seq. ID gsv701049893.h1

Method BLASTX
NCBI GI g2388586
BLAST score 362
E value 7.0e-35
Match length 85
% identity 85

NCBI Description (AC000098) Similar to Saccharomyces RAD16 (gb_X78993).

[Arabidopsis thaliana]

Seq. No. 44985

Seq. ID gsv701049911.h1

Method BLASTX
NCBI GI g1220180
BLAST score 154
E value 2.0e-10
Match length 74
% identity 49

NCBI Description (Z69996) dormancy related protein [Trollius ledebourii]

Seq. No. 44986

Seq. ID gsv701049935.hl

Method BLASTX
NCBI GI g2414593
BLAST score 167
E value 5.0e-12
Match length 78
% identity 42

NCBI Description (Z99258) molybdopterin biosynthesis [Schizosaccharomyces

pombe]

Seq. No. 44987

Seq. ID gsv701049936.h1

Method BLASTX
NCBI GI g1856971
BLAST score 235
E value 5.0e-20
Match length 49
% identity 90

NCBI Description (D26058) This gene is specifically expressed at the S phase

during the cell cycle in the synchronous culture of

periwinkle cells. [Catharanthus roseus]

Seq. No. 44988

Seq. ID gsv701049940.h1

Method BLASTX
NCBI GI g4218116
BLAST score 153
E value 2.0e-10
Match length 54
% identity 65

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]



gsv701049951.h1

Method BLASTX
NCBI GI g1086263
BLAST score 170
E value 2.0e-12
Match length 75
% identity 48

NCBI Description TMV resistance protein N - tobacco (Nicotiana glutinosa)

>gi 558887 (U15605) N [Nicotiana glutinosa]

Seq. No. 44990

Seq. ID gsv701049969.h1

Method BLASTX
NCBI GI g3047104
BLAST score 227
E value 4.0e-19
Match length 85
% identity 55

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 44991

Seq. ID gsv701049977.h1

Method BLASTN
NCBI GI g3694834
BLAST score 153
E value 9.0e-81
Match length 267
% identity 100

NCBI Description Glycine max alcohol dehydrogenase Adh-1 gene, partial cds

Seq. No. 44992

Seq. ID gsv701049982.h1

Method BLASTN
NCBI GI g602564
BLAST score 53
E value 3.0e-21
Match length 129
% identity 85

NCBI Description C.paradisi (Macf) INO1 gene

Seq. No. 44993

Seq. ID gsv701050045.h1

Method BLASTX
NCBI GI g3645899
BLAST score 198
E value 1.0e-15
Match length 93
% identity 45

NCBI Description (U68408) 5' end not determined experimentally [Zea mays]

Seq. No. 44994

Seq. ID gsv701050084.h1

Method BLASTX
NCBI GI g3329386
BLAST score 251



44996

```
7.0e-22
E value
Match length
                  88
% identity
                  51
                   (AF038958) synaptic glycoprotein SC2 spliced variant [Homo
NCBI Description
                  sapiens]
Seq. No.
                  44995
Seq. ID
                  gsv701050091.h1
Method
                  BLASTX
NCBI GI
                  q4567281
                  240
                  1.0e-20
```

BLAST score 240
E value 1.0eMatch length 90
% identity 48

Seq. No.

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. ID gsv701050192.h1
Method BLASTX
NCBI GI g2191168
BLAST score 185
E value 4.0e-14
Match length 60

% identity 60
NCBI Description (AF007270) contains similarity to myosin heavy chain

[Arabidopsis thaliana]

Seq. No. 44997

Seq. ID gsv701050203.h1

Method BLASTX
NCBI GI g267036
BLAST score 179
E value 2.0e-13
Match length 72
% identity 53

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR

(STEAROYL-ACP DESATURASE) >gi 169895 (M83199) stearoyl-acyl

carrier protein desaturase [Simmondsia chinensis] >gi 384336 prf 1905423A stearoyl-acyl carrier protein desaturase [Simmondsia chinensis]

Seq. No. 44998

Seq. ID gsv701050247.h1

Method BLASTX
NCBI GI g2160151
BLAST score 326
E value 1.0e-30
Match length 82
% identity 63

NCBI Description (AC000375) Strong similarity to Brassica aspartic protease

(gb_X77260). [Arabidopsis thaliana]

Seq. No. 44999

Seq. ID qsv701050316.h1

Method BLASTN
NCBI GI g2055227
BLAST score 197



E value 1.0e-107 Match length 261 % identity 94

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No.

45000

45001

45002

Seq. ID

gsv701050403.hl

Method BLASTX
NCBI GI g3334349
BLAST score 196
E value 2.0e-15
Match length 49
% identity 73

NCBI Description GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)

>gi 2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase

[Arabidopsis thaliana]

Seq. No.

Seq. ID gsv701050489.h1

Method BLASTN
NCBI GI g1808591
BLAST score 84
E value 1.0e-39
Match length 132
% identity 91

NCBI Description C.arietinum mRNA for SAM-synthetase

Seq. No.

Seq. ID gsv701050604.h1

Method BLASTN
NCBI GI g473604
BLAST score 56
E value 7.0e-23
Match length 80

% identity 93

NCBI Description Zea mays W-22 histone H2B mRNA, complete cds

Seq. No. 45003

Seq. ID gsv701050679.h1

Method BLASTX
NCBI GI g2462931
BLAST score 130
E value 7.0e-14
Match length 85
% identity 58

NCBI Description (Z83833) UDP-glucose:sterol glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 45004

Seq. ID gsv701050685.h1

Method BLASTX
NCBI GI g3377797
BLAST score 283
E value 1.0e-25
Match length 66
% identity 85

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for



by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

 Seq. No.
 45005

 Seq. ID
 gsv701050694.h1

 Method
 BLASTN

 NCBI GI
 g454847

 BLAST score
 37

 E value
 1.0e-11

 Match length
 177

Match length 177 % identity 89

NCBI Description Glycine max ribosomal protein S11 gene, complete cds

Seq. No. 45006

Seq. ID gsv701050702.h1

Method BLASTN
NCBI GI g454847
BLAST score 44
E value 4.0e-16
Match length 72
% identity 90

NCBI Description Glycine max ribosomal protein S11 gene, complete cds

Seq. No. 45007

Seq. ID gsv701050713.h1

Method BLASTX
NCBI GI g3281855
BLAST score 139
E value 9.0e-09
Match length 82
% identity 41

NCBI Description (AL031004) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45008

Seq. ID gsv701050808.h1

Method BLASTN
NCBI GI g4102896
BLAST score 41
E value 3.0e-14
Match length 41
% identity 100

NCBI Description Tilia sp 25S ribosomal RNA gene, partial sequence

Seq. No. 45009

Seq. ID gsv701050841.h1

Method BLASTX
NCBI GI g4558672
BLAST score 207
E value 6.0e-17
Match length 44
% identity 77

NCBI Description (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis

thaliana]

Seq. No. 45010

7205



Seq. ID gsv701050908.hl

Method BLASTN
NCBI GI g4103958
BLAST score 197
E value 1.0e-107
Match length 249
% identity 95

NCBI Description Phaseolus vulgaris calmodulin (CaM) mRNA, PvCaM-2 allele,

complete cds

Seq. No. 45011

Seq. ID gsv701050909.h1

Method BLASTN
NCBI GI g436782
BLAST score 48
E value 3.0e-18
Match length 108
% identity 86

NCBI Description Rice mRNA for cyc07, complete cds

Seq. No. 45012

Seq. ID gsv701050946.h1

Method BLASTX
NCBI GI g2252839
BLAST score 159
E value 2.0e-11
Match length 60
% identity 48

NCBI Description (AF013293) Similar to receptor-like protein kinase precusor

[Arabidopsis thaliana]

Seq. No. 45013

Seq. ID gsv701050966.hl

Method BLASTX
NCBI GI g3337361
BLAST score 157
E value 7.0e-11
Match length 37
% identity 78

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 45014

Seq. ID gsv701050983.h1

Method BLASTX
NCBI GI g4490325
BLAST score 165
E value 5.0e-12
Match length 63
% identity 52

NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45015

Seq. ID gsv701051045.hl

Method BLASTX
NCBI GI g3402679
BLAST score 270
E value 4.0e-24



Match length 90 % identity 66

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 45016

Seq. ID gsv701051061.h1

Method BLASTX
NCBI GI g2921500
BLAST score 170
E value 2.0e-12
Match length 75
% identity 45

NCBI Description (AF037222) XRCC3 [Homo sapiens]

Seq. No. 45017

Seq. ID gsv701051068.h1

Method BLASTX
NCBI GI g4033735
BLAST score 398
E value 4.0e-39
Match length 85
% identity 89

NCBI Description (AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No. 45018

Seq. ID gsv701051146.hl

Method BLASTX
NCBI GI g3395427
BLAST score 122
E value 1.0e-13
Match length 62
% identity 56

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 45019

Seq. ID gsv701051187.h1

Method BLASTX
NCBI GI g282980
BLAST score 166
E value 4.0e-12
Match length 63
% identity 54

NCBI Description helix-loop-helix protein DEL - garden snapdragon >gi_166428

(M84913) DEL [Antirrhinum majus]

Seq. No. 45020

Seq. ID gsv701051229.h1

Method BLASTX
NCBI GI g4455360
BLAST score 143
E value 4.0e-09
Match length 84
% identity 9

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 45021

Seq. ID gsv701051287.h1



```
Method
                   BLASTX
NCBI GI
                  g4580455
BLAST score
                  195
E value
                  2.0e-15
Match length
                  44
% identity
                  89
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                  45022
Seq. No.
Seq. ID
                  gsv701051337.h1
Method
                  BLASTX
NCBI GI
                  q1172571
BLAST score
                  329
                  1.0e-31
E value
Match length
                  73
% identity
                   95
                  PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)
NCBI Description
                  >gi 1076277 pir S52637 phosphoenolpyruvate carboxykinase
                   (ATP) (EC 4.1.1.49) - cucumber >gi 567102 (L31899)
                  phosphoenolpyruvate carboxykinase [Cucumis sativus]
Seq. No.
                   45023
Seq. ID
                  qsv701051362.h1
Method
                  BLASTX
                  q100226
NCBI GI
BLAST score
                   336
E value
                   5.0e-32
Match length
                   74
% identity
NCBI Description
                  hypothetical protein - tomato >gi 19275 emb CAA78112
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi 445619 prf 1909366A Leu zipper protein
                   [Lycopersicon esculentum]
Seq. No.
                   45024
Seq. ID
                   gsv701051368.h1
Method
                  BLASTN
NCBI GI
                   g3202019
BLAST score
                  71
E value
                   8.0e-32
Match length
                  139
% identity
                   88
NCBI Description
                  Medicago sativa DnaJ-like protein MsJ1 gene, complete cds
                   45025
Seq. No.
                   gsv701051372.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4455250
BLAST score
                   232
                  1.0e-19
E value
Match length
                  92
                  27
% identity
```

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No.

45026

gsv701051382.hl Seq. ID

Method BLASTX



```
g2217970
NCBI GI
BLAST score
                  140
                  8.0e-09
E value
                  89
Match length
                  20
% identity
NCBI Description (Z97074) p40 [Homo sapiens]
                  45027
Seq. No.
Seq. ID
                   gsv701051384.h1
                  BLASTN
Method
NCBI GI
                   q2695860
BLAST score
                   99
                   2.0e-48
E value
                   167
Match length
                   90
% identity
                  Pisum sativum mRNA for
NCBI Description
                   3-deoxy-D-manno-2-octulosonate-8-phosphate synthase, clone
                   pPS40
                   45028
Seq. No.
                   gsv701051412.h1
Seq. ID
                   BLASTX
Method
                   g1272349
NCBI GI
                   153
BLAST score
                   3.0e-10
E value
                   59
Match length
                   54
% identity
NCBI Description (U51740) secreted glycoprotein 3 [Ipomoea trifida]
                   45029
Seq. No.
                   gsv701051427.hl
Seq. ID
                   BLASTN
Method
                   g166379
NCBI GI
BLAST score
                   126
                   1.0e-64
E value
                   280
Match length
                   74
% identity
NCBI Description Alfalfa glucose-regulated endoplasmic reticular protein
                   mRNA, complete cds
                   45030
Seq. No.
Seq. ID
                   gsv701051515.h1
                   BLASTN
Method
NCBI GI
                   q217902
                   75
BLAST score
                   3.0e - 34
E value
                   235
Match length
                   83
% identity
NCBI Description Catharanthus roseus cyc07 mRNA, complete cds
                   45031
Seq. No.
Seq. ID ·
                   gsv701051546.hl
                   BLASTN
Method
NCBI GI
                   q2052028
BLAST score
                   279
```

1.0e-156

279

E value

Match length



```
% identity
                  G.max mRNA for glutathione transferase
NCBI Description
                  45032
Seq. No.
                  gsv701051549.h1
Seq. ID
Method
                  BLASTN
                  g18644
```

NCBI GI BLAST score 154 2.0e-81 E value 182 Match length % identity 97

NCBI Description Soybean mRNA for HMG-1 like protein

45033 Seq. No. gsv701051609.h1 Seq. ID Method BLASTN NCBI GI g3378649 BLAST score 91

9.0e-44 E value 187 Match length 87 % identity

NCBI Description M.sativa mRNA translated from abscisic activated gene

45034 Seq. No.

gsv701051653.h1 Seq. ID

BLASTX Method NCBI GI g123688 BLAST score 153 1.0e-10 E value Match length 41 71 % identity

DNAJ PROTEIN HOMOLOG HSJ1 (HSJ-1) >gi_284069_pir__S23508 NCBI Description

dnaJ protein homolog - human >gi_32469_emb_CAA44968_

(X63368) HSJ1b [Homo sapiens]

45035 Seq. No.

gsv701051717.hl Seq. ID

BLASTN Method g1183936 NCBI GI 42 BLAST score 8.0e-15 E value 62 Match length 92 % identity

NCBI Description P.sativum 5S rRNA gene

45036 Seq. No.

gsv701051786.h1 Seq. ID

BLASTX Method g1710546 NCBI GI BLAST score 163 9.0e-12 E value Match length 34 88 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative

ribosomal protein [Daucus carota]

45037 Seq. No.



Seq. ID gsv701051839.h1

Method BLASTN
NCBI GI g296408
BLAST score 173
E value 7.0e-93
Match length 193
% identity 97

NCBI Description G.max ADR12 mRNA

Seq. No. 45038

Seq. ID gsv701051846.h1

Method BLASTX
NCBI GI g3367522
BLAST score 161
E value 1.0e-11
Match length 60
% identity 50

NCBI Description (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 45039

Seq. ID gsv701051876.h1

Method BLASTX
NCBI GI g2262177
BLAST score 267
E value 5.0e-24
Match length 60
% identity 83

NCBI Description (AC002329) hypothetical protein similar to T18A10.3

[Arabidopsis thaliana]

Seq. No. 45040

Seq. ID gsv701051880.h1

Method BLASTX
NCBI GI g3386598
BLAST score 264
E value 1.0e-23
Match length 61
% identity 77

NCBI Description (AC004665) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No. 45041

Seq. ID gsv701051883.h1

Method BLASTN
NCBI GI g2879810
BLAST score 70
E value 2.0e-31
Match length 114
% identity 90

NCBI Description Lupinus luteus mRNA for ribosomal protein L30

Seq. No. 45042

Seq. ID gsv701051901.h1

Method BLASTN
NCBI GI g960288
BLAST score 82
E value 2.0e-38



```
Match length
% identity
                  87
                  Ruta graveolens anthranilate synthase alpha-subunit mRNA,
NCBI Description
                  complete cds
Seq. No.
                  45043
Seq. ID
                  gsv701051914.hl
Method
                  BLASTX
NCBI GI
                  q3046693
BLAST score
                  396
E value
                   4.0e-39
Match length
                   69
                  99
% identity
                   (AL022140) receptor like protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                   45044
Seq. No.
Seq. ID
                   qsv701051953.h1
                  BLASTN
Method
NCBI GI
                  q2565418
                  103
BLAST score
E value
                   5.0e-51
                  191
Match length
                   88
% identity
                  Onobrychis viciifolia histone H3 mRNA, complete cds
NCBI Description
                   45045
Seq. No.
                   gsv701051984.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q509810
BLAST score
                   168
                   2.0e-12
E value
Match length
                   65
                   54
% identity
                  (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
                   45046
Seq. No.
Seq. ID
                   gsv701051989.h1
Method
                   BLASTN
NCBI GI
                   q408793
BLAST score
                   152
E value
                   3.0e-80
Match length
                   196
% identity
                   95
NCBI Description Glycine soja chloroplast 3-omega faty acid desaturase
                   (Fad3) mRNA, complete cds
Seq. No.
                   45047
                   gsv701052056.h1
Seq. ID
```

Method BLASTX NCBI GI g4388818 BLAST score 175 E value 2.0e-15 Match length 85 % identity 52

(ACO06528) putative pol polyprotein with a Zn-finger CCHC NCBI Description

type domain (prosite:QDOC50158) and a DDE integrase



signature motif [Arabidopsis thaliana]

Seq. No. 45048

Seq. ID gsv701052059.hl

Method BLASTN
NCBI GI g4530125
BLAST score 172
E value 4.0e-92
Match length 260
% identity 92

NCBI Description Phaseolus vulgaris receptor-like protein kinase homolog

RK20-1 mRNA, complete cds

Seq. No. 45049

Seq. ID gsv701052184.h1

Method BLASTN
NCBI GI g902526
BLAST score 80
E value 3.0e-37
Match length 216
% identity 85

NCBI Description Zea mays clone MubG7 ubiquitin fusion protein gene,

complete cds

Seq. No. 45050

Seq. ID gsv701052218.h1

Method BLASTX
NCBI GI g2760830
BLAST score 346
E value 3.0e-33
Match length 70
% identity 89

NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 45051

Seq. ID gsv701052240.h1

Method BLASTX
NCBI GI g2911059
BLAST score 200
E value 4.0e-16
Match length 67
% identity 72

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 45052

Seq. ID gsv701052317.h1

Method BLASTX
NCBI GI g437327
BLAST score 250
E value 7.0e-22
Match length 62
% identity 73

NCBI Description (L04497) MYB A; putative [Gossypium hirsutum]

Seq. No. 45053

Seq. ID gsv701052338.h1

7213



Method BLASTN NCBI GI g904153 116 BLAST score 1.0e-58 E value Match length 272 % identity 96 Glycine max FAD2-2 microsomal omega-6 desaturase mRNA, NCBI Description complete cds 45054 Seq. No. Seq. ID gsv701052379.h1 Method BLASTX NCBI GI q4262186 BLAST score 343 E value 1.0e-32 97 Match length % identity (ACO05508) Highly similar to cullin 3 [Arabidopsis NCBI Description thaliana] 45055 Seq. No. Seq. ID gsv701052481.h1 Method BLASTX NCBI GI q4567235 BLAST score 188 5.0e-26 E value 78 Match length 71 % identity (AC007119) putative phosphatidylinositol/phophatidylcholine NCBI Description transfer protein [Arabidopsis thaliana] 45056 Seq. No. Seq. ID gsv701052483.h1 BLASTN Method q3869074 NCBI GI BLAST score 36 6.0e-11 E value Match length 48 % identity 94 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MMI9, complete sequence [Arabidopsis thaliana] Seq. No. 45057 Seq. ID gsv701052506.hl Method BLASTN NCBI GI q3449320 BLAST score 39

E value 9.0e-13 Match length 59 % identity 92

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MRB17, complete sequence [Arabidopsis thaliana]

Seq. No. 45058

gsv701052512.h1 Seq. ID

Method BLASTX g2832625 NCBI GI

Match length

% identity

64

94



```
BLAST score
                  7.0e-15
E value
                  45
Match length
                  78
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                  45059
Seq. No.
Seq. ID
                  gsv701052527.hl
                  BLASTN
Method
                  g3449334
NCBI GI
                  32
BLAST score
                  1.0e-08
E value
Match length
                  100
                  83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
                  45060
Seq. No.
Seq. ID
                  gsv701052540.h1
                  BLASTN
Method
NCBI GI
                  q3264758
BLAST score
                  36
                  6.0e-11
E value
Match length
                  60
% identity
                  90
NCBI Description Prunus armeniaca 40S ribosomal protein S8 (RPS8) mRNA,
                  complete cds
                   45061
Seq. No.
                   gsv701052547.hl
Seq. ID
                  BLASTN
Method
                  g3298610
NCBI GI
                  57
BLAST score
E value
                   2.0e-23
Match length
                  109
                   88
% identity
NCBI Description Arabidopsis thaliana BAC T2H3
Seq. No.
                   45062
Seq. ID
                   gsv701052569.h1
                   BLASTN
Method
NCBI GI
                   g2565339
BLAST score
                   94
E value
                   1.0e-45
Match length
                   214
                   86
% identity
NCBI Description Lupinus luteus ribosomal protein S14 (rps14) mRNA, complete
                   cds
                   45063
Seq. No.
                   gsv701052585.h1
Seq. ID
                   BLASTX
Method
                   g1362103
NCBI GI
BLAST score
                   334
E value
                   1.0e-31
```



NCBI Description ubiquitin conjugating enzyme - tomato

>gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating

enzyme [Lycopersicon esculentum]

Seq. No. 45064

Seq. ID gsv701052594.h1

Method BLASTN
NCBI GI g1184192
BLAST score 57
E value 2.0e-23
Match length 109

NCBI Description A.thaliana mRNA for DAD-1-like protein

Seq. No. 45065

% identity

Seq. ID gsv701052602.h1

88

Method BLASTN
NCBI GI g3327922
BLAST score 44
E value 1.0e-15
Match length 88
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 45066

Seq. ID gsv701052642.h1

Method BLASTX
NCBI GI g4063751
BLAST score 144
E value 2.0e-09
Match length 38
% identity 63

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi_4510409_gb_AAD21495.1_ (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 45067

Seq. ID gsv701052655.h1

Method BLASTX
NCBI GI g1170659
BLAST score 199
E value 8.0e-16
Match length 76
% identity 50

NCBI Description KINESIN-LIKE PROTEIN KIF4 >gi_1083417_pir__A54803

microtubule-associated motor KIF4 - mouse

>gi 563773 dbj BAA02167 (D12646) KIF4 [Mus musculus]

Seq. No. 45068

Seq. ID gsv701052718.h1

Method BLASTX
NCBI GI g2832622
BLAST score 163
E value 8.0e-12
Match length 63
% identity 49



NCBI Description (AL021711) cyclic phosphodiesterase - like protein [Arabidopsis thaliana]

Seq. No. 45069

Seq. ID gsv701052780.h1

Method BLASTX
NCBI GI g960291
BLAST score 219
E value 4.0e-18
Match length 49
% identity 88

NCBI Description (L34344) anthranilate synthase alpha subunit [Ruta

graveolens]

Seq. No. 45070

Seq. ID gsv701052930.h1

Method BLASTX
NCBI GI g140400
BLAST score 265
E value 2.0e-23
Match length 69
% identity 75

NCBI Description HYPOTHETICAL 37.2 KD PROTEIN IN CHA1-PRD1 INTERGENIC REGION

>gi_83176_pir__S19389 hypothetical protein YCL059c - yeast
(Saccharomyces cerevisiae) >gi_5300_emb_CAA42386_ (X59720)

YCL059c, len:316 [Saccharomyces cerevisiae]

Seq. No. 45071

Seq. ID gsv701052976.hl

Method BLASTN
NCBI GI g2281081
BLAST score 38

E value 4.0e-12 Match length 70 % identity 89

NCBI Description Arabidopsis thaliana chromosome II BAC F18019 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 45072

Seq. ID gsv701053014.h1

Method BLASTX
NCBI GI g3128228
BLAST score 263
E value 1.0e-23
Match length 55

% identity 91
NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis

thaliana] >gi_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 45073

Seq. ID gsv701053054.h1

Method BLASTX
NCBI GI g3860247
BLAST score 291
E value 1.0e-26
Match length 56



% identity

(AC005824) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

45074

Seq. ID Method

gsv701053061.h1 BLASTX

NCBI GI BLAST score

g3335354 191

E value 4.0e-15 Match length 73 % identity 55

NCBI Description

(AC004512) This gene is continued from gene F5I14.1 from BAC sequence gb AC001229 from A. thaliana. EST gb_AA585814

comes from this gene. [Arabidopsis thaliana]

45075 Seq. No.

gsv701053141.hl Seq. ID

BLASTX Method NCBI GI g2078350 194 BLAST score 5.0e-15 E value Match length 105 % identity 41

(U95923) transaldolase [Solanum tuberosum] NCBI Description

45076 Seq. No.

gsv701053150.h1 Seq. ID

Method BLASTN g2791947 NCBI GI BLAST score 52 2.0e-20 E value 121 Match length 86 % identity

NCBI Description Lupinus luteus mRNA for ribosomal protein L13a

45077 Seq. No.

Seq. ID gsv701053193.h1

BLASTX Method NCBI GI g3413716 BLAST score 115 2.0e-12 E value 51 Match length % identity

(AC004747) unknown protein [Arabidopsis thaliana] NCBI Description

>qi 3643589 (AC005395) unknown protein [Arabidopsis

thaliana]

Seq. No. 45078

qsv701053238.hl Seq. ID

BLASTX Method NCBI GI g2275202 BLAST score 397 E value 6.0e-39 Match length 93 % identity 72

(AC002337) acyl-CoA synthetase isolog [Arabidopsis NCBI Description

thaliana]



45079 Seq. No.

Seq. ID gsv701053255.h1

BLASTX Method NCBI GI g1345592 BLAST score 145 E value 2.0e-09 53 Match length

66 % identity

14-3-3-LIKE PROTEIN GF14 EPSILON >gi 1022778 (U36446) GF14 NCBI Description

epsilon isoform [Arabidopsis thaliana]

Seq. No. 45080

Seq. ID qsv701053328.h1

BLASTN Method NCBI GI g4103958 BLAST score 185 E value 1.0e-100 240 Match length 95 % identity

NCBI Description Phaseolus vulgaris calmodulin (CaM) mRNA, PvCaM-2 allele,

complete cds

Seq. No. 45081

Seq. ID qsv701053385.h1

BLASTX Method g3510261 NCBI GI BLAST score 130 2.0e-16 E value 70 Match length

% identity

NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45082

gsv701053401.hl Seq. ID

BLASTX Method g2506276 NCBI GI BLAST score 228 4.0e-19 E value Match length 81 % identity 59

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi_2129561_pir__S71235 chaperonin-60 alpha chain -Arabidopsis thaliana >qi 1223910 (U49357) chaperonin-60

alpha subunit [Arabidopsis thaliana]

>qi 4510416 gb AAD21502.1 (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]

Seq. No. 45083

Seq. ID gsv701053612.h1

Method BLASTN NCBI GI q414665 BLAST score 62 E value 8.0e-27

Match length 62 % identity 100





NCBI Description G.max gene for coproporphyrinogen oxidase 45084 Seq. No.

Seq. ID gsv701053727.hl

Method BLASTX NCBI GI g4204263 BLAST score 218 5.0e-18 E value

73 Match length % identity 55

NCBI Description (AC005223) 40409 [Arabidopsis thaliana]

Seq. No.

45085 Seq. ID gsv701053807.hl

Method BLASTX NCBI GI g1171429 BLAST score 386 E value 1.0e-37 Match length 90 % identity 45

NCBI Description (U44028) CKC [Arabidopsis thaliana]

Seq. No.

45086 Seq. ID gsv701053878.h1

BLASTN Method NCBI GI g395071 BLAST score 133 E value 8.0e-69 Match length 181 % identity 93

NCBI Description V.faba guanine nucleotide regulatory protein mRNA, complete

Seq. No. 45087

Seq. ID qsv701053935.h1

Method BLASTX NCBI GI g2852447 BLAST score 325 E value 1.0e-30 Match length 84 % identity

NCBI Description (D88206) protein kinase [Arabidopsis thaliana]

Seq. No. 45088

Seq. ID gsv701053971.hl

Method BLASTX NCBI GI q3928543 BLAST score 236 E value 4.0e-20 Match length 84 % identity

(AB016819) UDP-glucose glucosyltransferase [Arabidopsis NCBI Description

thaliana]

45089

Seq. No.

Seq. ID gsv701053982.h1

Method BLASTN



```
q886099
NCBI GI
BLAST score
                  114
E value
                  2.0e-57
Match length
                  154
% identity
NCBI Description
                  Glycine max putative water channel protein (Pip1) mRNA,
                  complete cds
Seq. No.
                  45090
Seq. ID
                  qsv701053989.h1
Method
                  BLASTX
NCBI GI
                  g3522941
BLAST score
                  178
E value
                  2.0e-13
                  41
Match length
% identity
                  76
NCBI Description
                  (AC004411) putative peptide chain release factor
                   [Arabidopsis thaliana]
                  45091
Seq. No.
Seq. ID
                  gsv701054015.hl
Method
                  BLASTX
NCBI GI
                  q4469009
BLAST score
                  430
                  8.0e-43
E value
                  93
Match length
% identity
                 (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  45092
Seq. ID
                  gsv701054029.h1
Method
                  BLASTN
NCBI GI
                  q473216
BLAST score
                  61
E value
                  7.0e-26
Match length
                  197
% identity
                  83
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
Seq. No.
                  45093
Seq. ID
                  qsv701054081.h1
Method
                  BLASTN
NCBI GI
                  q3241923
BLAST score
                  41
                  6.0e-14
E value
Match length
                  225
% identity
                  85
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMN10, complete sequence [Arabidopsis thaliana]
                  45094
Seq. No.
```

gsv701054091.h1 Seq. ID

Method BLASTN NCBI GI g458339 BLAST score 137 E value 3.0e-71Match length 189



% identity 93

NCBI Description Vigna radiata clone pVR-ACO2

1-aminocyclopropane-1-carboxylate oxidase homolog mRNA,

partial cds

Seq. No. 45095

Seq. ID gsv701054134.h1

Method BLASTX
NCBI GI g3080447
BLAST score 162
E value 2.0e-11
Match length 37
% identity 76

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Seq. No. 45096

Seq. ID gsv701054138.h1

Method BLASTX
NCBI GI g3297821
BLAST score 285
E value 8.0e-26
Match length 91
% identity 18

NCBI Description (AL031032) extensin-like protein [Arabidopsis thaliana]

Seq. No. 45097

Seq. ID gsv701054155.h1

Method BLASTX
NCBI GI g1946372
BLAST score 154
E value 2.0e-10
Match length 35
% identity 80

NCBI Description (U93215) yeast hypothetical protein YDB1_SCHPO isolog

[Arabidopsis thaliana]

Seq. No. 45098

Seq. ID gsv701054168.h1

Method BLASTX
NCBI GI g3337366
BLAST score 223
E value 1.0e-18
Match length 83
% identity 52

NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]

Seq. No. 45099

Seq. ID gsv701054174.h1

Method BLASTX
NCBI GI g3885342
BLAST score 145
E value 3.0e-09
Match length 41
% identity 63

NCBI Description (AC005623) putative DNA polymerase [Arabidopsis thaliana]

Seq. No. 45100



```
qsv701054224.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2337888
BLAST score
                  34
                  9.0e-10
E value
Match length
                  78
% identity
                  86
                  Genomic sequence for Arabidopsis thaliana BAC F14J16,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  45101
Seq. No.
                  gsv701054241.h1
Seq. ID
                  BLASTN
Method
                  g669002
NCBI GI
BLAST score
                  55
                  3.0e-22
E value
Match length
                  155
                  88
% identity
                  Glycine max calnexin mRNA, complete cds
NCBI Description
                  45102
Seq. No.
Seq. ID
                  gsv701054251.h1
                  BLASTN
Method
NCBI GI
                  g169980
                  82
BLAST score
                  2.0e-38
E value
                  189
Match length
                  87
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
                   45103
Seq. No.
Seq. ID
                  gsv701054280.hl
Method
                  BLASTX
                  g4538965
NCBI GI
                  137
BLAST score
                   1.0e-08
E value
                   82
Match length
% identity
                  (AL049488) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45104
Seq. No.
Seq. ID
                   gsv701054287.h1
Method
                   BLASTN
NCBI GI
                   q18764
BLAST score
                   182
                   4.0e-98
E value
Match length
                   213
                   97
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
```

Seq. No. 45105

Seq. ID gsv701054289.h1

Method BLASTX
NCBI GI g2735841
BLAST score 204
E value 2.0e-16
Match length 77



% identity (AF010283) No definition line found [Sorghum bicolor] NCBI Description 45106 Seq. No. gsv701054379.h1 Seq. ID BLASTX Method NCBI GI g3080385 245 BLAST score 2.0e-21 E value 71 Match length 66 % identity (AL022603) serine/threonine protein kinase [Arabidopsis NCBI Description thaliana] >gi 3402760_emb_CAA20206.1_ (AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana] 45107 Seq. No. Seq. ID gsv701054406.h1 BLASTX Method NCBI GI g462187 BLAST score 287 E value 4.0e-26 86 Match length 74 % identity SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR NCBI Description (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_282928_pir__A42906 serine hydroxymethyltransferase - garden pea >gi_169158 (M87649) serine hydroxymethyltransferase [Pisum sativum] 45108 Seq. No. Seq. ID gsv701054424.h1 BLASTX Method NCBI GI g2911042 BLAST score 156 1.0e-10 E value 44 Match length 64 % identity (AL021961) Phosphoglycerate dehydrogenase - like protein NCBI Description [Arabidopsis thaliana] 45109 Seq. No. Seq. ID gsv701054426.h1 Method BLASTX q2795806 NCBI GI 354 BLAST score 6.0e-34 E value 87 Match length % identity

NCBI Description (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No. 45110

Seq. ID gsv701054585.h1

Method BLASTX
NCBI GI g3549626
BLAST score 218
E value 4.0e-18



```
Match length
                  49
% identity
NCBI Description
                  (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
Seq. No.
                  45111
Seq. ID
                  gsv701054591.h1
                  BLASTX
Method
                  q3522956
NCBI GI
                  146
BLAST score
                  1.0e-09
E value
Match length
                  81
% identity
                  47
                  (AC004411) putative pectinacetylesterase precursor
NCBI Description
                  [Arabidopsis thaliana]
                  45112
Seq. No.
                  gsv701054633.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4038035
BLAST score
                  131
                  9.0e-11
E value
Match length
                  56
% identity
                  73
                  (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  45113
Seq. No.
Seq. ID
                  gsv701054642.h1
                  BLASTX
Method
NCBI GI
                  g2651310
                  177
BLAST score
                  3.0e-13
E value
Match length
                  86
% identity
                  37
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  45114
Seq. ID
                  gsv701054762.h1
Method
                  BLASTN
NCBI GI
                  g2905779
BLAST score
                  114
E value
                  2.0e-57
Match length
                  114
% identity
                  100
                 Glycine max hydroxyproline-rich glycoprotein (hrgp) mRNA,
NCBI Description
                  partial cds
```

Seq. No. 45115

Seq. ID gsv701054773.hl

Method BLASTX NCBI GI g3152566 BLAST score 192 E value 6.0e-27 Match length 83 % identity 70

(AC002986) Similar to hypothetical protein YLR002c, NCBI Description



gb_Z7314 from S. cerevisiae. [Arabidopsis thaliana]

45116 Seq. No. Seq. ID gsv701054826.h1 Method BLASTN NCBI GI g1161251 BLAST score 99 2.0e-48 E value 179 Match length 89 % identity NCBI Description

Glycine max nucleosome assembly protein 1 (SNAP-1) mRNA,

complete cds

45117 Seq. No.

Seq. ID gsv701054831.h1

BLASTX Method NCBI GI q3157936 BLAST score 392 E value 2.0e-38 Match length 90 % identity 69

(AC002131) Contains similarity to NFATc3 gb U28807 from Mus NCBI Description

musculus. [Arabidopsis thaliana]

45118 Seq. No.

Seq. ID gsv701054890.hl

BLASTXMethod NCBI GI g3914056 BLAST score 272 2.0e-24 E value Match length 66 77 % identity

DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706) NCBI Description

MutS homolog 2 [Arabidopsis thaliana] >gi 2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana]

>gi 2547236 (AF026549) DNA mismatch repair protein MSH2

[Arabidopsis thaliana]

Seq. No. 45119

Seq. ID gsv701054924.h1

Method BLASTX NCBI GI q3273202 BLAST score 247 E value 2.0e-21 Match length 82 % identity

(AB010918) responce reactor4 [Arabidopsis thaliana] NCBI Description

Seq. No. 45120

Seq. ID gsv701054957.h1

Method BLASTN NCBI GI g2160155 BLAST score 32 E value 5.0e-09 Match length 76 % identity

NCBI Description Sequence of BAC F21M12 from Arabidopsis thaliana chromosome



1, complete sequence [Arabidopsis thaliana]

45121 Seq. No. gsv701054964.h1 Seq. ID Method ${\tt BLASTX}$ NCBI GI g585536 BLAST score 177 3.0e-13E value 68 Match length % identity 51 MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) NCBI Description >gi 1362006 pir S56653 thioglucosidase (EC 3.2.3.1) -Arabidopsis thaliana >gi 304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi 871990 emb CAA55786 (X79194) thioglucosidase [Arabidopsis thaliana] Seq. No. 45122 Seq. ID gsv701055058.h1 BLASTN Method NCBI GI q1498333 BLAST score 113 E value 6.0e-57 Match length 113 100 % identity NCBI Description Glycine max actin (Soy57) gene, partial cds Seq. No. 45123 Seq. ID gsv701055152.h1 Method BLASTX NCBI GI g3819699 BLAST score 159 E value 4.0e-11 79 Match length % identity 46 (AJ009609) BnMAP4K alpha2 [Brassica napus] NCBI Description Seq. No. 45124 Seq. ID gsv701055162.h1 BLASTX Method NCBI GI g2072393 BLAST score 457 E value 5.0e-46 Match length 91 97 % identity NCBI Description (U29168) similar to human Xeroderma pigmentosum group B DNA repair protein, Swiss-Prot Accession Number P19447 [Arabidopsis thaliana] 45125 Seq. No. gsv701055206.h1 Seq. ID BLASTX Method

Method BLASTX
NCBI GI g2832707
BLAST score 141
E value 5.0e-09
Match length 38
% identity 82

NCBI Description (AL021713) translation initiation factor eIF-2 gamma



chain-like protein [Arabidopsis thaliana]

45126 Seq. No. Seq. ID gsv701055216.h1 Method BLASTX NCBI GI g4490316 BLAST score 172 1.0e-12 E value 82 Match length 49 % identity (AL035678) nucellin-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 45127 Seq. ID gsv701055359.h1 BLASTX Method g285395 NCBI GI BLAST score 184 5.0e-14 E value Match length 74 46 % identity ribosomal protein L13 homolog - Haemophilus somnus NCBI Description >gi 241866 bbs 75164 (S75161) ribosomal protein L13 homolog=rplM [Haemophilus somnus, HS25, Peptide, 142 aa] [Haemophilus somnus] 45128 Seq. No. Seq. ID gsv701055380.h1 Method BLASTX g3776579 NCBI GI BLAST score 328 E value 6.0e-31 Match length 62 % identity NCBI Description (AC005388) Strong similarity to F22013.22 gi 3063460 myosin homolog from A. thaliana BAC gb AC003981. [Arabidopsis thaliana] Seq. No. 45129 Seq. ID gsv701055405.h1 BLASTN Method NCBI GI q170073 BLAST score 205 E value 1.0e-112 Match length 251 % identity 96 NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds 45130 Seq. No. Seq. ID gsv701055479.hl Method BLASTN NCBI GI g1732360 BLAST score 42 E value 2.0e-14 Match length 74

% identity Malus domestica translation initiation factor 2 beta NCBI Description (eIF-2beta) mRNA, partial cds

89

% identity

Seq. No.

NCBI Description

71

45136



```
45131
Seq. No.
Seq. ID
                  gsv701055484.h1
                  BLASTN
Method
                  g217902
NCBI GI
BLAST score
                  74
                  1.0e-33
E value
                  234
Match length
                  83
% identity
NCBI Description Catharanthus roseus cyc07 mRNA, complete cds
                  45132
Seq. No.
                  gsv701055514.h1
Seq. ID
                  BLASTX
Method
                  g3122933
NCBI GI
                  274
BLAST score
                  2.0e-24
E value
Match length
                  81
% identity
                  PUTATIVE QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
NCBI Description
                  TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)
                  >gi_3881825_emb_CAA98076_ (Z73899) Similarity to
                  Haemophilus Queuine tRNA-ribosyltransferase (SW:TGT_HAEIN)
                   [Caenorhabditis elegans]
                   45133
Seq. No.
Seq. ID
                   gsv701055548.h1
                  BLASTX
Method
                   g2459420
NCBI GI
                  393
BLAST score
                   2.0e-38
E value
Match length
                  77
% identity
                  (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                   thaliana]
                   45134
Seq. No.
Seq. ID
                   gsv701055573.h1
                   BLASTX
Method
                   g2911070
NCBI GI
                   309
BLAST score
                   1.0e-28
E value
                   90
Match length
% identity
                   62
NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]
                   45135
Seq. No.
Seq. ID
                   qsv701055637.hl
Method
                   BLASTX
NCBI GI
                   g3080375
BLAST score
                   324
E value
                   2.0e-30
Match length
                   84
```

7229

(AL022580) putative protein [Arabidopsis thaliana]

Method

NCBI GI

BLAST score

BLASTN

188

q2444419



```
qsv701055674.h1
Seq. ID
                  BLASTX
Method
                  g3927831
NCBI GI
BLAST score
                  212
                  2.0e-17
E value
                  52
Match length
                  73
% identity
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                  thaliana]
                  45137
Seq. No.
                  gsv701055739.h1
Seq. ID
                  BLASTX
Method
                  g4220514
NCBI GI
BLAST score
                  228
                  3.0e-19
E value
Match length
                  54
                  76
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                   45138
Seq. ID
                   gsv701055762.h1
Method
                  BLASTN
                  g2905779
NCBI GI
                  59
BLAST score
                   1.0e-24
E value
Match length
                  144
                   93
% identity
NCBI Description Glycine max hydroxyproline-rich glycoprotein (hrgp) mRNA,
                  partial cds
                   45139
Seq. No.
                   gsv701055785.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4204293
                   374
BLAST score
                   2.0e-36
E value
                   77
Match length
                   87
% identity
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   45140
Seq. No.
Seq. ID
                   gsv701055814.hl
Method
                   BLASTX
NCBI GI
                   g2244902
BLAST score
                   253
                   5.0e-22
E value
                   93
Match length
                   57
% identity
NCBI Description (Z97339) allene oxide synthase [Arabidopsis thaliana]
                   45141
Seq. No.
Seq. ID
                   gsv701055834.h1
```



```
1.0e-101
E value
Match length
                  199
                  99
% identity
                  Glycine max ribosome-associated protein p40 mRNA, complete
NCBI Description
                  cds
                   45142
Seq. No.
Seq. ID
                  qsv701055886.h1
Method
                  BLASTX
                  g3600039
NCBI GI
                  183
BLAST score
                   3.0e - 30
E value
                  88
Match length
% identity
                   65
                  (AF080119) similar to Schizosaccharomyces pombe isp4
NCBI Description
                  protein (GB:D14061) [Arabidopsis thaliana]
Seq. No.
                   gsv701055922.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3021268
BLAST score
                   416
E value
                   4.0e-41
Match length
                   94
% identity
                  (AL022347) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45144
                   gsv701056147.h1
Seq. ID
Method
                   BLASTX
                   g4220529
NCBI GI
                   331
BLAST score
                   3.0e-31
E value
Match length
                   93
% identity
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                   45145
Seq. No.
Seq. ID
                   gsv701056213.h1
                   BLASTX
Method
                   q1174599
NCBI GI
BLAST score
                   433
                   4.0e-45
E value
Match length
                   94
% identity
                   100
                   TUBULIN BETA-2 CHAIN >gi 1076659 pir S50748 beta-tubulin -
NCBI Description
                   potato >gi 609270 emb CAA83853 (Z33402) beta-tubulin
                   [Solanum tuberosum]
                   45146
Seq. No.
Seq. ID
                   gsv701056219.h1
                   BLASTX
Method
```

NCBI GI g2444271
BLAST score 391
E value 1.0e-39
Match length 97
% identity 77



(AF019637) putative amino acid or GABA permease NCBI Description [Arabidopsis thaliana] 45147 Seq. No.

gsv701056237.h1 Seq. ID ${\tt BLASTN}$ Method NCBI GI g20755 93 BLAST score 6.0e-45 E value 172 Match length

% identity P.sativum mRNA rab for ras-related GTP-binding protein NCBI Description

Seq. No. 45148

gsv701056318.h1 Seq. ID

98

BLASTX Method g3834323 NCBI GI BLAST score 160 E value 3.0e-1153 Match length % identity 53

NCBI Description (AC005679) F9K20.25 [Arabidopsis thaliana]

45149 Seq. No.

qsv701056421.h1 Seq. ID

BLASTN Method g2780782 NCBI GI BLAST score 246 E value 1.0e-136 266 Match length 98 % identity

NCBI Description Homo sapiens OS-9 mRNA, complete cds

45150 Seq. No.

gsv701056449.h1 Seq. ID

BLASTN Method g1006656 NCBI GI BLAST score 270 E value 1.0e-150 270 Match length 100 % identity

H.sapiens mRNA for cathepsin C NCBI Description

>gi 4503140_ref_NM_001814.1_CTSC_ Homo sapiens cathepsin C

(CTSC) mRNA

Seq. No. 45151

gsv701056451.h1 Seq. ID

BLASTX Method NCBI GI g3687230 258 BLAST score 1.0e-22 E value Match length 82 62 % identity

(AC005169) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

gsv701056511.h1 Seq. ID



Method BLASTX
NCBI GI g3152584
BLAST score 172
E value 2.0e-12
Match length 55
% identity 64

NCBI Description (AC002986) YUP8H12R.31 [Arabidopsis thaliana]

Seq. No.

45153

Seq. ID gsv701056581.h1

Method BLASTN
NCBI GI g3378649
BLAST score 93
E value 6.0e-45
Match length 193
% identity 87

NCBI Description M.sativa mRNA translated from abscisic activated gene

Seq. No.

45154

Seq. ID gsv701056615.h1

Method BLASTX
NCBI GI g4490316
BLAST score 207
E value 1.0e-16
Match length 59
% identity 58

NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.

45155

Seq. ID gsv701056647.hl

Method BLASTX
NCBI GI g630724
BLAST score 148
E value 9.0e-10
Match length 66
% identity 50

NCBI Description

R07E5.1 protein (clone R07E5) - Caenorhabditis elegans >gi_3878945_emb_CAA83621_ (Z32683) cDNA EST EMBL:Z14902 comes from this gene; cDNA EST EMBL:M89155 comes from this gene; cDNA EST yk212g12.3 comes from this gene; cDNA EST yk212g12.5 comes from this gene; cDNA EST yk403b9.3 comes

from this gene; cDNA ES

Seq. No. 45156

Seq. ID gsv701056674.h1

Method BLASTX
NCBI GI g2980768
BLAST score 157
E value 7.0e-11
Match length 73
% identity 48

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 45157

Seq. ID gsv701056816.h1

Method BLASTX NCBI GI g2832708

% identity

99



```
BLAST score
                  3.0e-27
E value
                  88
Match length
                   65
% identity
                   (AL021713) beta-1, 3-glucanase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   45158
Seq. No.
                  gsv701056828.h1
Seq. ID
                  {\tt BLASTX}
Method
                   g4322940
NCBI GI
                   330
BLAST score
E value
                   4.0e-31
                   79
Match length
                   38
% identity
                  (AF096299) DNA-binding protein 2 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   45159
                   gsv701056831.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3860247
                   209
BLAST score
                   6.0e-17
E value
Match length
                   43
% identity
                   93
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   45160
Seq. No.
Seq. ID
                   gsv701056883.h1
                   BLASTX
Method
NCBI GI
                   g4455237
BLAST score
                   256
                   2.0e-22
E value
Match length
                   56
                   88
% identity
                   (AL035523) ubiquitin activating enzyme-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   45161
                   has700548118.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3176662
BLAST score
                   220
E value
                   2.0e-18
                   48
Match length
                   77
% identity
                   (AC004393) Similar to mannosyl-oligosaccharide glucosidase
NCBI Description
                   gb X87237 from Homo sapiens. [Arabidopsis thaliana]
                   45162
Seq. No.
Seq. ID
                   has700548195.h1
Method
                   BLASTN
NCBI GI
                   g296444
BLAST score
                   242
E value
                   1.0e-134
Match length
                   257
```



```
NCBI Description G.max ADR6 mRNA
```

Seq. No. 45163

Seq. ID has700548208.h1

Method BLASTX
NCBI GI 94417287
BLAST score 187
E value 2.0e-14
Match length 76
% identity 51

NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 45164

Seq. ID has700548245.hl

Method BLASTX
NCBI GI g1402900
BLAST score 317
E value 1.0e-29
Match length 90
% identity 69

NCBI Description (X98322) peroxidase [Arabidopsis thaliana]

>gi 1429219 emb CAA67312_ (X98776) peroxidase ATP13a

[Arabidopsis thaliana]

Seq. No. 45165

Seq. ID has700548258.h1

Method BLASTX
NCBI GI g4314370
BLAST score 283
E value 1.0e-25
Match length 74
% identity 70

NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45166

Seq. ID has700548261.h1

Method BLASTX
NCBI GI g3402690
BLAST score 356
E value 3.0e-34
Match length 89
% identity 72

NCBI Description (AC004697) hypothetical protein, 3' partial [Arabidopsis

thaliana]

Seq. No. 45167

Seq. ID has700548276.h1

Method BLASTX
NCBI GI g3850584
BLAST score 283
E value 1.0e-25
Match length 83
% identity 66

NCBI Description (AC005278) ESTs gb_H37641 and gb_AA651422 come from this

gene. [Arabidopsis thaliana]

Seq. No. 45168

7235



has700548279.h1 Seq. ID BLASTX Method g3522956 NCBI GI 234 BLAST score 7.0e-20 E value 88 Match length % identity 49 (AC004411) putative pectinacetylesterase precursor NCBI Description [Arabidopsis thaliana] 45169 Seq. No. hrw701056908.h1 Seq. ID BLASTX Method NCBI GI g4567274 BLAST score 438 8.0e-44E value 87 Match length % identity 87 (AC006841) putative cysteine proteinase precursor NCBI Description [Arabidopsis thaliana] 45170 Seq. No. hrw701057038.h2 Seq. ID Method BLASTN NCBI GI g2304954 BLAST score 262 E value 1.0e-146 Match length 266 % identity 100 NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds 45171 Seq. No. Seq. ID hrw701057042.h2 BLASTX Method NCBI GI g1083217 BLAST score 164 1.0e-11 E value 64 Match length 48 % identity alpha-mannosidase (EC 3.2.1.24) - mouse >gi_474276 (U03457) NCBI Description alpha-mannosidase [Mus musculus] 45172 Seq. No. Seq. ID hrw701057063.h2 BLASTX Method NCBI GI g1814401 150 BLAST score 5.0e-10 E value 37 Match length % identity 70 (U84888) phosphoglucomutase [Mesembryanthemum crystallinum] NCBI Description

Seq. No. 45173

Seq. ID hrw701057210.h1

Method BLASTX NCBI GI g3047104 BLAST score 148



E value 5.0e-10
Match length 47
% identity 57
NCBI Description (AF0589

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 45174

Seq. ID hrw701057224.h1

Method BLASTN
NCBI GI g310560
BLAST score 118
E value 4.0e-60
Match length 150
% identity 95

NCBI Description Soybean ascorbate peroxidase mRNA, complete cds

Seq. No. 45175

Seq. ID hrw701057241.h1

Method BLASTN
NCBI GI g1055367
BLAST score 76
E value 5.0e-35
Match length 124
% identity 90

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 45176

Seq. ID hrw701057301.h1

Method BLASTN
NCBI GI g3478668
BLAST score 226
E value 1.0e-124
Match length 270
% identity 96

NCBI Description Homo sapiens PAC clone DJ0620P06 from 7p21-p22, complete

sequence [Homo sapiens]

Seq. No. 45177

Seq. ID hrw701057307.hl

Method BLASTN
NCBI GI g3043721
BLAST score 250
E value 1.0e-138
Match length 266
% identity 98

NCBI Description Homo sapiens mRNA for KIAA0599 protein, partial cds

Seq. No. 45178

Seq. ID hrw701057309.h1

Method BLASTN
NCBI GI g4003384
BLAST score 241
E value 1.0e-133
Match length 270
% identity 97

NCBI Description Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer,



segment 7/11

```
45179
Seq. No.
Seq. ID
                  hrw701057310.hl
                  BLASTN
Method
NCBI GI
                  g434770
BLAST score
                  240
E value
                  1.0e-132
                  264
Match length
                  98
% identity
NCBI Description Human mRNA for KIAA0111 gene, complete cds
                   45180
Seq. No.
Seq. ID
                  hrw701057312.h1
                  BLASTN
Method
NCBI GI
                  g3327379
                  207
BLAST score
                   1.0e-113
E value
Match length
                   238
                   73
% identity
                  Homo sapiens small proline-rich protein 1 (SPRR1A) gene,
NCBI Description
                   complete cds
                   45181
Seq. No.
Seq. ID
                  hrw701057314.h1
                  BLASTN
Method
NCBI GI
                   g432361
BLAST score
                   198
                   1.0e-107
E value
                   262
Match length
                   94
% identity
                  Human mRNA for ribosomal protein L37, complete cds
NCBI Description
                   >gi 4506640 ref NM 000997.1 RPL37 Homo sapiens ribosomal
                   protein L37 (RPL37) mRNA
                   45182
Seq. No.
Seq. ID
                   hrw701057317.h1
                   {\tt BLASTN}
Method
NCBI GI
                   q291926
BLAST score
                   216
                   1.0e-118
E value
Match length
                   255
                   97
% identity
NCBI Description Homo sapiens cystatin B mRNA, complete cds
                   45183
Seq. No.
Seq. ID
                   hrw701057318.hl
                   BLASTN
Method
NCBI GI
                   g264772
BLAST score
                   269
E value
                   1.0e-150
Match length
                   277
```

Seq. No. 45184

% identity

NCBI Description

100

mRNA, 453 nt]

thymosin beta-10 [human, metastatic melanoma cell line,



hrw701057321.h1 Seq. ID BLASTN Method g32106 NCBI GI 239 BLAST score 1.0e-132 E value 268 Match length 96 % identity NCBI Description Human gene for histone H1(0) 45185 Seq. No. hrw701057323.hl Seq. ID Method BLASTN g2264345 NCBI GI BLAST score 251 E value 1.0e-139 Match length 271 99 % identity Homo sapiens GOK (STIM1) mRNA, complete cds NCBI Description $>gi_4507268_ref_NM_003156.1_STIM1_$ Homo sapiens stromal interaction molecule 1 (STIM1) mRNA Seq. No. 45186 hrw701057324.h1 Seq. ID Method BLASTN NCBI GI g184426 BLAST score 116 7.0e-59 E value Match length 168 % identity 94 Human heparan sulfate proteoglycan (HSPG2) mRNA, complete NCBI Description cds Seq. No. Seq. ID 45187 hrw701057326.hl Method BLASTN g1079565 NCBI GI BLAST score 264 E value 1.0e-147 272 Match length 99 % identity NCBI Description Human Hep27 protein mRNA, complete cds Seq. No. 45188 Seq. ID hrw701057339.h1 Method BLASTN NCBI GI g3342793 BLAST score 54 9.0e-22 E value Match length 68

93 % identity

Homo sapiens calcium binding protein (ALG-2) mRNA, complete NCBI Description

cds

45189 Seq. No.

Seq. ID hrw701057350.h1

BLASTN Method q1620016 NCBI GI

Match length

NCBI Description

% identity

268

92

and additional ORF



```
BLAST score
                  1.0e-106
E value
                  262
Match length
                  94
% identity
NCBI Description Human heart mRNA for heat shock protein 90, partial cds
                  45190
Seq. No.
                  hrw701057355.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3183910
                  229
BLAST score
                  1.0e-126
E value
                  257
Match length
% identity
                  98
NCBI Description Homo sapiens partial mRNA; ID YG81-2B
                  45191
Seq. No.
                  hrw701057356.h1
Seq. ID
Method
                  BLASTN
                  g29508
NCBI GI
                  188
BLAST score
                  1.0e-101
E value
                  248
Match length
                  94
% identity
                  Human BTG1 mRNA >gi 4502472 ref NM 001731.1_BTG1_ Homo
NCBI Description
                  sapiens B-cell translocation protein 1 (BTG1) mRNA
Seq. No.
                   45192
                  hrw701057365.h1
Seq. ID
Method
                  BLASTN
                   g2366751
NCBI GI
BLAST score
                   237
                   1.0e-131
E value
                   273
Match length
                   97
% identity
NCBI Description Homo sapiens mRNA for Lysyl tRNA Synthetase, complete cds
                   45193
Seq. No.
Seq. ID
                   hrw701057366.h1
                   BLASTN
Method
                   g297407
NCBI GI
BLAST score
                   139
                   2.0e-72
E value
Match length
                   254
% identity
                   93
NCBI Description H.sapiens p63 mRNA for transmembrane protein
                   45194
Seq. No.
Seq. ID
                   hrw701057367.h1
Method
                   BLASTN
NCBI GI
                   g32998
BLAST score
                   169
                   3.0e-90
E value
```

7240

Human DNA for insulin-like growth factor II (IGF-2); exon 7

% identity

NCBI Description

41



```
45195
Seq. No.
Seq. ID
                  hrw701057368.h1
                  BLASTN
Method
NCBI GI
                  g3184497
BLAST score
                  120
                  4.0e-61
E value
Match length
                  226
% identity
                  98
                  Homo sapiens chromosome 19, cosmid R31546, complete
NCBI Description
                  sequence [Homo sapiens]
                  45196
Seq. No.
Seq. ID
                  hrw701057369.h1
Method
                  BLASTN
NCBI GI
                  g28338
BLAST score
                  235
                  1.0e-129
E value
Match length
                  263
                   97
% identity
                  Human mRNA for cytoskeletal gamma-actin
NCBI Description
                  >gi 4501886 ref NM 001614.1_ACTG1_ Homo sapiens actin,
                  gamma 1 (ACTG1) mRNA
                   45197
Seq. No.
Seq. ID
                  hrw701057372.h1
                  BLASTN
Method
NCBI GI
                  g31371
                   256
BLAST score
E value
                   1.0e-142
                   264
Match length
                   99
% identity
NCBI Description
                  Human FGFR-4 mRNA for fibroblast growth factor receptor
                   (FGFR-4) >qi 4503712 ref NM 002011.1 FGFR4 Homo sapiens
                   fibroblast growth factor receptor 4 (FGFR4) mRNA
                   45198
Seq. No.
Seq. ID
                   hrw701057381.h1
Method
                   BLASTN
NCBI GI
                   q576478
BLAST score
                   132
E value
                   2.0e-68
Match length
                   136
% identity
                   99
                  Homo sapiens (clone pMF17) MHC class I HLA-Cw7 mRNA, 3'
NCBI Description
                   end, haplotype A1/A2, B8/Bw62, Cw3/Cw7
Seq. No.
                   45199
                  hrw701057385.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g631129
BLAST score
                   187
E value
                   2.0e-14
Match length
                   82
```

7241

endosomal protein [Homo sapiens]

endosomal protein - human >gi_475934_emb_CAA55632_ (X78998)



Seq. No. 45200

Seq. ID hrw701057386.h1

Method BLASTN
NCBI GI g897556
BLAST score 256
E value 1.0e-142
Match length 264
% identity 99

NCBI Description Human T-lymphoma invasion and metastasis inducing TIAM1

protein (TIAM1) mRNA, complete cds.

>gi 4507500 ref NM 003253.1 TIAM1 Homo sapiens T-cell

lymphoma invasion and metastasis 1 (TIAM1) mRNA

Seq. No. 45201

Seq. ID hrw701057387.h1

Method BLASTN
NCBI GI g2911586
BLAST score 237
E value 1.0e-131
Match length 264
% identity 97

NCBI Description Homo sapiens mRNA for putative methyltransferase

Seq. No. 45202

Seq. ID hrw701057391.h1

Method BLASTX
NCBI GI g1175453
BLAST score 156
E value 1.0e-10
Match length 65
% identity 43

NCBI Description HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I

>gi 2130268 pir S62433 hypothetical protein SPAC13G6.04 -

fission yeast (Schizosaccharomyces pombe)

>gi 1008989 emb CAA91097 (Z54308) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 45203

Seq. ID hrw701057393.h1

Method BLASTN
NCBI GI g2897866
BLAST score 257
E value 1.0e-143
Match length 265
% identity 99

NCBI Description Homo sapiens NRD convertase mRNA, complete cds

Seq. No. 45204

Seq. ID hrw701057402.h1

Method BLASTN
NCBI GI g2230868
BLAST score 149
E value 2.0e-78
Match length 248
% identity 91

NCBI Description H.sapiens mRNA for ferritin L-chain



```
Seq. No.
                  45205
Seq. ID
                  hrw701057415.h1
                  BLASTN
Method
NCBI GI
                  g3789933
                  177
BLAST score
E value
                  3.0e-95
Match length
                  192
% identity
                   99
                  Homo sapiens RGS-GAIP interacting protein GIPC mRNA,
NCBI Description
                  complete cds
Seq. No.
                   45206
Seq. ID
                  hrw701057417.h1
Method
                  BLASTN
NCBI GI
                  q34772
BLAST score
                  251
E value
                   1.0e-139
Match length
                   273
% identity
                   99
                  Human mRNA for calcium-binding protein in macrophages
NCBI Description
                   (MRP-8) macrophage migration inhibitory factor
                   (MIF)-related protein >gi_3938041_gb_I93571_I93571 Sequence
                   15 from patent US
Seq. No.
                   45207
                  hrw701057420.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3721662
BLAST score
                   253
E value
                   1.0e-140
Match length
                   272
                   99
% identity
NCBI Description Homo sapiens mRNA for KIP2, complete cds
Seq. No.
                   45208
Seq. ID
                  hrw701057421.h1
                  BLASTX
Method
NCBI GI
                   g2078441
BLAST score
                   243
                   7.0e-21
E value
Match length
                   80
% identity
                   53
                  (U56964) weak similarity to S. cerevisiae intracellular
NCBI Description
                   protein transport protein US)1 (SP:P25386) [Caenorhabditis
                   elegans]
                   45209
Seq. No.
Seq. ID
                   hrw701057426.h1
Method
                   BLASTN
```

BLAST score 256 E value 1.0e-142 Match length 263 % identity 100

NCBI GI

NCBI Description Human profilin mRNA, complete cds

g190385



```
45210
Seq. No.
                  hrw701057428.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3413937
                  273
BLAST score
                  1.0e-152
E value
                  273
Match length
% identity
                  100
NCBI Description Homo sapiens mRNA for KIAA0494 protein, complete cds
                  45211
Seq. No.
                  hrw701057430.hl
Seq. ID
Method
                  BLASTN
                  g3005586
```

NCBI GI BLAST score 152 E value 4.0e-80 Match length 231 100 % identity

Homo sapiens Ser/Arg-related nuclear matrix protein NCBI Description

(SRM160) mRNA, complete cds

Seq. No. 45212 hrw701057436.h1 Seq. ID BLASTN Method g3413292 NCBI GI 272 BLAST score

E value 1.0e-152 279 Match length 100 % identity

Homo sapiens mRNA for ERp28 protein NCBI Description

45213 Seq. No.

hrw701057437.h1 Seq. ID

Method BLASTN NCBI GI q603801 BLAST score 271 1.0e-151 E value 279 Match length 99 % identity

NCBI Description Human mRNA for KIAA0024 gene, complete cds

45214 Seq. No.

hrw701057439.h1 Seq. ID

BLASTN Method NCBI GI g30150 BLAST score 118 7.0e-60 E value 276 Match length 87 % identity

H.sapiens coxVIIb mRNA for cytochrome c oxidase subunit NCBI Description

VIIb >gi_4502990_ref_NM_001866.1 COX7B Homo sapiens cytochrome c oxidase subunit VIIb (COX7B), nuclear gene

encoding mitochondrial protein, mRNA

45215 Seq. No.

Seq. ID hrw701057440.h1

Method BLASTN



```
q1835126
NCBI GI
BLAST score
                   71
                   8.0e-32
E value
                  107
Match length
                   92
% identity
                  M.musculus E800 mRNA
NCBI Description
Seq. No.
                   45216
Seq. ID
                   hrw701057444.h1
Method
                   BLASTN
                   q181036
NCBI GI
BLAST score
                   247
                   1.0e-137
E value
Match length
                   266
                   99
% identity
                   Human carbonyl reductase mRNA, complete cds.
NCBI Description
                   reductase 1 (CBR1) mRNA
                   45217
Seq. No.
```

>gi 4502598 ref NM 001757.1_CBR1_ Homo sapiens carbonyl

Seq. ID hrw701057456.hl Method BLASTN NCBI GI g2645204 BLAST score 59 E value 1.0e-24 Match length 150 % identity 85

Mus musculus p160 myb-binding protein (P160) mRNA, complete NCBI Description cds

45218 Seq. No. hrw701057457.h1 Seq. ID Method BLASTN g187460 NCBI GI BLAST score 146 1.0e-76 E value 181 Match length

95 % identity

Human mineralocorticoid receptor mRNA (hMR), complete cds. NCBI Description

>gi 4505198 ref NM 000901.1_MLR_ Homo sapiens

mineralocorticoid receptor (aldosterone receptor) (MLR)

mRNA

45219 Seq. No.

Seq. ID hrw701057462.h1

BLASTN Method g348706 NCBI GI BLAST score 246 E value 1.0e-136 Match length 265 99 % identity

NCBI Description Homo sapiens cathepsin B mRNA, 3' UTR with a stem-loop

structure providing mRNA stability

Seq. No. 45220 Seq. ID

hrw701057463.h1

Method BLASTN



NCBI GI g181291 BLAST score 263 E value 1.0e-146 Match length 270 % identity 100

NCBI Description Human sterol 27-hydroxylase (CYP27) mRNA, complete cds.

>gi_4503208_ref_NM_000105.1_CYP27A1a_ Homo sapiens

cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1a) mRNA >gi 4503210 ref NM 000784.1 CYP27A1b Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b)

mRNA

Seq. No. 45221

Seq. ID hrw701057465.hl

Method BLASTN
NCBI GI 9456190
BLAST score 121
E value 8.0e-62
Match length 188
% identity 92

NCBI Description H.sapiens mRNA for rho GDP-dissociation Inhibitor

Seq. No. 45222

Seq. ID hrw701057467.h1

Method BLASTN
NCBI GI g287644
BLAST score 265
E value 1.0e-147
Match length 272
% identity 100

NCBI Description H.sapiens cDNA for TREB protein

Seq. No. 45223

Seq. ID hrw701057470.h1

Method BLASTN
NCBI GI g2957144
BLAST score 210
E value 1.0e-115
Match length 228
% identity 99

NCBI Description Homo sapiens carboxyl terminal LIM domain protein (CLIM1)

mRNA, complete cds

Seq. No. 45224

Seq. ID hrw701057477.h1

Method BLASTN
NCBI GI g186701
BLAST score 257
E value 1.0e-143
Match length 264
% identity 100

NCBI Description Human cytokeratin 8 mRNA, complete cds

Seq. No. 45225

Seq. ID hrw701057478.h1



BLASTN Method g537513 NCBI GI 232 BLAST score 1.0e-128 E value 239 Match length 100 % identity

Human arylacetamide deacetylase mRNA, complete cds. NCBI Description >gi 4557226 ref NM 001086.1_AADAC_ Homo sapiens

arylacetamide deacetylase (esterase) (AADAC) mRNA

45226 Seq. No.

hrw701057482.hl Seq. ID

Method BLASTN NCBI GI q452984 BLAST score 214 E value 1.0e-117 Match length 221 100 % identity

smooth muscle myosin heavy chain isoform SM1 [human, NCBI Description umbilical cord, fetal aorta, mRNA Partial, 1039 nt]

Seq. No. 45227

Seq. ID hrw701057492.h1

Method BLASTN NCBI GI q862619 BLAST score 256 1.0e-142 E value Match length 263 100 % identity

Human cystic fibrosis antigen mRNA, complete cds. NCBI Description

>gi_4506772_ref_NM_002965.1_S100A9 Homo sapiens S100 calcium-binding protein A9 (calgranulin B) (S100A9) mRNA

Seq. No. 45228

Seq. ID hrw701057494.h1

Method BLASTN g2474095 NCBI GI 217 BLAST score 1.0e-119 E value 224 Match length 100 % identity

Human XMP mRNA, complete cds NCBI Description

>gi 4503560 ref NM 001424.1 EMP2 Homo sapiens epithelial

membrane protein 2 (EMP2) mRNA

45229 Seq. No.

Seq. ID hrw701057505.h1

BLASTN Method g2988396 NCBI GI BLAST score 70 3.0e-31 E value

Match length 245 83 % identity

Homo sapiens chromosome 19, cosmid F23858, complete NCBI Description

sequence [Homo sapiens]

45230 Seq. No.



hrw701057512.h1 Seq. ID BLASTN Method NCBI GI g1922316 153 BLAST score 9.0e-81 E value 173 Match length 97 % identity H.sapiens DNA for muscle nicotinic acetylcholine receptor NCBI Description gene promotor, clone ICRFc105F02104 Seq. No. Seq. ID 45231 hrw701057517.h1 BLASTN Method NCBI GI q337515 207 BLAST score 1.0e-113 E value 240 Match length 96 % identity Human ribosomal protein S6 mRNA, complete cds. NCBI Description >gi 4506730_ref_NM_001010.1_RPS6_ Homo sapiens ribosomal protein S6 (RPS6) mRNA Seq. No. 45232 hrw701057520.h1 Seq. ID Method BLASTN NCBI GI q2347183 272 BLAST score 1.0e-152 E value Match length 272 % identity 100 Genomic sequence from Human 17, complete sequence [Homo NCBI Description sapiens] 45233 Seq. No. hrw701057521.hl Seq. ID BLASTN Method NCBI GI q339688 BLAST score 263 E value 1.0e-146 271 Match length 99 % identity NCBI Description Human thymosin beta-4 mRNA, complete cds 45234 Seq. No. Seq. ID hrw701057522.h1 BLASTN Method g559370

NCBI GI BLAST score 135 E value 5.0e-70 Match length 250 89 % identity

Rattus norvegicus mRNA for Crk-associated substrate, p130, NCBI Description

complete cds

Seq. No. 45235

hrw701057525.hl Seq. ID

Method BLASTN



```
q182860
NCBI GI
                  262
BLAST score
E value
                  1.0e-146
                  270
Match length
                  100
% identity
                  Human glyceraldehyde-3-phosphate dehydrogenase mRNA,
NCBI Description
                  complete cds
Seq. No.
                   45236
                  hrw701057527.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3868777
BLAST score
                   108
                   7.0e-54
E value
Match length
                   240
                   86
% identity
                  Rattus norvegicus mRNA for atypical PKC specific binding
NCBI Description
                  protein, complete cds
Seq. No.
                   45237
                   hrw701057528.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2267586
BLAST score
                   69
                   1.0e-30
E value
Match length
                   211
                   91
% identity
                   Rattus norvegicus enhancer-of-split and hairy-related
NCBI Description
                   protein 1 (SHARP-1) mRNA, complete cds
                   45238
Seq. No.
                   hrw701057533.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1054883
BLAST score
                   46
E value
                   7.0e-17
                   235
Match length
                   81
% identity
                   Rattus norvegicus prostaglandin F2a receptor regulatory
NCBI Description
                   protein precursor, mRNA, complete cds
                   45239
Seq. No.
                   hrw701057534.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g414348
                   267
BLAST score
                   1.0e-149
E value
                   271
Match length
                   100
% identity
                   Human homolog of yeast ribosomal protein S28, complete cds
NCBI Description
```

>gi 4506700 ref NM 001025.1 RPS23 Homo sapiens ribosomal

protein S23 (RPS23) mRNA

45240 Seq. No.

Seq. ID hrw701057535.h1

BLASTN Method q311340 NCBI GI



BLAST score E value 8.0e-69 257 Match length 88 % identity

B. taurus mRNA for gamma-COP NCBI Description

Seq. No.

45241

Seq. ID

hrw701057536.h1

Method BLASTN NCBI GI g37503 259 BLAST score 1.0e-144 E value 259 Match length % identity 100

Human tyk2 mRNA for non-receptor protein tyrosine kinase NCBI Description

>gi 4507748 ref_NM_003331.1_TYK2_ Homo sapiens tyrosine

kinase 2 (TYK2) mRNA

Seq. No.

45242

hrw701057541.h1 Seq. ID

Method BLASTN NCBI GI g619906 BLAST score 88 6.0e-42E value Match length 256 % identity 91

R.norvegicus C15 mRNA NCBI Description

45243

Seq. No.

hrw701057543.h1 Seq. ID

BLASTN Method NCBI GI g2988396 BLAST score 259 E value 1.0e-144 Match length 267 99

% identity

Homo sapiens chromosome 19, cosmid F23858, complete NCBI Description

sequence [Homo sapiens]

Seq. No. 45244

hrw701057550.h1 Seq. ID

BLASTN Method g182178 NCBI GI BLAST score 261 E value 1.0e-145 Match length 273 99 % identity

Human DNA repair helicase (ERCC3) mRNA, complete cds. NCBI Description

>qi 4557562 ref NM 000122.1 ERCC3 Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B

complementing) (ERCC3) mRNA

45245 Seq. No.

Seq. ID hrw701057551.hl

Method BLASTN NCBI GI g348706



BLAST score 217 E value 1.0e-119 Match length 245 % identity 98

NCBI Description Homo sapiens cathepsin B mRNA, 3' UTR with a stem-loop

structure providing mRNA stability

Seq. No. 45246

Seq. ID hrw701057552.h1

Method BLASTN
NCBI GI g2224600
BLAST score 270
E value 1.0e-150
Match length 270
% identity 100

NCBI Description Human mRNA for KIAA0330 gene, partial cds

Seq. No. 45247

Seq. ID hrw701057553.h1

Method BLASTN
NCBI GI g1665724
BLAST score 217
E value 1.0e-119
Match length 265
% identity 95

NCBI Description Human mRNA for KIAA0109 gene, complete cds

Seq. No. 45248

Seq. ID hrw701057554.hl

Method BLASTN
NCBI GI g3668108
BLAST score 148
E value 9.0e-78
Match length 244
% identity 90

NCBI Description Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete

sequence [Homo sapiens]

Seq. No. 45249

Seq. ID hrw701057555.h1

Method BLASTN
NCBI GI g57128
BLAST score 170
E value 6.0e-91
Match length 254
% identity 92

NCBI Description Rat mRNA for ribosomal protein S14

Seq. No. 45250

Seq. ID hrw701057558.h1

Method BLASTN
NCBI GI g3335505
BLAST score 253
E value 1.0e-140
Match length 265
% identity 99

NCBI Description Homo sapiens b(2)gcn homolog mRNA, complete cds



>gi_4504770_ref_NM_002212.1_ITGB4BP_ Homo sapiens integrin beta 4 binding protein (ITGB4BP) mRNA

Seq. No. 45251

Seq. ID hrw701057559.h1

Method BLASTN
NCBI GI g3599572
BLAST score 213
E value 1.0e-116
Match length 237
% identity 98

NCBI Description Homo sapiens flotillin-1 mRNA, complete cds

Seq. No. 45252

Seq. ID hrw701057560.h1

Method BLASTN
NCBI GI g452047
BLAST score 262
E value 1.0e-146
Match length 269
% identity 100

NCBI Description Homo sapiens HnRNP F protein mRNA, complete cds

Seq. No. 45253

Seq. ID hrw701057562.h1

Method BLASTN
NCBI GI g3779225
BLAST score 33
E value 3.0e-09
Match length 137
% identity 81

NCBI Description Homo sapiens secreted cement gland protein XAG-2 homolog

(hAG-2/R) mRNA, complete cds

Seq. No. 45254

Seq. ID hrw701057564.h1

Method BLASTN
NCBI GI g2385366
BLAST score 97
E value 2.0e-47
Match length 177
% identity 89

NCBI Description H.sapiens MLN51 mRNA

Seq. No. 45255

Seq. ID hrw701057568.h1

Method BLASTN
NCBI GI g3420928
BLAST score 242
E value 1.0e-134
Match length 262
% identity 98

NCBI Description Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds

Seq. No. 45256

Seq. ID hrw701057570.h1

Method BLASTN



q32998 NCBI GI BLAST score 182 E value 4.0e-98 186 Match length 99 % identity Human DNA for insulin-like growth factor II (IGF-2); exon 7 NCBI Description and additional ORF Seq. No. 45257 Seq. ID hrw701057572.h1 Method BLASTN NCBI GI g2745717 BLAST score 174 E value 3.0e-93 Match length 178 % identity 99

NCBI Description Homo sapiens nucleophosmin phosphoprotein (NPM) gene, intron 9, partial sequence

Seq. No. 45258

Seq. ID hrw701057573.h1

Method BLASTN
NCBI GI g30346
BLAST score 216
E value 1.0e-118
Match length 252
% identity 96

NCBI Description Human cytochrome P-450c gene and flanking regions

Seq. No. 45259

Seq. ID hrw701057575.h1

Method BLASTN
NCBI GI g854123
BLAST score 234
E value 1.0e-129
Match length 257
% identity 98

NCBI Description H.sapiens mRNA for human giant larvae homolog

Seq. No. 45260

Seq. ID hrw701057576.h1

Method BLASTN
NCBI GI g3043629
BLAST score 244
E value 1.0e-135
Match length 248
% identity 100

NCBI Description Homo sapiens mRNA for KIAA0553 protein, partial cds

Seq. No. 45261

Seq. ID hrw701057577.h1

Method BLASTN
NCBI GI g2739354
BLAST score 228
E value 1.0e-125
Match length 248
% identity 98

7253



NCBI Description Homo sapiens DNA from chromosome 19, cosmid R33485 containing pNORF1, complete sequence [Homo sapiens]

Seq. No. 45262

Seq. ID hrw701057578.h1

Method BLASTN
NCBI GI g28333
BLAST score 264
E value 1.0e-147
Match length 268
% identity 100

NCBI Description Human mRNA for alpha-actinin

Seq. No. 45263

Seq. ID hrw701057587.h1

Method BLASTN
NCBI GI g4309892
BLAST score 215
E value 1.0e-118
Match length 263
% identity 96

NCBI Description Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete

sequence [Homo sapiens]

Seq. No. 45264

Seq. ID hrw701057591.h1

Method BLASTN
NCBI GI g179767
BLAST score 265
E value 1.0e-147
Match length 265
% identity 100

NCBI Description Human prolactin receptor-associated protein (PRA) gene,

complete cds

Seq. No. 45265

Seq. ID hrw701057594.h1

Method BLASTN
NCBI GI g338826
BLAST score 175
E value 7.0e-94
Match length 226
% identity 100

NCBI Description Human TCB gene encoding cytosolic thyroid hormone-binding

protein, complete cds

Seq. No. 45266

Seq. ID hrw701057595.h1

Method BLASTN
NCBI GI g2281061
BLAST score 188
E value 1.0e-101
Match length 208
% identity 98

NCBI Description Human Chromosome 11 Cosmid cSRL16b6, complete sequence

[Homo sapiens]



```
45267
Seq. No.
Seq. ID
                  hrw701057624.h1
Method
                  BLASTN
NCBI GI
                   g515765
BLAST score
                   192
E value
                   1.0e-104
                   259
Match length
                   94
% identity
                  H.sapiens mRNA for IG light chain V-region, V lambda gene
NCBI Description
Seq. No.
                   45268
                   hrw701057625.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3327169
BLAST score
                   184
E value
                   3.0e-99
Match length
                   227
                   96
% identity
NCBI Description
                  Homo sapiens mRNA for KIAA0678 protein, partial cds
Seq. No.
                   45269
Seq. ID
                   hrw701057628.h1
Method
                   BLASTN
NCBI GI
                   q187192
BLAST score
                   248
E value
                   1.0e-137
Match length
                   257
% identity
                   99
NCBI Description
                   Human lipoxygenase mRNA, complete cds.
                   >gi_4502056_ref_NM_000698.1_ALOX5 Homo sapiens
                   arachidonate 5-lipoxygenase (ALOX5) mRNA
                   45270
Seq. No.
Seq. ID
                   hrw701057632.hl
Method
                   BLASTN
                   g1296606
NCBI GI
BLAST score
                   141
                   1.0e-73
E value
                   273
Match length
                   94
% identity
NCBI Description H.sapiens mRNS for clathrin-associated protein
Seq. No.
                   45271
Seq. ID
                   hrw701057636.h1
Method
                   BLASTN
NCBI GI
                   g31923
BLAST score
                   251
                   1.0e-139
E value
Match length
                   258
```

100 % identity

Human mRNA for glutathione S-transferase subunit 4 (EC NCBI Description

2.5.1.18)

Seq. No.

45272

Seq. ID hrw701057639.h1

BLASTN Method NCBI GI g1737070



BLAST score 250 E value 1.0e-138 Match length 257 % identity 100

NCBI Description Human periodic tryptophan protein 2 (PWP2) gene, exons 15

to 21, and complete cds

Seq. No. 45273

Seq. ID hrw701057642.h1

Method BLASTN
NCBI GI g1871197
BLAST score 242
E value 1.0e-134
Match length 261
% identity 42

NCBI Description Human chromosome 16 BAC clone CIT987SK-A-962B4, complete

sequence [Homo sapiens]

Seq. No. 45274

Seq. ID hrw701057656.hl

Method BLASTN
NCBI GI g2565062
BLAST score 175
E value 7.0e-94
Match length 193
% identity 98

NCBI Description Homo sapiens CTG4a mRNA, complete cds

Seq. No. 45275

Seq. ID hrw701057666.h1

Method BLASTN
NCBI GI g2706516
BLAST score 248
E value 1.0e-137
Match length 255
% identity 100

NCBI Description Homo sapiens IGF2 gene, exon

Seq. No. 45276

Seq. ID hrw701057676.h1

Method BLASTN
NCBI GI g1718194
BLAST score 250
E value 1.0e-138
Match length 261
% identity 99

NCBI Description Homo sapiens translation initiation factor eIF3 p36 subunit

mRNA, complete cds >gi_4503512_ref_NM_003757.1_EIF3S2_ Homo sapiens eukaryotic translation initiation factor 3, subunit

2 (beta, 36kD) (EIF3S2) mRNA

Seq. No. 45277

Seq. ID hrw701057678.hl

Method BLASTN
NCBI GI g463890
BLAST score 240
E value 1.0e-132



Match length 266 98 % identity

Human voltage-gated calcium channel beta subunit mRNA, NCBI Description

complete cds

45278 Seq. No.

hrw701057682.h1 Seq. ID

BLASTN Method NCBI GI q184648 223 BLAST score E value 1.0e-122 251 Match length

97 % identity Homo sapiens interferon regulatory factor 1 gene, complete NCBI Description

45279 Seq. No.

hrw701057687.h1 Seq. ID

BLASTN Method NCBI GI g3540172 244 BLAST score E value 1.0e-135 Match length 255 99 % identity

Homo sapiens chromosome 16, P1 clone 109-8C (LANL), NCBI Description

complete sequence [Homo sapiens]

45280 Seq. No.

hrw701057688.hl Seq. ID

BLASTN Method NCBI GI q3360400 236 BLAST score 1.0e-130 E value Match length 251 99

% identity

NCBI Description Homo sapiens clone 23698 mRNA sequence

45281 Seq. No.

hrw701057691.h1 Seq. ID

Method BLASTN NCBI GI g36137 BLAST score 127 1.0e-65 E value Match length 131 99 % identity

H.sapiens mRNA for ribosomal protein L6 NCBI Description

>gi 4506656 ref_NM_000970.1_RPL6_ Homo sapiens ribosomal

protein L6 (RPL6) mRNA

45282 Seq. No.

hrw701057694.h1 Seq. ID

BLASTN Method NCBI GI g761715 BLAST score 254 1.0e-141 E value Match length 265 99 % identity



NCBI Description H.sapiens hH3.3B gene for histone H3.3

Seq. No. 45283

Seq. ID hrw701057706.hl

Method BLASTX
NCBI GI g3818624
BLAST score 357
E value 3.0e-34
Match length 78

% identity 87 NCBI Description (AF095912) actin related protein 2; ARP2 [Arabidopsis

thaliana]

Seq. No. 45284

Seq. ID hrw701057720.h1

Method BLASTX
NCBI GI 9419812
BLAST score 160
E value 3.0e-11
Match length 81
% identity 42

NCBI Description crm1+ protein - fission yeast (Schizosaccharomyces pombe)

Seq. No. 45285

Seq. ID hrw701057772.h1

Method BLASTN
NCBI GI g2780193
BLAST score 85
E value 3.0e-40
Match length 179
% identity 91

NCBI Description Lupinus albus mRNA for adenine nucleotide translocator

Seq. No. 45286

Seq. ID hrw701057815.h1

Method BLASTN
NCBI GI g2304954
BLAST score 270
E value 1.0e-150
Match length 270
% identity 100

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No. 45287

Seq. ID hrw701057830.h1

Method BLASTX
NCBI GI g4417296
BLAST score 198
E value 3.0e-29
Match length 85
% identity 78

NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 45288

Seq. ID hrw701057850.h1

Method BLASTX NCBI GI g1326161



```
BLAST score
                  8.0e-09
E value
Match length
                  63
% identity
                  60
                  (U54703) dehydrin [Phaseolus vulgaris]
NCBI Description
                  45289
Seq. No.
Seq. ID
                  hrw701057853.h1
Method
                  BLASTN
NCBI GI
                  g2304954
BLAST score
                  159
                  2.0e-84
E value
Match length
                  250
                  92
% identity
NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds
                  45290
Seq. No.
                  hrw701057895.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1001263
BLAST score
                   140
                   7.0e-09
E value
Match length
                  84
                   39
% identity
                  (D64003) hypothetical protein [Synechocystis sp.]
NCBI Description
                   45291
Seq. No.
                  hrw701057896.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g422495
BLAST score
                   162
                   1.0e-11
E value
                   45
Match length
% identity
                   76
                   ribosomal protein S3 - fruit fly (Drosophila melanogaster)
NCBI Description
                   >gi_296094_emb_CAA51425_ (X72921) ribosomal protein S3
                   [Drosophila melanogaster]
                   45292
Seq. No.
Seq. ID
                   hrw701057901.h1
                   BLASTX
Method
NCBI GI
                   g1174779
                   201
BLAST score
                   3.0e-16
E value
                   47
Match length
% identity
                   83
                   TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi_166894
NCBI Description
                   (M81620) tryptophan synthase beta-subunit [Arabidopsis
                   thaliana] >gi_4490703_emb_CAB38837.1_ (AL035680) tryptophan
                   synthase beta-subunit (TSB2) [Arabidopsis thaliana]
                   45293
Seq. No.
                   hrw701057936.h1
Seq. ID
```

BLASTN Method NCBI GI g3832527 BLAST score 50 E value 3.0e-19



Match length 122 % identity 85

NCBI Description Glycine max unknown mRNA

Seq. No.

45294

Seq. ID hrw701057990.h1

Method BLASTN
NCBI GI g170091
BLAST score 163
E value 7.0e-87
Match length 207
% identity 95

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No.

45295

Seq. ID hrw701058012.h1

Method BLASTN
NCBI GI g2905771
BLAST score 144
E value 2.0e-75
Match length 156
% identity 98

NCBI Description Glycine max glyceraldehyde-3 phosphate dehydrogenase

(GAPDH) mRNA, partial cds

Seq. No. 45296

Seq. ID hrw701058014.hl

Method BLASTN
NCBI GI g516853
BLAST score 174
E value 3.0e-93
Match length 226
% identity 27

NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No. 45297

Seq. ID hrw701058070.h1

Method BLASTN
NCBI GI g218082
BLAST score 102
E value 3.0e-50
Match length 246
% identity 85

NCBI Description Rice mRNA for initiation factor eIF-4D (225 gene), partial

sequence

Seq. No. 45298

Seq. ID hrw701058088.h1

Method BLASTN
NCBI GI g2739266
BLAST score 63
E value 5.0e-27
Match length 175
% identity 84

NCBI Description Allium cepa DNA for Tyl-copia retrotransposon



```
45299
Seq. No.
Seq. ID
                  hrw701058096.h1
Method
                  BLASTN
NCBI GI
                  g296444
BLAST score
                  271
                  1.0e-151
E value
                  282
Match length
% identity
                  99
NCBI Description
                  G.max ADR6 mRNA
Seq. No.
                  45300
                  hrw701058114.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2959767
BLAST score
                  255
E value
                  1.0e-22
Match length
                  67
% identity
                  72
NCBI Description
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
Seq. No.
                  45301
                  hrw701058206.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3982595
BLAST score
                  131
E value
                  1.0e-67
Match length
                  266
% identity
                  94
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                  45302
Seq. No.
Seq. ID
                  hrw701058290.h1
Method
                  BLASTX
NCBI GI
                  q1514643
BLAST score
                  359
E value
                  2.0e-34
                  90
Match length
                   40
% identity
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                  45303
Seq. No.
                  hrw701058294.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642432
BLAST score
                  168
E value
                   4.0e-12
                  39
Match length
% identity
                  (AC002391) putative elicitor response element binding
NCBI Description
                  protein (WRKY3) [Arabidopsis thaliana]
```

45304 Seq. No.

Seq. ID hrw701058323.h1

Method BLASTX NCBI GI g1865677



BLAST score 246 E value 3.0e-21 Match length 78 % identity 62

NCBI Description (Y08568) trehalose-6-phosphate synthase [Arabidopsis

thaliana]

Seq. No. 45305

Seq. ID hrw701058372.h1

Method BLASTN
NCBI GI g16511
BLAST score 35
E value 2.0e-10
Match length 71
% identity 87

NCBI Description A.thaliana mRNA for suppressor-like protein

Seq. No. 45306

Seq. ID hrw701058512.h1

Method BLASTX
NCBI GI g3559816
BLAST score 166
E value 7.0e-12
Match length 53
% identity 60

NCBI Description (Y15782) transketolase 2 [Capsicum annuum]

Seq. No. 45307

Seq. ID hrw701058723.h1

Method BLASTN
NCBI GI g18764
BLAST score 241
E value 1.0e-133
Match length 264
% identity 98

NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No. 45308

Seq. ID hrw701058748.hl

Method BLASTX
NCBI GI g4512667
BLAST score 435
E value 2.0e-43
Match length 88
% identity 94

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 45309

Seq. ID hrw701058768.h1

Method BLASTN
NCBI GI g18662
BLAST score 110
E value 4.0e-55
Match length 174
% identity 91

NCBI Description Glycine max hsp 70 gene

Method

NCBI GI

BLAST score

BLASTX

231

g3461817



```
Seq. No.
Seq. ID
                  hrw701058769.h1
Method
                  BLASTN
NCBI GI
                   g456713
                   255
BLAST score
E value
                   1.0e-141
                   259
Match length
% identity
                   27
NCBI Description Glycine max gene for ubiquitin, complete cds
                   45311
Seq. No.
Seq. ID
                   hrw701058804.h1
Method
                   BLASTX
                   q2852449
NCBI GI
BLAST score
                   303
                   6.0e-28
E value
                   76
Match length
                   80
% identity
                   (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061
NCBI Description
                   (AC002521) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   45312
Seq. ID
                   hrw701058828.hl
Method
                   BLASTX
NCBI GI
                   g3355490
                   355
BLAST score
E value
                   5.0e-34
Match length
                   91
                   73
% identity
                   (AC004218) putative dolichyl-phosphate
NCBI Description
                   beta-glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                   45313
Seq. ID
                   hrw701058850.h1
Method
                   BLASTX
NCBI GI
                   g1001263
BLAST score
                   184
                   5.0e-14
E value
Match length
                   73
% identity
                   47
                  (D64003) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   45314
Seq. ID
                   hrw701058858.h1
Method
                   BLASTX
NCBI GI
                   g1769899
BLAST score
                   192
                   6.0e-15
E value
                   76
Match length
                   46
% identity
                  (Y08010) lectin receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45315
Seq. ID
                   hrw701058886.h1
```



```
E value 2.0e-19 Match length 85
```

% identity 55

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 45316

Seq. ID hrw701058910.h1

Method BLASTN
NCBI GI g1531764
BLAST score 32
E value 1.0e-08

Match length 40 % identity 95

NCBI Description D.stramonium mRNA for S-adenosylmethionine decarboxylase

Seq. No. 45317

Seq. ID hrw701058921.h1

Method BLASTN
NCBI GI g296444
BLAST score 257
E value 1.0e-143
Match length 277
% identity 98

NCBI Description G.max ADR6 mRNA

Seq. No. 45318

Seq. ID hrw701058933.h1

Method BLASTX
NCBI GI g136636
BLAST score 275
E value 1.0e-24
Match length 51
% identity 98

NCBI Description

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>qi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 45319

Seq. ID hrw701058990.h1

Method BLASTN
NCBI GI g296408
BLAST score 114
E value 2.0e-57
Match length 175
% identity 91

NCBI Description G.max ADR12 mRNA

Seq. No. 45320

Seq. ID hrw701059083.h1

Method BLASTN NCBI GI g441205



BLAST score 122 E value 3.0e-62 Match length 242 % identity 88

NCBI Description Soybean lox1gm4 gene encoding lipxygenase L-4

Seq. No. 45321

Seq. ID hrw701059089.h1

Method BLASTN
NCBI GI g170087
BLAST score 150
E value 5.0e-79
Match length 198
% identity 95

NCBI Description G.max vegetative storage protein mRNA (VSP25 gene)

Seq. No. 45322

Seq. ID hrw701059108.h1

Method BLASTN
NCBI GI g441205
BLAST score 135
E value 4.0e-70
Match length 194
% identity 93

NCBI Description Soybean lox1gm4 gene encoding lipxygenase L-4

Seq. No. 45323

Seq. ID hrw701059120.h1

Method BLASTX
NCBI GI g3980377
BLAST score 352
E value 1.0e-33
Match length 93
% identity 72

NCBI Description (AC004561) unknown protein [Arabidopsis thaliana]

Seq. No. 45324

Seq. ID hrw701059365.h1

Method BLASTN
NCBI GI g499067
BLAST score 221
E value 1.0e-121
Match length 225
% identity 100

NCBI Description G.max gmr2 gene

Seq. No. 45325

Seq. ID hrw701059373.h1

Method BLASTX
NCBI GI g1420924
BLAST score 307
E value 2.0e-28
Match length 85
% identity 64

NCBI Description (U57899) IN1 [Zea mays]

Seq. No. 45326



```
hrw701059432.h1
Seq. ID
                  BLASTX
Method
                  g2739279
NCBI GI
BLAST score
                  174
                  9.0e-13
E value
                  86
Match length
% identity
                  43
                  (AJ223177) short chain alcohol dehydrogenase [Nicotiana
NCBI Description
                  tabacum] >gi 2791348 emb CAA11154 (AJ223178) short chain
                  alcohol dehydrogenase [Nicotiana tabacum]
                  45327
Seq. No.
                  hrw701059487.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3461848
BLAST score
                  151
                  3.0e-10
E value
                  89
Match length
% identity
                  35
                  (AC005315) putative ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  hrw701059514.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g126151
BLAST score
                  169
E value
                  2.0e-12
Match length
                  56
% identity
                  61
                  LECTIN PRECURSOR (AGGLUTININ) (SBA) >gi_282898_pir__S27365
NCBI Description
                  lectin precursor - soybean >gi_170006 (K00821) lectin
                  prepeptide [Glycine max]
Seq. No.
                  45329
Seq. ID
                  hrw701059519.hl
Method
                  BLASTX
NCBI GI
                  g2832700
                  270
BLAST score
                  4.0e-24
E value
Match length
                  88
% identity
                  (AL021713) unknown protein [Arabidopsis thaliana]
NCBI Description
                  45330
Seq. No.
Seq. ID
                  hrw701059690.hl
Method
                  BLASTX
                  g1360141
NCBI GI
                  143
BLAST score
                  3.0e-09
E value
Match length
                  82
% identity
                  48
                  (X97980) protein kinase [Solanum berthaultii]
NCBI Description
```

Seq. No. 45331

Seq. ID hrw701059715.hl

Method BLASTN NCBI GI g3982595

% identity

NCBI Description

thaliana]



```
BLAST score
                  3.0e-62
E value
                  189
Match length
                  94
% identity
                  Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
NCBI Description
                   45332
Seq. No.
Seq. ID
                  hrw701059720.h1
Method
                  BLASTN
                  g169958
NCBI GI
                  72
BLAST score
                   2.0e-32
E value
Match length
                  96
% identity
                   94
NCBI Description Glycine max G-box binding factor (GBF2A) mRNA, 3' end
Seq. No.
                   45333
                  hrw701059748.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g166915
BLAST score
                   50
E value
                   2.0e-19
Match length
                   70
% identity
                   93
                  Arabidopsis thaliana alpha-4 tubulin (TUA4) gene, complete
NCBI Description
                   45334
Seq. No.
                  hrw701059759.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g18642
BLAST score
                   33
                   2.0e-09
E value
Match length
                   81
% identity
                   85
NCBI Description G.max mRNA from stress-induced gene (H4)
                   45335
Seq. No.
                   hrw701059763.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g310575
BLAST score
                   195
                   1.0e-106
E value
                   234
Match length
                   97
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   45336
Seq. No.
Seq. ID
                   hrw701059807.h1
                   BLASTX
Method
NCBI GI
                   g2842480
                   Ī71
BLAST score
                   2.0e-12
E value
Match length
                   64
```

7267

(AL021749) ADP, ATP carrier-like protein [Arabidopsis



```
45337
Seq. No.
                  hrw701059813.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3128190
BLAST score
                   144
                   3.0e-09
E value
Match length
                   50
% identity
                   (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
                   45338
Seq. No.
                   hrw701059836.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3420055
BLAST score
                   169
                   3.0e-12
E value
Match length
                   44
                   70
% identity
                   (AC004680) cyclophilin [Arabidopsis thaliana]
NCBI Description
                   45339
Seq. No.
Seq. ID
                   hrw701059852.hl
Method
                   BLASTN
                   q2905771
NCBI GI
BLAST score
                   136
                   1.0e-70
E value
                   156
Match length
                   97
% identity
                   Glycine max glyceraldehyde-3 phosphate dehydrogenase
NCBI Description
                   (GAPDH) mRNA, partial cds
Seq. No.
                   45340
Seq. ID
                   hrw701059890.h1
Method
                   BLASTX
NCBI GI
                   g542034
BLAST score
                   140
                   7.0e-09
E value
Match length
                   54
% identity
                   54
                   TDR3 protein - tomato >gi_19380_emb_CAA43168_ (X60756) TDR3
NCBI Description
                   [Lycopersicon esculentum]
                   45341
Seq. No.
Seq. ID
                   hrw701060018.h2
Method
                   BLASTX
NCBI GI
                   g3929325
                   282
BLAST score
                   2.0e-25
E value
                   85
Match length
% identity
                   66
                   (AF100333) putative DNA-binding protein [Dendrobium grex
NCBI Description
                   Madame Thong-IN]
```

Seq. No. 45342

Seq. ID hrw701060023.h2

Method BLASTX



NCBI GI g2244965
BLAST score 259
E value 4.0e-23
Match length 81
% identity 75
NCBI Description (Z97340) unnamed

NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]

Seq. No. 45343

Seq. ID hrw701060036.h2

Method BLASTX
NCBI GI g2342666
BLAST score 223
E value 1.0e-18
Match length 83
% identity 52

NCBI Description (AF014502) seed coat peroxidase precursor [Glycine max]

Seq. No. 45344

Seq. ID hrw701060060.h2

Method BLASTN
NCBI GI g1022364
BLAST score 70
E value 1.0e-31
Match length 134
% identity 88

NCBI Description V.faba mRNA for sucrose phosphate synthase

Seq. No. 45345

Seq. ID hrw701060061.h2

Method BLASTX
NCBI GI g2440044
BLAST score 291
E value 1.0e-26
Match length 70
% identity 83

NCBI Description (AJ001293) major intrinsic protein PIPB [Craterostigma

plantagineum]

Seq. No. 45346

Seq. ID hrw701060138.h1

Method BLASTN
NCBI GI g170091
BLAST score 237
E value 1.0e-131
Match length 264
% identity 98

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 45347

Seq. ID hrw701060153.hl

Method BLASTX
NCBI GI g3878570
BLAST score 200
E value 3.0e-32
Match length 87
% identity 70



(Z46381) similar to lipoic acid synthase; cDNA EST NCBI Description yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3 45348 Seq. No. hrw701060220.h1 Seq. ID BLASTX Method g4049341 NCBI GI 141 BLAST score 2.0e-12 E value 51 Match length % identity 84 NCBI Description (AL034567) putative protein [Arabidopsis thaliana] 45349 Seq. No. hrw701060221.h1 Seq. ID BLASTN Method g170091 NCBI GI 78 BLAST score 3.0e - 36E value 78 Match length 100 % identity Glycine max vegetative storage protein (vspB) gene, NCBI Description complete cds 45350 Seq. No. hrw701060235.h1 Seq. ID BLASTN Method g18727 NCBI GI 120 BLAST score 3.0e-61E value 120 Match length 100 % identity Soybean mRNA for reductase involved in deoxychalcone NCBI Description synthesis (NAD(P)H dependent 6'-deoxychalcone synthase) 45351 Seq. No. Seq. ID hrw701060262.h1 Method BLASTX q2801536 NCBI GI BLAST score 167 3.0e-12 E value Match length 51 53 % identity (AF039531) lysophospholipase homolog [Oryza sativa] NCBI Description 45352 Seq. No. Seq. ID hrw701060284.h1 BLASTN Method q3021374 NCBI GI 58 BLAST score

E value 2.0e-24 Match length 102 % identity 90

NCBI Description Glycine max mRNA for profilin, PRO1

Seq. No.

Seq. ID

Method

NCBI GI

45358

BLASTX

g4490316

hrw701060469.h1



```
45353
Seq. No.
Seq. ID
                  hrw701060325.h1
                  BLASTX
Method
                  g4455274
NCBI GI
                  338
BLAST score
                  5.0e-32
E value
                  77
Match length
                  81
% identity
                  (AL035527) spliceosome associated protein-like [Arabidopsis
NCBI Description
                  thaliana]
                  45354
Seq. No.
                  hrw701060335.h1
Seq. ID
                  BLASTN
Method
                  g256142
NCBI GI
                  265
BLAST score
                  1.0e-147
E value
                  277
Match length
                   99
% identity
NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var
                   Prize, mRNA, 1450 nt]
                   45355
Seq. No.
                  hrw701060353.hl
Seq. ID
                  BLASTX
Method
                   g1935909
NCBI GI
BLAST score
                  212
                   3.0e-17
E value
                   55
Match length
                   71
% identity
NCBI Description (U77345) lethal leaf-spot 1 [Zea mays]
                   45356
Seq. No.
                   hrw701060413.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2224732
BLAST score
                   117
                   3.0e-59
E value
                   177
Match length
                   92
% identity
NCBI Description Vigna radiata mRNA for Aux22e, complete cds
Seq. No.
                   45357
                   hrw701060463.hl
Seq. ID
                   BLASTN
Method
                   q19506
NCBI GI
BLAST score
                   111
E value
                   1.0e-55
                   203
Match length
                   89
% identity
NCBI Description L.polyphyllus mRNA for pPLZ02 protein
```



BLAST score 214
E value 2.0e-17
Match length 53
% identity 68

NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

* **

Seq. No. 45359

Seq. ID hrw701060496.h1

Method BLASTN
NCBI GI g169980
BLAST score 56
E value 7.0e-23
Match length 181
% identity 87

NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds

Seq. No. 45360

Seq. ID hrw701060534.hl

Method BLASTX
NCBI GI g3461846
BLAST score 313
E value 3.0e-29
Match length 81
% identity 33

NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis

thaliana]

Seq. No. 45361

Seq. ID hrw701060593.h1

Method BLASTN
NCBI GI 9475597
BLAST score 139
E value 2.0e-72
Match length 191
% identity 98

NCBI Description Glycine max Century 84 BiP isoform C mRNA, partial cds

Seq. No. 45362

Seq. ID hrw701060607.h1

Method BLASTX
NCBI GI g2130133
BLAST score 155
E value 1.0e-10
Match length 32
% identity 88

NCBI Description heat shock factor (clone hsfa) - maize (fragment)

Seq. No. 45363

Seq. ID hrw701060684.hl

Method BLASTN
NCBI GI 9473604
BLAST score 55
E value 3.0e-22
Match length 67
% identity 96

NCBI Description Zea mays W-22 histone H2B mRNA, complete cds



Seq. No. 45364 hrw701060719.h1 Seq. ID Method BLASTX NCBI GI g4544431 BLAST score 219 E value 4.0e-18 Match length 84 60 % identity (AC006955) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 45365 Seq. ID hrw701060761.h1 Method BLASTN NCBI GI q18651 BLAST score 66 7.0e-29 E value Match length 206 % identity 88 Soybean gene for heat shock protein Gmhsp17.9-D (class VI) NCBI Description 45366 Seq. No. hrw701060764.h1 Seq. ID Method BLASTN NCBI GI q170089 87 BLAST score E value 2.0e-41 Match length 183 87 % identity NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds Seq. No. 45367 hrw701060775.h1 Seq. ID Method BLASTX NCBI GI g1174162 BLAST score 296 E value 3.0e-27 56 Match length 93 % identity (U44976) ubiquitin-conjugating enzyme [Arabidopsis NCBI Description thaliana] >gi 3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana] 45368 Seq. No. hrw701060808.hl Seq. ID BLASTN Method NCBI GI g1061039 40 BLAST score 3.0e-13 E value 44 Match length 98 % identity NCBI Description A.thaliana mRNA for sterol-C-methyltransferase

Seq. No. 45369

Seq. ID hrw701060850.h1

Method BLASTN
NCBI GI g170091
BLAST score 177



E value 5.0e-95 Match length 272 % identity 95

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 45370

Seq. ID hrw701060859.h1

Method BLASTN
NCBI GI g296444
BLAST score 215
E value 1.0e-118
Match length 250
% identity 98

NCBI Description G.max ADR6 mRNA

Seq. No. 45371

Seq. ID hrw701060884.hl

Method BLASTX
NCBI GI g1360090
BLAST score 189
E value 1.0e-14
Match length 84
% identity 36

NCBI Description (X95576) C1C-Nt1 [Nicotiana tabacum]

Seq. No. 45372

Seq. ID hrw701060891.h1

Method BLASTN
NCBI GI g170091
BLAST score 142
E value 3.0e-74
Match length 226
% identity 94

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 45373

Seq. ID hrw701060905.h1

Method BLASTN
NCBI GI g2661127
BLAST score 74
E value 1.0e-33
Match length 245
% identity 91

NCBI Description Glycine max arginase (pAG1) mRNA, complete cds

Seq. No. 45374

Seq. ID hrw701060925.h1

Method BLASTX
NCBI GI g2507281
BLAST score 137
E value 5.0e-13
Match length 57
% identity 70

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_

(X97380) atran2 [Arabidopsis thaliana]



```
45375
Seq. No.
                  hrw701060947.hl
Seq. ID
                  BLASTN
Method
                  g1435059
NCBI GI
BLAST score
                  143
E value
                  7.0e-75
                  162
Match length
                  97
% identity
NCBI Description Soybean mRNA for cytochrome P450 (CYP93A1), complete cds
                  45376
Seq. No.
                  hrw701060963.h1
Seq. ID
                  BLASTN
Method
                  g296444
NCBI GI
                  239
BLAST score
                  1.0e-132
E value
                  239
Match length
                  100
% identity
NCBI Description G.max ADR6 mRNA
                  45377
Seq. No.
Seq. ID
                  hrw701060976.hl
                  BLASTX
Method
                  q1170659
NCBI GI
                  141
BLAST score
                  4.0e-09
E value
Match length
                  56
                  45
% identity
NCBI Description KINESIN-LIKE PROTEIN KIF4 >gi 1083417 pir_A54803
                  microtubule-associated motor KIF4 - mouse
                  >gi_563773_dbj_BAA02167_ (D12646) KIF4 [Mus musculus]
Seq. No.
                  45378
                  hrw701060995.h1
Seq. ID
                  BLASTN
Method
                  g296444
NCBI GI
BLAST score
                  231
                  1.0e-127
E value
                  235
Match length
                  100
% identity
NCBI Description G.max ADR6 mRNA
Seq. No.
                   45379
Seq. ID
                   hrw701061006.h1
                  BLASTN
Method
                   q2463568
NCBI GI
BLAST score
                   77
E value
                   2.0e-35
                   81
Match length
% identity
NCBI Description Glycine max mRNA for squalene synthase, complete cds
```

Seq. No. 45380

Seq. ID hrw701061091.h1

Method BLASTN NCBI GI g1902893



BLAST score 95 E value 3.0e-46 Match length 235 % identity 85

NCBI Description Solanum melongena mRNA for QM family protein, complete cds

Seq. No. 45381

Seq. ID hrw701061118.hl

Method BLASTN
NCBI GI g533691
BLAST score 79
E value 1.0e-36
Match length 83
% identity 99

NCBI Description Glycine max Essex protease inhibitor mRNA, complete cds

Seq. No.

Seq. ID hrw701061120.h1

45382

Method BLASTX
NCBI GI g4510362
BLAST score 260
E value 6.0e-23
Match length 90

% identity 54 NCBI Description (AC007017) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45383

Seq. ID hrw701061133.h1

Method BLASTX
NCBI GI g3201554
BLAST score 388
E value 6.0e-38
Match length 91
% identity 77

NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 45384

Seq. ID hrw701061167.h1

Method BLASTN
NCBI GI g170089
BLAST score 189
E value 1.0e-102
Match length 253
% identity 94

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds

Seq. No. 45385

Seq. ID hrw701061195.h1

Method BLASTN
NCBI GI g296444
BLAST score 250
E value 1.0e-138
Match length 261
% identity 99

NCBI Description G.max ADR6 mRNA

Seq. No. 45386



hrw701061216.h1 Seq. ID BLASTN Method g4115336 NCBI GI 85 BLAST score 2.0e-40 E value Match length 137 % identity 19 NCBI Description Pisum sativum (Alaska) ubiquitin (PUB3) gene, complete cds 45387 Seq. No. hrw701061255.hl Seq. ID BLASTX Method g4510381 NCBI GI 142 BLAST score 2.0e-09 E value Match length 45 % identity NCBI Description (AC007017) unknown protein [Arabidopsis thaliana] 45388 Seq. No. hrw701061313.hl Seq. ID BLASTN Method q1183936 NCBI GI 42 BLAST score 1.0e-14 E value 73 Match length 91 % identity NCBI Description P.sativum 5S rRNA gene 45389 Seq. No. hrw701061375.hl Seq. ID BLASTN Method NCBI GI q2317899 BLAST score 246 1.0e-136 E value Match length 269 % identity 98 NCBI Description Glycine max Sali3-2 mRNA, complete cds 45390 Seq. No. hrw701061407.h1 Seq. ID Method BLASTX NCBI GI g3355474 BLAST score 227 5.0e-19 E value Match length 81 % identity 54 NCBI Description (AC004218) unknown protein [Arabidopsis thaliana] 45391 Seq. No. hrw701061414.h1 Seq. ID BLASTN Method NCBI GI g217902 75 BLAST score 3.0e-34 E value

7277

235

83

Match length

% identity



NCBI Description Catharanthus roseus cyc07 mRNA, complete cds

Seq. No. 45392

Seq. ID hrw701061442.hl

Method BLASTN
NCBI GI g169157
BLAST score 138
E value 8.0e-72
Match length 266
% identity 88

NCBI Description Pisum sativum serine hydroxymethyltransferase mRNA,

complete cds

Seq. No. 45393

Seq. ID hrw701061471.hl

Method BLASTN
NCBI GI g18761
BLAST score 51
E value 7.0e-20
Match length 174
% identity 87

NCBI Description Soybean stem mRNA for 31 kD glycoprotein

Seq. No. 45394

Seq. ID hrw701061561.h1

Method BLASTN
NCBI GI g3047074
BLAST score 53
E value 4.0e-21
Match length 241
% identity 80

NCBI Description Arabidopsis thaliana BAC F21E10

Seq. No. 45395

Seq. ID hrw701061581.hl

Method BLASTX
NCBI GI g4567310
BLAST score 199
E value 1.0e-15
Match length 83
% identity 52

NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 45396

Seq. ID hrw701061642.h1

Method BLASTN
NCBI GI g18695
BLAST score 43
E value 4.0e-15
Match length 83
% identity 88

NCBI Description Soybean nodulin 22 gene

Seq. No. 45397

Seq. ID hrw701061661.h1

Method BLASTX NCBI GI g3298540



```
BLAST score
                   7.0e-24
E value
                   61
Match length
                   80
% identity
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
Seq. No.
                   45398
Seq. ID
                   hrw701061671.h1
                   BLASTN
Method
                   g441205
NCBI GI
                   70
BLAST score
                   2.0e-31
E value
                   134
Match length
                   88
% identity
NCBI Description Soybean lox1gm4 gene encoding lipxygenase L-4
                   45399
Seq. No.
                   hrw701061673.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1163180
                   85
BLAST score
                   2.0e-40
E value
                   141
Match length
                   91
% identity
NCBI Description Glycine max arginine decarboxylase mRNA, complete cds
                    45400
Seq. No.
Seq. ID
                   hrw701061683.h1
                   BLASTX
Method
                    q3914303
NCBI GI
BLAST score
                    140
                    7.0e-09
E value
                    83
Match length
% identity
                    39
                   PEROXISOMAL ASSEMBLY PROTEIN PEX3 (PEROXIN-3)
NCBI Description
                    >gi 3336882_emb_CAA04879_ (AJ001625) Pex3 protein [Homo
                    sapiens] >gi 4092648 emb CAA10362 (AJ131389) PEX3 protein
                    [Homo sapiens] >gi_4\overline{2}184\overline{2}6_{emb}CA\overline{A}08904_{A}(AJ009866) Pex3p
                    [Homo sapiens] >gi_4505727_ref_NP_00362\overline{1}.1_pPEX3_
                    peroxisomal biogenesis factor
                    45401
Seq. No.
Seq. ID
                    hrw701061720.hl
Method
                    BLASTX
                    q4455171
NCBI GI
BLAST score
                    159
                    3.0e-11
E value
                    59
Match length
 % identity
                   (AL035521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    45402
 Seq. No.
 Seq. ID
                    hrw701061834.hl
```

Method BLASTN
NCBI GI g434344
BLAST score 52
E value 1.0e-20



Match length 141 % identity 89

NCBI Description A.thaliana (Columbia) mRNA for S18 ribosomal protein

(641bp)

Seq. No. 45403

Seq. ID hrw701061845.h1

Method BLASTX
NCBI GI g3643607
BLAST score 278
E value 3.0e-25
Match length 58
% identity 86

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 45404

Seq. ID hrw701061859.h1

Method BLASTN
NCBI GI g1498052
BLAST score 62
E value 1.0e-26

Match length 138 % identity 86

NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds

Seq. No. 45405

Seq. ID hrw701061862.h1

Method BLASTN
NCBI GI g1173641
BLAST score 107
E value 2.0e-53
Match length 123
% identity 98

NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds

Seq. No. 45406

Seq. ID hrw701061893.h1

Method BLASTN
NCBI GI g170071
BLAST score 234
E value 1.0e-129
Match length 238
% identity 100

NCBI Description Soybean calmodulin (SCaM-2) mRNA, complete cds

Seq. No. 45407

Seq. ID hrw701061950.h1

Method BLASTN
NCBI GI g310575
BLAST score 97
E value 2.0e-47
Match length 199
% identity 91

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 45408

Seq. ID hrw701061962.h1



Method BLASTX
NCBI GI g3176710
BLAST score 136
E value 1.0e-08
Match length 50
% identity 52
NCBI Description (AC00239

NCBI Description (AC002392) unknown protein [Arabidopsis thaliana]

Seq. No. 45409

Seq. ID hrw701061985.hl

Method BLASTN
NCBI GI g18651
BLAST score 188
E value 1.0e-102
Match length 208
% identity 98

NCBI Description Soybean gene for heat shock protein Gmhsp17.9-D (class VI)

Seq. No. 45410

Seq. ID hrw701062087.h1

Method BLASTX
NCBI GI g4510403
BLAST score 139
E value 2.0e-14
Match length 64
% identity 69

NCBI Description (AC006587) putative DNA repair protein [Arabidopsis

thaliana]

Seq. No. 45411

Seq. ID hrw701062125.h1

Method BLASTX
NCBI GI g1617036
BLAST score 155
E value 1.0e-10
Match length 52
% identity 65

NCBI Description (Y08624) Ted2 [Vigna unguiculata]

Seq. No. 45412

Seq. ID hrw701062126.hl

Method BLASTX
NCBI GI g4191791
BLAST score 272
E value 2.0e-24
Match length 88
% identity 56

NCBI Description (AC005917) putative sf21 {Helianthus annuus} protein

[Arabidopsis thaliana]

Seq. No. 45413

Seq. ID hrw701062285.h1

Method BLASTN
NCBI GI g170091
BLAST score 209
E value 1.0e-114
Match length 268

% identity



```
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                  45414
Seq. No.
                  hrw701062335.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2959324
                  391
BLAST score
                  2.0e-38
E value
                  81
Match length
                  88
% identity
NCBI Description (Y15224) Importin alpha-like protein [Arabidopsis thaliana]
                  45415
Seq. No.
                  hrw701062338.h1
Seq. ID
                  BLASTX
Method
                   q3242728
NCBI GI
                  152
BLAST score
                   2.0e-10
E value
                   57
Match length
                   53
% identity
NCBI Description (AC003040) unknown protein [Arabidopsis thaliana]
Seq. No.
                   45416
                   hrw701062352.h1
Seq. ID
                   BLASTX
Method
                   g1723271
NCBI GI
                   112
BLAST score
                   1.0e-08
E value
                   62
Match length
                   51
% identity
                   PUTATIVE ATP-DEPENDENT RNA HELICASE C13F4.11C
NCBI Description
                   >gi_2130219_pir__S67386 hypothetical protein - fission
                   yeast (Schizosaccharomyces pombe) >gi_3451298_emb_CAA20430_
                   (AL031322) putative atp-dependent rna helicase
                   [Schizosaccharomyces pombe]
                   45417
Seq. No.
                   hrw701062378.h1
Seq. ID
                   BLASTN
Method
                   g4204858
NCBI GI
                   73
BLAST score
                   5.0e-33
E value
                   176
Match length
 % identity
                   86
NCBI Description Triticum aestivum heat shock protein 80 mRNA, complete cds
                   45418
 Seq. No.
                   hrw701062414.hl
 Seq. ID
                   BLASTX
 Method
                   g3176098
 NCBI GI
                   239
 BLAST score
                   7.0e-26
 E value
                   84
 Match length
```

NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No.

Seq. ID



```
45419
Seq. No.
                  hrw701062484.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  355
                  2.0e-34
E value
                  86
Match length
                  80
% identity
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  45420
Seq. No.
                  hrw701062553.hl
Seq. ID
                  BLASTX
Method
                  g4138581
NCBI GI
BLAST score
                  311
                  7.0e-29
E value
                  87
Match length
                  71
% identity
                   (X98474) mitochondrial energy transfer protein [Solanum
NCBI Description
                  tuberosum]
                   45421
Seq. No.
                  hrw701062574.h1
Seq. ID
Method
                  BLASTN
                  g3860320
NCBI GI
BLAST score
                   112
                   3.0e-56
E value
                   240
Match length
                   87
% identity
                  Cicer arietinum mRNA for beta-galactosidase, clone
NCBI Description
                   CanBGal-5
                   45422
Seq. No.
                   hrw701062577.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q16508
BLAST score
                   98
                   6.0e-48
E value
Match length
                   150
                   91
% identity
                   A.thaliana DNA for S-adenosylmethionine synthetase gene
NCBI Description
                   sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana
                   S-adenosylmethionine synthetase gene, complete cds
                   45423
Seq. No.
Seq. ID
                   hrw701062646.hl
Method
                   BLASTN
NCBI GI
                   q3378649
BLAST score
                   80
                   3.0e-37
E value
Match length
                   160
                   88
% identity
                  M.sativa mRNA translated from abscisic activated gene
NCBI Description
```

hrw701062693.h1



Method BLASTX
NCBI GI g2347088
BLAST score 172
E value 1.0e-12
Match length 67
% identity 55

NCBI Description (U72765) non-specific lipid transfer protein PvLTP-24

[Phaseolus vulgaris]

Seq. No. 45425

Seq. ID hrw701062717.h1

Method BLASTX
NCBI GI g571484
BLAST score 141
E value 3.0e-09
Match length 49
% identity 55

NCBI Description (U16727) peroxidase precursor [Medicago truncatula]

Seq. No. 45426

Seq. ID hrw701062850.h1

Method BLASTN
NCBI GI g479144
BLAST score 84
E value 1.0e-39
Match length 184
% identity 87

NCBI Description G.max mRNA for ATP synthase subunit

Seq. No. 45427

Seq. ID hrw701062912.h1

Method BLASTX
NCBI GI g1495259
BLAST score 329
E value 5.0e-31
Match length 84
% identity 75

NCBI Description (X97826) orf04 [Arabidopsis thaliana]

Seq. No. 45428

Seq. ID hrw701062936.h1

Method BLASTN
NCBI GI g533691
BLAST score 122
E value 3.0e-62
Match length 140
% identity 98

NCBI Description Glycine max Essex protease inhibitor mRNA, complete cds

Seq. No. 45429

Seq. ID hrw701062937.h1

Method BLASTN
NCBI GI g2905773
BLAST score 120
E value 4.0e-61
Match length 174
% identity 98



NCBI Description Glycine max putative channel protein 1 (SPCP1) mRNA, partial cds

Seq. No. 45430

Seq. ID hrw701063006.h1

Method BLASTN
NCBI GI g3241925
BLAST score 35
E value 2.0e-10
Match length 155
% identity 87

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOK9, complete sequence [Arabidopsis thaliana]

Seq. No. 45431

Seq. ID hrw701063011.hl

Method BLASTX
NCBI GI g3559816
BLAST score 150
E value 5.0e-10
Match length 42
% identity 74

NCBI Description (Y15782) transketolase 2 [Capsicum annuum]

Seq. No. 45432

Seq. ID hrw701063032.h1

Method BLASTX
NCBI GI g4572671
BLAST score 166
E value 7.0e-12
Match length 88
% identity 40

NCBI Description (AC006954) putative cyclic nucleotide regulated ion channel

[Arabidopsis thaliana]

Seq. No. 45433

Seq. ID hrw701063057.h1

Method BLASTN
NCBI GI g1518539
BLAST score 78
E value 4.0e-36
Match length 125
% identity 91

NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds

Seq. No. 45434

Seq. ID hrw701063105.h1

Method BLASTX
NCBI GI g1052973
BLAST score 352
E value 1.0e-33
Match length 88
% identity 80

NCBI Description (U37838) fructokinase [Beta vulgaris]

Seq. No. 45435

Seq. ID hrw701063155.h1



```
Method
                  BLASTX
NCBI GI
                  g3242721
BLAST score
                  230
E value
                  2.0e-19
Match length
                  85
% identity
                  53
NCBI Description
                  (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
                  thalianal
                  45436
Seq. No.
Seq. ID
                  hrw701063184.h1
Method
                  BLASTN
NCBI GI
                  g256142
BLAST score
                  248
E value
                  1.0e-137
Match length
                  252
% identity
                  100
NCBI Description
                 cytosolic glutamine synthetase [Glycine max=soybeans, var
                  Prize, mRNA, 1450 nt]
                  45437
Seq. No.
Seq. ID
                  hrw701063186.hl
Method
                  BLASTX
NCBI GI
                  g2842490
BLAST score
                  137
E value
                  1.0e-08
Match length
                  36
% identity
                  69
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  45438
Seq. ID
                  hrw701063270.h1
Method
                  BLASTX
NCBI GI
                  g2565436
BLAST score
                  194
E value
                  4.0e-15
Match length
                  92
% identity
                  46
NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana]
Seq. No.
                  45439
Seq. ID
                  hrw701063280.h1
Method
                  BLASTX
NCBI GI
                  g2194121
BLAST score
                  206
E value
                  1.0e-16
Match length
                  85
% identity
                  46
                  (AC002062) Strong similarity to Arabidopsis cyclin delta-1
NCBI Description
                  (gb_ATCD1). EST gb ATTS4338 comes from this gene.
```

[Arabidopsis thaliana]

Seq. No. 45440

Seq. ID hrw701063281.h1

Method BLASTX NCBI GI g461736 BLAST score 314



E value 3.0e-29

Match length 78 % identity 79

NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR

>gi_478786_pir__S29316 chaperonin 60 - cucurbit

>gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita

sp.]

Seq. No. 45441

Seq. ID hrw701063295.h1

Method BLASTX
NCBI GI g3688188
BLAST score 339
E value 3.0e-32
Match length 90
% identity 71

NCBI Description (AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis

thaliana]

Seq. No. 45442

Seq. ID hrw701063302.h1

Method BLASTN
NCBI GI g4566613
BLAST score 46
E value 7.0e-17
Match length 122
% identity 84

NCBI Description Populus alba x Populus tremula actin depolymerizing factor

mRNA, partial cds

Seq. No. 45443

Seq. ID hrw701063319.h1

Method BLASTX
NCBI GI g4335731
BLAST score 233
E value 9.0e-20
Match length 86
% identity 56

NCBI Description (AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No. 45444

Seq. ID hrw701063321.h1

Method BLASTN
NCBI GI g20061
BLAST score 79
E value 1.0e-36
Match length 151
% identity 88

NCBI Description Oenothera elata subsp. hookeri mRNA for protein kinase C

inhibitor homologue

Seq. No. 45445

Seq. ID hrw701063345.h1

Method BLASTX
NCBI GI g3337367
BLAST score 145
E value 2.0e-09



Match length 72 % identity 47

NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45446

Seq. ID hrw701063361.h1

Method BLASTX
NCBI GI g2642157
BLAST score 378
E value 9.0e-37
Match length 90
% identity 73

NCBI Description (AC003000) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 45447

Seq. ID hrw701063390.h1

Method BLASTX
NCBI GI g2317908
BLAST score 317
E value 1.0e-29
Match length 84
% identity 74

NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]

Seq. No. 45448

Seq. ID hrw701063442.h1

Method BLASTX
NCBI GI g3135263
BLAST score 170
E value 3.0e-12
Match length 74
% identity 50

NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45449

Seq. ID hrw701063454.h1

Method BLASTX
NCBI GI g1707018
BLAST score 261
E value 6.0e-23
Match length 67
% identity 76

NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]

Seq. No. 45450

Seq. ID hrw701063465.h1

Method BLASTN
NCBI GI g3107930
BLAST score 107
E value 3.0e-53
Match length 248
% identity 88

NCBI Description Pyrus pyrifolia mRNA for UDP-glucose pyrophosphorylase,

complete cds

Seq. No. 45451

Seq. ID hrw701063485.h1

% identity

NCBI Description

55



```
Method
                   BLASTX
NCBI GI
                   g1546706
BLAST score
                   237
E value
                   4.0e-20
Match length
                   55
% identity
                   78
NCBI Description
                  (X98855) peroxidase ATP8a [Arabidopsis thaliana]
Seq. No.
                   45452
Seq. ID
                   hrw701063494.h1
Method
                   BLASTX
NCBI GI
                   q1155090
BLAST score
                   222
E value
                   2.0e-18
Match length
                   65
% identity
                   60
NCBI Description
                  (X94986) beta glucosidase [Manihot esculenta]
Seq. No.
                   45453
Seq. ID
                   hrw701063527.h1
Method
                   BLASTN
NCBI GI
                   q18764
BLAST score
                   134
E value
                   2.0e-69
Match length
                   202
                   92
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                   45454
Seq. ID
                   hrw701063535.h1
Method
                   BLASTN
NCBI GI
                   q4204760
BLAST score
                   49
E value
                   1.0e-18
Match length
                   151
% identity
                   88
NCBI Description Glycine max peroxidase precursor (sEPa2) mRNA, partial cds
Seq. No.
                   45455
Seq. ID
                   hrw701063573.h1
Method
                   BLASTN
NCBI GI
                   g515691
BLAST score
                   107
E value
                   2.0e-53
Match length
                   167
% identity
                   91
NCBI Description Glycine max Forrest beta-tubulin (tubB3) mRNA, partial cds
Seq. No.
                   45456
Seq. ID
                   hrw701063574.h1
Method
                   BLASTX
NCBI GI
                   g1184123
BLAST score
                   142
E value
                   4.0e-10
Match length
                   71
```

(U20809) auxin-induced protein [Vigna radiata]



Seq. No. 45457

Seq. ID hrw701063579.h1

Method BLASTN
NCBI GI g169984
BLAST score 56
E value 7.0e-23
Match length 166
% identity 87

NCBI Description Soybean (Glycine max) low MW heat shock protein gene

(Gmhsp17.6-L)

Seq. No. 45458

Seq. ID hrw701063618.h1

Method BLASTX
NCBI GI g3176690
BLAST score 173
E value 6.0e-13
Match length 56
% identity 41

NCBI Description (AC003671) Similar to ubiquitin ligase gb_D63905 from S.

cerevisiae. EST gb_R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 45459

Seq. ID hrw701063634.h1

Method BLASTN
NCBI GI g170091
BLAST score 40
E value 1.0e-13
Match length 52
% identity 94

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 45460

Seq. ID hrw701063636.h1

Method BLASTN
NCBI GI g558542
BLAST score 108
E value 4.0e-54
Match length 189
% identity 99

NCBI Description G.max (Evans) mRNA for zinc-finger protein (C-terminal)

Seq. No. 45461

Seq. ID hyd700724942.h1

Method BLASTN
NCBI GI g3142328
BLAST score 68
E value 5.0e-30

Match length 185 % identity 93

NCBI Description Glycine max partial SIRE-1 sequence ribonuclease H and

envelope-like genes, partial cds, and long terminal repeat,

complete sequence



```
Seq. No.
                   45462
Seq. ID
                   hyd700725047.h1
Method
                   BLASTX
NCBI GI
                   g2209358
BLAST score
                   384
E value
                   2.0e-37
Match length
                   85
% identity
                   79
NCBI Description
                  (AF004812) beta-D-galactosidase [Mangifera indica]
Seq. No.
                   45463
Seq. ID
                   hyd700725069.h1
Method
                   BLASTX
NCBI GI
                   g4406820
BLAST score
                   329
E value
                   3.0e-31
Match length
                   82
% identity
                   78
                   (AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                   thalianal
Seq. No.
                   45464
Seq. ID
                   hyd700725163.h1
Method
                   BLASTX
NCBI GI
                   g2660669
BLAST score
                   138
E value
                   7.0e-09
Match length
                   67
% identity
                   51
                   (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   45465
Seq. ID
                   hyd700725212.h1
Method
                   BLASTX
NCBI GI
                   g2583128
BLAST score
                   205
E value
                   1.0e-16
Match length
                   80
                   49
% identity
NCBI Description
                  (AC002387) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   45466
Seq. ID
                  hyd700725318.h1
Method
                  BLASTN
                  g3426033
                   64
                  1.0e-27
                  164
                  85
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F12C2O genomic
```

NCBI GI BLAST score

E value Match length % identity

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 45467

Seq. ID hyd700725328.h1

Method BLASTX NCBI GI g3687230

Match length

NCBI Description

% identity

37

68



```
BLAST score
E value
                   9.0e-09
Match length
                   32
% identity
                   84
NCBI Description
                  (AC005169) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   45468
Seq. ID
                   hyd700725350.h1
Method
                   BLASTX
NCBI GI
                   g2244805
BLAST score
                   208
E value
                   5.0e-17
Match length
                   66
% identity
                   52
NCBI Description
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   45469
Seq. ID
                   hyd700725488.h1
Method
                   BLASTX
NCBI GI
                   q4006827
BLAST score
                   379
E value
                   7.0e-37
Match length
                   88
% identity
                   82
NCBI Description
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                   45470
Seq. ID
                   hyd700725537.h1
Method
                   BLASTX
NCBI GI
                   g2911053
BLAST score
                   111
E value
                   1.0e-08
Match length
                   42
% identity
                   76
NCBI Description
                  (AL021961) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   45471
Seq. ID
                  hyd700725669.h1
Method
                  BLASTX
NCBI GI
                  g4490746
BLAST score
                  154
E value
                   2.0e-10
Match length
                  50
% identity
                  52
NCBI Description
                  (AL035708) cytochrome P450-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  45472
Seq. ID
                  hyd700725734.h1
Method
                  BLASTX
                  g4508070
NCBI GI
BLAST score
                  143
E value
                  3.0e-09
```

(AC005882) 24349 [Arabidopsis thaliana]

Match length

NCBI Description

% identity

43

81



```
Seq. No.
                   45473
Seq. ID
                   hyd700725757.h1
Method
                   BLASTX
                   g3033377
NCBI GI
BLAST score
                   253
E value
                   4.0e-22
Match length
                   79
% identity
                   59
NCBI Description
                  (AC004238) putative berberine bridge enzyme [Arabidopsis
                   thaliana]
                   45474
Seq. No.
Seq. ID
                   hyd700725791.h1
Method
                  BLASTX
NCBI GI
                   g2493046
BLAST score
                  163
E value
                  1.0e-11
Match length
                  59
% identity
                  53
NCBI Description
                  ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi 82297 pir A41740 H+-transporting ATP synthase (EC
                   3.6.1.34) delta' chain precursor - sweet potato
                   >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                   delta subunit [Ipomoea batatas]
Seq. No.
                  45475
Seq. ID
                  hyd700725819.h1
Method
                  BLASTX
NCBI GI
                  g3080412
BLAST score
                  146
E value
                  8.0e-10
Match length
                  52
% identity
                  56
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  45476
Seq. ID
                  hyd700725839.h1
Method
                  BLASTX
NCBI GI
                  q4454463
BLAST score
                  168
E value
                  2.0e-12
Match length
                  43
% identity
                  74
NCBI Description
                  (AC006234) putative leucine rich protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  45477
Seq. ID
                  hyd700725891.h1
Method
                  BLASTX
NCBI GI
                  g2494113
BLAST score
                  227
E value
                  2.0e-19
```

7293

from this gene. [Arabidopsis thaliana]

(AC002376) Strong similarity to Musa pectate lyase

(gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come

NCBI GI

BLAST score

```
Seq. No.
                   45478
Seq. ID
                   hyd700726002.h1
Method
                   BLASTX
NCBI GI
                   g2827663
BLAST score
                   143
E value
                   3.0e-09
Match length
                   86
% identity
NCBI Description
                   (AL021637) membrane-associated salt-inducible-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   45479
Seq. ID
                   hyd700726019.h1
Method
                   BLASTN
NCBI GI
                   q2765444
BLAST score
                   168
E value
                   9.0e-90
Match length
                   249
% identity
                   100
NCBI Description Glycine max mRNA for ferredoxin thioredoxin reductase
Seq. No.
                   45480
Seq. ID
                   hyd700726028.h1
Method
                   BLASTX
NCBI GI
                   g2864625
BLAST score
                   414
E value
                   5.0e-41
Match length
                   87
% identity
                   94
NCBI Description
                  (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   45481
Seq. ID
                   hyd700726062.h1
Method
                   BLASTX
NCBI GI
                   g2464864
BLAST score
                   161
E value
                   2.0e-11
Match length
                   77
% identity
                   27
NCBI Description
                  (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   45482
Seq. ID
                  hyd700726090.h1
Method
                  BLASTX
NCBI GI
                   g4160292
BLAST score
                   377
E value
                   1.0e-36
Match length
                  81
% identity
                  81
NCBI Description
                  (Y18209) alpha-N-acetylglucosaminidase [Nicotiana tabacum]
Seq. No.
                  45483
Seq. ID
                  hyd700726094.h1
Method
                  BLASTX
```

g2245077

256



```
E value
                   2.0e-22
Match length
                  81
% identity
                  60
NCBI Description (Z97343) glucanase homolog [Arabidopsis thaliana]
                  45484
Seq. No.
                  hyd700726141.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g807698
BLAST score
                  146
E value
                  1.0e-09
Match length
                  53
% identity
                  49
NCBI Description (D32206) prepro-cucumisin [Cucumis melo]
Seq. No.
                  45485
                  hyd700726152.h1
                  BLASTN
                  g1183936
                  68
```

Seq. ID Method NCBI GI BLAST score E value 4.0e-30 Match length 119

% identity 90 NCBI Description P.sativum 5S rRNA gene

Seq. No. 45486

Seq. ID hyd700726177.h1

Method BLASTX NCBI GI q3360289 BLAST score 255 E value 2.0e-22 Match length 68 % identity 71

NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase

1 [Zea mays]

Seq. No. 45487

Seq. ID hyd700726285.h1

Method BLASTX NCBI GI g2317905 BLAST score 179 E value 2.0e-13 Match length 41 % identity 83

NCBI Description (U89959) bZIP-like protein [Arabidopsis thaliana]

Seq. No. 45488

Seq. ID hyd700726306.h1 Method

BLASTX NCBI GI g3372671 BLAST score 262 E value 3.0e-23 Match length 86 % identity 60

NCBI Description (AF061286) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No. 45489

7295



```
Seq. ID
                   hyd700726346.h1
Method
                   BLASTX
NCBI GI
                   q4262228
BLAST score
                   388
E value
                   6.0e-38
Match length
                   90
% identity
                   81
NCBI Description
                   (AC006200) putative receptor protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   45490
                  hyd700726372.h1
Method
                  BLASTN
```

Seq. ID

NCBI GI g217902 BLAST score 36 E value 4.0e-11 Match length 100 % identity 84

NCBI Description Catharanthus roseus cyc07 mRNA, complete cds

Seq. No.

45491

Seq. ID hyd700726393.h1

Method BLASTX NCBI GI g2826900 BLAST score 291 E value 1.0e-26 Match length 87 % identity 68

NCBI Description (AB004461) DNA polymerase alpha catalytic subunit [Oryza

sativa]

Seq. No. 45492

Seq. ID hyd700726406.h1

Method BLASTX NCBI GI g4567286 BLAST score 193 2.0e-31 E value Match length 87 % identity 82

(AC006841) putative coatomer alpha subunit [Arabidopsis NCBI Description

thaliana]

Seq. No. 45493

Seq. ID hyd700726414.h1

Method BLASTX NCBI GI g3377800 BLAST score 216 E value 2.0e-33 Match length 88 % identity 77

NCBI Description (AF075597) similar to glycosyl hydrolases family 9

(PFam:glycosyl_hydro5.hmm, score: 100.70) [Arabidopsis

thalianal

Seq. No. 45494

Seq. ID hyd700726522.h1

Method BLASTX



NCBI GI g2829903 BLAST score 246 E value 2.0e-21 Match length 51 % identity 92

NCBI Description (AC002311) unknown protein [Arabidopsis thaliana]

Seq. No. 45495

Seq. ID hyd700726612.h1

Method BLASTN
NCBI GI g3063391
BLAST score 33
E value 2.0e-09
Match length 89
% identity 85

NCBI Description Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds

Seq. No. 45496

Seq. ID hyd700726642.h1

Method BLASTX
NCBI GI g2351566
BLAST score 210
E value 3.0e-17
Match length 74
% identity 50

NCBI Description (U76003) carboxypeptidase [Metarhizium anisopliae]

Seq. No. 45497

Seq. ID hyd700726644.h1

Method BLASTN
NCBI GI g1053046
BLAST score 67
E value 1.0e-29
Match length 186
% identity 96

NCBI Description Glycine max histone H3 gene, partial cds, clone S2

Seq. No. 45498

Seq. ID hyd700726661.h1

Method BLASTX
NCBI GI g4567278
BLAST score 339
E value 3.0e-32
Match length 76
% identity 82

NCBI Description (AC006841) putative anthracycline associated resistance ARX

protein [Arabidopsis thaliana]

Seq. No. 45499

Seq. ID hyd700726714.h1

Method BLASTX
NCBI GI g2979542
BLAST score 417
E value 3.0e-41
Match length 93
% identity 78

NCBI Description (AC003680) putative Ser/Thr kinase [Arabidopsis thaliana]



Seq. No. 45500
Seq. ID hyd70

hyd700726758.h1

Method BLASTX
NCBI GI g3540199
BLAST score 222
E value 2.0e-18
Match length 75
% identity 53

NCBI Description (AC004260) Putative monosaccharide transport protein

[Arabidopsis thaliana]

Seq. No. 45501

Seq. ID hyd700726770.h1

Method BLASTX
NCBI GI g2586127
BLAST score 215
E value 1.0e-17
Match length 75
% identity 59

NCBI Description (U89510) b-keto acyl reductase [Hordeum vulgare]

Seq. No.

Seq. ID hyd700726925.h1

45502

45503

Method BLASTN
NCBI GI g1236948
BLAST score 172
E value 4.0e-92
Match length 231
% identity 94

NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds

Seq. No.

Seq. ID hyd700727017.h1

Method BLASTX
NCBI GI g2341032
BLAST score 158
E value 4.0e-11
Match length 33
% identity 82

NCBI Description (AC000104) EST gb ATTS0956 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 45504

Seq. ID hyd700727041.h1

Method BLASTX
NCBI GI g3928090
BLAST score 161
E value 2.0e-11
Match length 80
% identity 42

NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana]

Seq. No. 45505

Seq. ID hyd700727059.h1

Method BLASTX NCBI GI g2760324



BLAST score 213 E value 2.0e-17 Match length 83 % identity 66

NCBI Description (AC002130) F1N21.9 [Arabidopsis thaliana]

Seq. No. 45506

Seq. ID hyd700727070.h1

Method BLASTN
NCBI GI g169036
BLAST score 50
E value 3.0e-19
Match length 70
% identity 93

NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No. 45507

Seq. ID hyd700727110.h1

Method BLASTN
NCBI GI g488738
BLAST score 38
E value 2.0e-12
Match length 74
% identity 88

NCBI Description G.hirsutum (DPL 62) mRNA for ribosomal protein small

subunit 4e

Seq. No. 45508

Seq. ID hyd700727124.h1

Method BLASTX
NCBI GI g3548802
BLAST score 140
E value 4.0e-09
Match length 53
% identity 57

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi 4335769 gb AAD17446 (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 45509

Seq. ID hyd700727182.h1

Method BLASTX
NCBI GI g4432819
BLAST score 141
E value 3.0e-09
Match length 32
% identity 75

NCBI Description (AC006593) putative kinesin light chain [Arabidopsis

thaliana]

Seq. No. 45510

Seq. ID hyd700727187.h1

Method BLASTX
NCBI GI 94006888
BLAST score 146
E value 8.0e-10
Match length 38

NCBI Description



```
% identity
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                  45511
Seq. No.
                  hyd700727258.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2143220
                  185
BLAST score
                  1.0e-20
E value
                  77
Match length
                  59
% identity
                  (Y13338) cellular serine proteinase [Aspergillus fumigatus]
NCBI Description
Seq. No.
                  45512
                  hyd700727267.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173198
BLAST score
                  277
                  5.0e-25
E value
                  58
Match length
                  90
% identity
                  40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal
NCBI Description
                  protein S13.e - garden pea >gi_396639_emb_CAA80974_
                  (Z25509) ribosomal protein S13 [Pisum sativum]
Seq. No.
                  45513
                  hyd700727294.h1
Seq. ID
Method
                  BLASTX
                  g479805
NCBI GI
BLAST score
                  165
                  5.0e-12
E value
Match length
                  39
                  77
% identity
NCBI Description
                  SNF2 protein homolog - human (fragment) >gi_292498 (M89907)
                  transcription activator [Homo sapiens]
                  45514
Seq. No.
                  hyd700727339.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4558564
BLAST score
                  192
                  5.0e-15
E value
Match length
                  74
                  62
% identity
NCBI Description
                   (AC007138) predicted protein of unknown function
                   [Arabidopsis thaliana]
                  45515
Seq. No.
Seq. ID
                  hyd700727354.h1
Method
                  BLASTX
NCBI GI
                  q4415914
BLAST score
                  150
E value
                   4.0e-10
Match length
                  77
% identity
                  44
                  (AC006282) unknown protein [Arabidopsis thaliana]
```

Seq. No.

Seq. ID Method

NCBI GI

45521

BLASTX

q2708741

hyd700727648.h1



```
45516
Seq. No.
Seq. ID
                  hyd700727361.h1
Method
                  BLASTN
NCBI GI
                  g12134
BLAST score
                  158
                  8.0e-84
E value
Match length
                  230
% identity
                  92
NCBI Description
                  Pisum sativum chloroplast psaA1 and psaA2 genes for P700
                  chlorophyll a-apoproteins (84 and 82 kD polypeptides)
                  45517
Seq. No.
Seq. ID
                  hyd700727381.h1
Method
                  BLASTX
NCBI GI
                  g3372233
BLAST score
                  153
E value
                  1.0e-10
Match length
                  56
% identity
                  54
NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
                   [Arabidopsis thaliana]
Seq. No.
                  45518
Seq. ID
                  hyd700727416.h1
Method
                  BLASTX
NCBI GI
                  g4454043
BLAST score
                  287
E value
                  4.0e-26
Match length
                  84
% identity
                  64
NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]
                  45519
Seq. No.
Seq. ID
                  hyd700727589.h1
Method
                  BLASTX
NCBI GI
                  q4097880
BLAST score
                  393
E value
                  1.0e-38
Match length
                  80
% identity
                  94
NCBI Description (U70866) polyprotein [Bean pod mottle virus]
Seq. No.
                  45520
Seq. ID
                  hyd700727609.h1
Method
                  BLASTN
NCBI GI
                  g3264758
BLAST score
                  52
                  2.0e-20
E value
                  104
Match length
                  88
% identity
NCBI Description Prunus armeniaca 40S ribosomal protein S8 (RPS8) mRNA,
                  complete cds
```



```
BLAST score
                  3.0e-36
E value
                  79
Match length
% identity
                  86
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45522
Seq. No.
                  hyd700727728.h1
Seq. ID
                  BLASTX
Method
                   q4314358
NCBI GI
BLAST score
                   177
                   3.0e-13
E value
                   68
Match length
                   51
% identity
                   (AC006340) putative kinesin heavy chain protein
NCBI Description
                   [Arabidopsis thaliana]
                   45523
Seq. No.
                   hyd700727744.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1362162
BLAST score
                   301
                   1.0e-27
E value
                   75
Match length
                   71
% identity
                  beta-glucosidase BGQ60 precursor - barley >gi_804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                   45524
Seq. ID
                   hyd700727776.h1
                   BLASTX
Method
                   g3924594
NCBI GI
BLAST score
                   254
                   3.0e-22
E value
                   56
Match length
                   30
% identity
                   (AF069442) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana] >gi_4262139_gb_AAD14439_ (AC005275) putative
                   ribonucleoprotein [Arabidopsis thaliana]
                   45525
Seq. No.
Seq. ID
                   hyd700727869.h1
Method.
                   BLASTX
NCBI GI
                   q1931641
BLAST score
                   300
                   1.0e-27
E value
                   79
Match length
                   77
% identity
                   (U95973) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45526
                   hyd700728037.hl
Seq. ID
Method
                   BLASTN
```

98 6.0e-48

q4097879

E value 6.0 Match length 201

NCBI GI

BLAST score



```
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  45527
Seq. No.
                  hyd700728048.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2618689
BLAST score
                  314
                   4.0e-32
E value
                  78
Match length
% identity
                   89
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                   45528
Seq. No.
                   hyd700728109.h1
Seq. ID
                   BLASTX
Method
                   g1402878
NCBI GI
BLAST score
                   235
                   5.0e-20
E value
                   80
Match length
                   54
% identity
                  (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                   45529
Seq. No.
                   hyd700728113.h1
Seq. ID
                   BLASTX
Method
                   g3738306
NCBI GI
                   326
BLAST score
                   9.0e-31
E value
                   80
Match length
                   82
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45530
                   hyd700728145.h1
Seq. ID
                   BLASTN
Method
                   g2343056
NCBI GI
                   220
BLAST score
                   1.0e-121
E value
                   232
Match length
                   99
 % identity
                   Rattus norvegicus organic cation transporter OCT1A mRNA,
NCBI Description
                   complete cds
                   45531
 Seq. No.
                   hyd700728193.h1
 Seq. ID
                   BLASTN
Method
                   g1872490
NCBI GI
 BLAST score
                   39
                   6.0e-13
 E value
                   88
```

Match length

% identity NCBI Description Mus musculus ion channel homolog RIC mRNA, complete cds

45532 Seq. No.

hyd700728279.hl Seq. ID

BLAST score

E value

63

2.0e-27



```
BLASTX
Method
                  q2347199
NCBI GI
BLAST score
                  346
                  4.0e-33
E value
Match length
                  82
% identity
                  80
                  (AC002338) protein kinase isolog [Arabidopsis thaliana]
NCBI Description
                  45533
Seq. No.
Seq. ID
                  hyd700728422.h1
Method
                  BLASTX
                   g1771162
NCBI GI
BLAST score
                   332
                   2.0e-31
E value
                   80
Match length
% identity
                   80
                   (X98930) SBT2 [Lycopersicon esculentum]
NCBI Description
                   >gi 3687307 emb CAA07000 (AJ006379) subtilisin-like
                  protease [Lycopersicon esculentum]
                   45534
Seq. No.
Seq. ID
                   hyd700728433.h1
                   BLASTX
Method
                   g3646340
NCBI GI
                   344
BLAST score
                   7.0e-33
E value
Match length
                   80
% identity
                  (AJ000763) MADS-box protein [Malus domestica]
NCBI Description
                   45535
Seq. No.
Seq. ID
                   hyd700728456.h1
Method
                   BLASTX
NCBI GI
                   q3047125
BLAST score
                   245
                   3.0e-21
E value
Match length
                   74
% identity
                   66
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45536
                   hyd700728520.h1
Seq. ID
Method
                   BLASTN
                   q166379
NCBI GI
                   107
BLAST score
                   3.0e-53
E value
Match length
                   167
% identity
                   71
                   Alfalfa glucose-regulated endoplasmic reticular protein
NCBI Description
                   mRNA, complete cds
Seq. No.
                   45537
                   hyd700728537.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1173641
```



Match length 95 92 % identity

NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds

Seq. No.

45538

Seq. ID hyd700728543.h1

BLASTX Method NCBI GI g3402719 BLAST score 211 3.0e-17 E value 84 Match length

50 % identity

NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.

45539

Seq. ID hyd700728590.h1

Method BLASTN NCBI GI q3021356 BLAST score 90 3.0e-43E value 241 Match length % identity

NCBI Description Cyamopsis tetragonoloba mRNA for UDP-galactose 4-epimerase,

clone GEPI48

Seq. No.

45540

hyd700728637.h1 Seq. ID

Method BLASTX NCBI GI q1053047 BLAST score 405 6.0e-40 E value Match length 82 99 % identity

(U38425) histone H3 [Glycine max] >gi 1053049 (U38426) NCBI Description

histone H3 [Glycine max] >gi 1053051 (U38427) histone H3

[Glycine max]

Seq. No. 45541

Seq. ID hyd700728670.h1

Method BLASTX q2370595 NCBI GI BLAST score 142 4.0e-09 E value Match length 83 33 % identity

NCBI Description (AJ001414) GTPase activating protein [Yarrowia lipolytica]

Seq. No.

45542

Seq. ID hyd700728672.h1

BLASTX Method q1703029 NCBI GI BLAST score 276 8.0e-25 E value Match length 83 % identity 59

CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 (CLATHRIN NCBI Description COAT ASSOCIATED PROTEIN AP47 HOMOLOG 2) (GOLGI ADAPTOR AP-1



47 KD PROTEIN HOMOLOG 2) (HA1 47 KD SUBUNIT HOMOLOG 2) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX... >qi 468382 (L07074) clathrin-associated adaptor protein [Rattus norvegicus]

Seq. No. 45543 Seq. ID hyd700728683.h1 Method BLASTX NCBI GI g1568480 BLAST score 406 E value 4.0e-40 Match length 84 92 % identity NCBI Description (Z71703) cdc2-like protein kinase [Beta vulgaris] Seq. No. 45544 Seq. ID hyd700728813.h1 Method BLASTX NCBI GI q2827554 BLAST score 229 E value 2.0e-19 Match length 79 % identity NCBI Description (AL021635) putative DNA binding protein [Arabidopsis thaliana] Seq. No. 45545 hyd700728821.h1 Seq. ID Method BLASTX g4432824 NCBI GI BLAST score 268 6.0e-24E value Match length 82 % identity 46 NCBI Description (AC006593) putative membrane-associated salt-inducible protein [Arabidopsis thaliana] Seq. No. 45546 Seq. ID hyd700728866.h1 BLASTX Method NCBI GI g3641252 BLAST score 302 6.0e-28 E value

Match length 81 % identity

NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

domestica]

Seq. No. 45547

Seq. ID hyd700728867.h1

Method BLASTN NCBI GI g20657 BLAST score 79 1.0e-36 E value Match length 164 % identity 91

NCBI Description P.sativum Cab II gene for chlorophyll a/b-binding protein



```
Seq. No.
                  45548
Seq. ID
                  hyd700728877.h1
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  152
E value
                  3.0e-80
Match length
                  248
                  90
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
Seq. No.
                  45549
Seq. ID
                  hyd700728933.h1
Method
                  BLASTN
NCBI GI
                  g473216
BLAST score
                  74
E value
                  1.0e-33
                  162
Match length
                  88
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
                   45550
Seq. No.
                  hyd700728946.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3241923
BLAST score
                   35
E value
                   2.0e-10
Match length
                   99
% identity
                   93
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.
                   45551
                   hyd700728951.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3548808
                   335
BLAST score
                   7.0e-32
E value
Match length
                   79
% identity
                   71
                   (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                   45552
Seq. No.
                   hyd700729025.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4432846
                   141
BLAST score
                   5.0e-09
E value
                   85
Match length
% identity
                   45
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 45553

Seq. ID hyd700729091.h1

Method BLASTN NCBI GI g4097879



```
BLAST score
                  1.0e-45
E value
                  201
Match length
                  87
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  45554
Seq. No.
                  hyd700729112.h1
Seq. ID
                  BLASTX
Method
                  g3176726
NCBI GI
                  283
BLAST score
                  1.0e-25
E value
                  71
Match length
                  79
% identity
                  (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                  thaliana]
                   45555
Seq. No.
                  hyd700729143.h1
Seq. ID
                  BLASTX
Method
                   g3522933
NCBI GI
BLAST score
                   167
                   5.0e-12
E value
                   38
Match length
                   74
% identity
                   (AC004411) putative anion exchange protein 3 [Arabidopsis
NCBI Description
                   thaliana]
                   45556
Seq. No.
                   hyd700729225.h1
Seq. ID
                   BLASTX
Method
                   g4455294
NCBI GI
                   167
BLAST score
                   4.0e-12
E value
                   68
Match length
                   47
% identity
                  (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   45557
Seq. No.
                   hyd700729234.h1
Seq. ID
                   BLASTX
Method
                   g4415918
NCBI GI
BLAST score
                   250
E value
                   1.0e-21
Match length
                   91
                   25
% identity
                  (AC006282) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45558
Seq. ID
                   hyd700729246.h1
                   BLASTX
Method
NCBI GI
                   a3372493
```

Method BLASTX
NCBI GI g3372493
BLAST score 156
E value 1.0e-10
Match length 87
% identity 40



NCBI Description (AF045583) tubby like protein 3 [Homo sapiens] >gi_4507739_ref_NP_003315.1_pTULP3_ tubby like protein

Seq. No. 45559

Seq. ID hyd700729308.h1

Method BLASTX
NCBI GI g135418
BLAST score 439
E value 6.0e-44
Match length 84
% identity 96

NCBI Description TUBULIN ALPHA-3 AND ALPHA-7 CHAINS >gi_2119267_pir__I77426

alpha-tubulin isotype M-alpha-6 - mouse >gi_202212 (M13442) alpha-tubulin isotype M-alpha-6 [Mus musculus] >gi_202219 (M13443) alpha-tubulin isotype M-alpha-6 [Mus musculus]

Seq. No. 45560

Seq. ID hyd700729356.h1

Method BLASTX
NCBI GI g322801
BLAST score 157
E value 7.0e-11
Match length 59
% identity 63

NCBI Description promotes sex organ development protein ple - Antirrhinum

majus >gi_264223_bbs_123356 (S53900) promotes sex organ
development=ple [Antirrhinum majus, Peptide, 239 aa]

[Antirrhinum majus]

Seq. No. 45561

Seq. ID hyd700729372.h1

Method BLASTX
NCBI GI g2088645
BLAST score 156
E value 8.0e-11
Match length 82
% identity 39

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45562

Seq. ID hyd700729409.h1

Method BLASTX
NCBI GI g1363479
BLAST score 258
E value 1.0e-22
Match length 64
% identity 75

NCBI Description photosystem I protein psaL - cucumber

gi_801740_dbj_BAA09047_ (D50456) PsaL [Cucumis sativus]

Seq. No. 45563

Seq. ID hyd700729463.hl

Method BLASTX
NCBI GI g2462925
BLAST score 341
E value 2.0e-32
Match length 84



```
% identity
                  (AJ000053) GTP cyclohydrolase II /
NCBI Description
                  3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                  thaliana]
Seq. No.
                  45564
                  hyd700729473.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4263718
                  336
BLAST score
                  7.0e-32
E value
Match length
                  86
% identity
                  69
                  (AC006223) putative DNA topoisomerase III beta [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   45565
Seq. ID
                  hyd700729489.h1
                  BLASTN
Method
                   g1071696
NCBI GI
                   67
BLAST score
                   2.0e-29
E value
Match length
                  154
                   86
% identity
NCBI Description M.sativa mRNA for cyclin
                   45566
Seq. No.
Seq. ID
                   hyd700729493.h1
                   BLASTX
Method
NCBI GI
                   q100226
                   303
BLAST score
                   4.0e-28
E value
Match length
                   67
                   85
% identity
NCBI Description hypothetical protein - tomato >gi_19275_emb_CAA78112_
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi_445619_prf__1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                   45567
Seq. No.
Seq. ID
                   hyd700729532.h1
Method
                   BLASTN
NCBI GI
                   q296442
BLAST score
                   40
                   2.0e-13
E value
Match length
                   52
                   94
% identity
NCBI Description G.max ADR11 mRNA
                   45568
Seq. No.
                   hyd700729567.h1
Seq. ID
                   BLASTX
Method
                   g3080389
NCBI GI
                   143
BLAST score
```

2.0e-09

56

59

E value

Match length

% identity



NCBI Description (AL022603) putative membrane associated protein [Arabidopsis thaliana] Seq. No. 45569 Seq. ID hyd700729688.h1 Method BLASTX NCBI GI g2344901 BLAST score 297 E value 2.0e-27 74 Match length

78 % identity NCBI Description (AC002388) serine/threonine protein kinase isolog [Arabidopsis thaliana]

45570 Seq. No. Seq. ID hyd700729737.h1

Method BLASTX NCBI GI q4091810 239 BLAST score E value 2.0e-20 79 Match length

% identity 62

NCBI Description (AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1 [Arabidopsis thaliana]

Seq. No. 45571

Seq. ID hyd700729743.h1

Method BLASTN NCBI GI g20728 BLAST score 64 E value 1.0e-27 176 Match length 84 % identity

NCBI Description Pea chloroplast GAPA mRNA encoding

glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A

(EC 1.2.1.13)

Seq. No. 45572

Seq. ID hyd700729808.h1

Method BLASTX NCBI GI q2809251 BLAST score 173 9.0e-13 E value Match length 85 % identity 47

NCBI Description (AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No. 45573

Seq. ID hyd700729819.h1

Method BLASTX NCBI GI g1905775 BLAST score 362 7.0e-35 E value 81 Match length % identity

NCBI Description (Y11930) putative protein kinase [Arabidopsis thaliana]



```
Seq. No.
                  hyd700729832.h1
Seq. ID
                  BLASTX
Method
                  g4008006
NCBI GI
BLAST score
                  142
E value
                   4.0e-09
                   78
Match length
                   42
% identity
                   (AF084034) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   45575
Seq. No.
                   hyd700729859.h1
Seq. ID
                   BLASTN
Method
                   g1208702
NCBI GI
                   79
BLAST score
                   1.0e-36
E value
                   141
Match length
                   100
% identity
NCBI Description Glycine max histone H3 gene, partial cds, clone H3-DMAX
                   45576
Seq. No.
                   hyd700729877.h1
Seq. ID
                   BLASTX
Method
                   g1209655
NCBI GI
                   266
BLAST score
                   1.0e-23
E value
                   79
Match length
                   62
% identity
NCBI Description (U37428) gl1 [Zea mays]
                   45577
Seq. No.
Seq. ID
                   hyd700729909.h1
                   BLASTN
Method
                   q4063730
NCBI GI
                   62
BLAST score
E value
                   2.0e-26
Match length
                   261
                   82
% identity
                   Arabidopsis thaliana BAC F21J6 from chromosome V,
NCBI Description
                   containing KNAT3 and mapping near 60.5 cM, complete
                   sequence [Arabidopsis thaliana]
Seq. No.
                   45578
                   hyd700729941.h1
Seq. ID
                   BLASTX
Method
                   q3096944
NCBI GI
BLAST score
                   141
                   5.0e-09
E value
                   51
Match length
 % identity
                   (AL023094) putative protein [Arabidopsis thaliana]
```

NCBI Description

Seq. No. 45579

hyd700730001.hl Seq. ID

Method BLASTX g2129651 NCBI GI



BLAST score 326 E value 1.0e-30 Match length 91 % identity 67

NCBI Description myosin heavy chain ATM2 - Arabidopsis thaliana (fragment)

>gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis

thaliana]

Seq. No. 45580

Seq. ID hyd700730004.h1

Method BLASTX
NCBI GI 94510345
BLAST score 145
E value 2.0e-09
Match length 36
% identity 67

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 45581

Seq. ID hyd700730101.h1

Method BLASTX
NCBI GI g3193306
BLAST score 142
E value 3.0e-09
Match length 78
% identity 7

NCBI Description (AF069300) contains similarity to Arabidopsis

membrane-associated salt-inducible-like protein

(GB:AL021637) [Arabidopsis thaliana]

Seq. No. 45582

Seq. ID hyd700730108.h1

Method BLASTX
NCBI GI g1724097
BLAST score 223
E value 9.0e-19
Match length 76
% identity 54

NCBI Description (U79772) female sex protein [Mercurialis annua]

Seq. No. 45583

Seq. ID hyd700730132.h1

Method BLASTN
NCBI GI g2832782
BLAST score 51
E value 6.0e-20
Match length 131
% identity 85

NCBI Description Egeria densa mRNA for potassium channel beta subunit

Seq. No. 45584

Seq. ID hyd700730215.h1

Method BLASTX
NCBI GI g1402883
BLAST score 271
E value 3.0e-24
Match length 86



```
% identity
                  (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                  >gi 1495263_emb_CAA66119_ (X97487) orf09 [Arabidopsis
                  thaliana]
Seq. No.
                  45585
                  hyd700730218.h1
Seq. ID
                  BLASTX
Method
                  q4220521
NCBI GI
                  205
BLAST score
                  2.0e-16
E value
                  59
Match length
                  63
% identity
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  45586
Seq. No.
Seq. ID
                  hyd700730221.h1
                  BLASTX
Method
                  q3860321
NCBI GI
                  341
BLAST score
                  1.0e-32
E value
                  83
Match length
% identity
                  (AJ012687) beta-galactosidase [Cicer arietinum]
NCBI Description
                   45587
Seq. No.
Seq. ID
                  hyd700730303.h1
                   BLASTX
Method
                   q3121727
NCBI GI
BLAST score
                   302
                   6.0e-28
E value
                   62
Match length
                   94
% identity
NCBI Description ALCOHOL DEHYDROGENASE CLASS III (GLUTATHIONE-DEPENDENT
                   FORMALDEHYDE DEHYDROGENASE) (FDH) (FALDH)
                   45588
Seq. No.
Seq. ID
                   hyd700730544.h1
                   BLASTN
Method
                   q516853
NCBI GI
BLAST score
                   87
                   2.0e-41
E value
Match length
                   175
% identity
                   30
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
                   45589
Seq. No.
                   hyd700730549.h1
Seq. ID
Method
                   BLASTN
                   g1575730
NCBI GI
BLAST score
                   169
                   2.0e-90
E value
```

Match length 185 % identity 98

NCBI Description Glycine max 14-3-3 related protein SGF14D mRNA, complete

cds



Seq. No. 45590

Seq. ID hyd700730562.h1

Method BLASTX
NCBI GI g3915847
BLAST score 291
E value 1.0e-26
Match length 82
% identity 69

NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative

40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 45591

Seq. ID hyd700730613.h1

Method BLASTX
NCBI GI g4033469
BLAST score 200
E value 6.0e-16
Match length 65
% identity 41

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP41

>qi 1707370 emb CAA67799 (X99436) splicing factor

[Arabidopsis thaliana]

Seq. No. 45592

Seq. ID hyd700730632.hl

Method BLASTN
NCBI GI g1724103
BLAST score 96
E value 8.0e-47
Match length 224
% identity 86

NCBI Description Mesembryanthemum crystallinum methionine

adenosyltransferase mRNA, complete cds

Seq. No. 45593

Seq. ID hyd700730716.h1

Method BLASTN
NCBI GI g169036
BLAST score 47
E value 2.0e-17
Match length 59
% identity 95

NCBI Description Pisum sativum L. aldolase gene, 3' end cds

Seq. No. 45594

Seq. ID hyd700730731.h1

Method BLASTX
NCBI GI g3402684
BLAST score 312
E value 4.0e-29
Match length 79
% identity 73

NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45595

Seq. ID hyd700730817.h1

Method BLASTX



NCBI GI g2130051
BLAST score 252
E value 5.0e-22
Match length 60
% identity 72
NCBI Description values i

NCBI Description xylose isomerase (EC 5.3.1.5) - barley

>gi_1296807_emb_CAA64544_ (X95256) xylose isomerase
[Hordeum vulgare] >gi_1588664_prf__2209268A xylose

isomerase [Hordeum vulgare]

Seq. No. 45596

Seq. ID hyd700730849.h1

Method BLASTX
NCBI GI g3582436
BLAST score 348
E value 2.0e-33
Match length 76
% identity 82

NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No. 45597

Seq. ID hyd700730911.h1

Method BLASTX
NCBI GI g2687726
BLAST score 260
E value 4.0e-23
Match length 72
% identity 64

NCBI Description (AJ003246) 2'-hydroxydihydrodaidzein reductase [Glycine

max]

Seq. No. 45598

Seq. ID hyd700730932.h1

Method BLASTN
NCBI GI g4097879
BLAST score 68
E value 4.0e-30
Match length 180
% identity 85

NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein

gene, complete cds

Seq. No. 45599

Seq. ID hyd700730933.h1

Method BLASTX
NCBI GI g4325338
BLAST score 107
E value 2.0e-11
Match length 55
% identity 63

NCBI Description (AF128392) No definition line found [Arabidopsis thaliana]

Seq. No. 45600

Seq. ID hyd700730961.h1

Method BLASTX
NCBI GI g1706130
BLAST score 347



```
3.0e-33
E value
Match length
                  79
                  86
% identity
                  CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052
NCBI Description
                  calcium-dependent protein kinase homolog - carrot
                  >gi 1103386 emb_CAA58750_ (X83869) CDPK-related protein
                  kinase [Daucus carota]
                  45601
Seq. No.
                  hyd700730982.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4097879
BLAST score
                  117
                   2.0e-59
E value
                   233
Match length
% identity
                   88
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                   gene, complete cds
                   45602
Seq. No.
Seq. ID
                   hyd700730989.h1
Method
                   BLASTN
                   g4567090
NCBI GI
                   38
BLAST score
                   2.0e-12
E value
                   103
Match length
% identity
                   90
                   Glycine max SNF-1-like serine/threonine protein kinase
NCBI Description
                   mRNA, complete cds
                   45603
Seq. No.
                   hyd700731048.h1
Seq. ID
                   BLASTX
Method
                   g2924247
NCBI GI
BLAST score
                   246
                   2.0e-21
E value
Match length
                   54
% identity
                   83
                   (Y07782) expansin [Oryza sativa]
NCBI Description
                   45604
Seq. No.
                   hyd700731096.hl
Seq. ID
                   BLASTX
Method
                   g3786009
NCBI GI
                   158
BLAST score
                   3.0e-11
E value
                   61
Match length
                   62
% identity
                   (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
```

45605 Seq. No.

hyd700731102.h1 Seq. ID

BLASTX Method NCBI GI q4567301 205 BLAST score 2.0e-16 E value 90 Match length



% identity 50 NCBI Description (AC005956) putative protein kinase [Arabidopsis thaliana]

Seq. No. 45606

Seq. ID hyd700731193.h1

Method BLASTX
NCBI GI g2529675
BLAST score 141
E value 3.0e-09
Match length 29
% identity 86

NCBI Description (AC002535) putative AP2 domain containing protein

[Arabidopsis thaliana]

Seq. No. 45607

Seq. ID hyd700731233.h1

Method BLASTN
NCBI GI g1675195
BLAST score 100
E value 4.0e-49
Match length 184
% identity 89

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

Seq. No. 45608

Seq. ID jC-gmf102220050d09d1

Method BLASTX
NCBI GI g3355486
BLAST score 386
E value 2.0e-37
Match length 93
% identity 76

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 45609

Seq. ID jC-gmf102220050e07d1

Method BLASTX
NCBI GI g2576361
BLAST score 261
E value 7.0e-23
Match length 57
% identity 75

NCBI Description (U39782) lysine and histidine specific transporter

[Arabidopsis thaliana]

Seq. No. 45610

Seq. ID jC-gmf102220050e09a1

Method BLASTX
NCBI GI g2499535
BLAST score 193
E value 9.0e-15
Match length 110
% identity 56

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]



45611 Seq. No. jC-gmf102220050e10d1 Seq. ID Method BLASTX q2754849 NCBI GI BLAST score 210 7.0e-17 E value 49 Match length 82 % identity (AF039000) putative serine-glyoxylate aminotransferase NCBI Description [Fritillaria agrestis] 45612 Seq. No. jC-gmf102220051a05a1 Seq. ID Method BLASTX NCBI GI g3779024 BLAST score 375 3.0e-36 E value 98 Match length 76 % identity (AC005171) unknown protein [Arabidopsis thaliana] NCBI Description 45613 Seq. No. jC-gmfl02220051a09a1 Seq. ID BLASTX Method NCBI GI g3582328 BLAST score 224 E value 3.0e-18 149 Match length % identity 14 (AC005496) hypothetical protein [Arabidopsis thaliana] NCBI Description 45614 Seq. No. jC-gmf102220051b10a1 Seq. ID Method BLASTX NCBI GI g1871192 BLAST score 418 E value 4.0e-41 Match length 104 % identity NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana] 45615 Seq. No. jC-gmf102220052b06a1 Seq. ID Method BLASTX NCBI GI g3242705 BLAST score 525 E value 2.0e-53 Match length 168 % identity 64 (AC003040) putative nicotinate phosphoribosyltransferase NCBI Description [Arabidopsis thaliana]

Seq. No. 45616

Seq. ID jC-gmf102220052c09a1

Method BLASTN

Match length

% identity

67

37



```
NCBI GI
                  g310575
BLAST score
                  277
                  1.0e-154
E value
                  344
Match length
                  99
% identity
                  Glycine max nodulin-26 mRNA, complete cds
NCBI Description
                  45617
Seq. No.
                  jC-gmf102220052e03a1
Seq. ID
                  BLASTN
Method
                  g1431621
NCBI GI
                  95
BLAST score
                  6.0e-46
E value
Match length
                  115
% identity
                  96
NCBI Description
                  T.repens mRNA for protein kinase
                  45618
Seq. No.
                  jC-gmf102220052g08a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1053215
BLAST score
                   467
                  0.0e+00
E value
                   475
Match length
                  100
% identity
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
                   45619
Seq. No.
                   jC-gmf102220052g09d1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g101813
BLAST score
                   316
                   2.0e-29
E value
Match length
                   92
% identity
                   67
                  NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 -
NCBI Description
                  Emericella nidulans mitochondrion (SGC3)
                   45620
Seq. No.
Seq. ID
                   jC-gmf102220053a02a1
Method
                  BLASTX
NCBI GI
                   g3608155
BLAST score
                   177
E value
                   2.0e-21
Match length
                   125
% identity
                   39
NCBI Description
                   (AC005314) putative RNA helicase [Arabidopsis thaliana]
Seq. No.
                   45621
                   jC-gmfl02220053d12a1
Seq. ID
Method
                   BLASTX
                   q481812
NCBI GI
BLAST score
                   238
E value
                   2.0e-20
```



NCBI Description DNA-binding protein GT-2 - Arabidopsis thaliana

>gi 416490 emb CAA51289_ (X72780) GT-2 factor [Arabidopsis

thaliana]

Seq. No. 45622

Seq. ID jC-gmf102220054b06d1

Method BLASTX
NCBI GI g4539397
BLAST score 220
E value 7.0e-18
Match length 77
% identity 52

NCBI Description (AL035526) cellulose synthase-like protein [Arabidopsis

thaliana]

Seq. No. 45623

Seq. ID jC-gmf102220054c02a1

Method BLASTX
NCBI GI g1931640
BLAST score 307
E value 3.0e-28
Match length 111
% identity 52

NCBI Description (U95973) Serine carboxypeptidase isolog [Arabidopsis

thaliana]

Seq. No. 45624

Seq. ID jC-gmfl02220054f11a1

Method BLASTX
NCBI GI g731042
BLAST score 155
E value 3.0e-10
Match length 81
% identity 35

NCBI Description UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 5 (UBIQUITIN

THIOLESTERASE 5) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 5)

(DEUBIQUITINATING ENZYME 5) >gi_1078451_pir__S50277 ubiquitin-specific proteinase UBP5 (EC 3.4.-.-) - yeast

(Saccharomyces cerevisiae) >gi_595377 (U10082)

ubiquitin-specific protease [Saccharomyces cerevisiae] >gi_603384 (U18917) Ubp5p: ubiquitin-specific protease

[Saccharomyces cerevisiae]

Seq. No. 45625

Seq. ID jC-gmf102220054g01a1

Method BLASTX
NCBI GI g2827638
BLAST score 291
E value 3.0e-29
Match length 133
% identity 52

NCBI Description (AL021636) Cytochrome P450-like protein [Arabidopsis

thaliana]

Seq. No. 45626

Seq. ID jC-gmf102220055c12a1

Method BLASTX



NCBI GI g3184285 BLAST score 143 E value 9.0e-09 Match length 31 % identity 77

NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45627

Seq. ID jC-gmf102220055d05a1

Method BLASTX
NCBI GI g1086586
BLAST score 247
E value 5.0e-21
Match length 139
% identity 35

NCBI Description (U41007) similar to G beta repeats (PROSITE: PS00670)

[Caenorhabditis elegans]

Seq. No. 45628

Seq. ID jC-gmf102220055d08a1

Method BLASTX
NCBI GI g2558655
BLAST score 145
E value 5.0e-09
Match length 156
% identity 39

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No. 45629

Seq. ID jC-gmf102220055d10d1

Method BLASTX
NCBI GI g399112
BLAST score 191
E value 2.0e-14
Match length 133
% identity 37

NCBI Description BETA-GALACTOSIDASE (LACTASE) >gi_101123_pir__JC1266

beta-galactosidase (EC 3.2.1.23) - yeast (Kluyveromyces

marxianus var. lactis) >gi_173305 (M84410)
beta-D-galactosidase [Kluyveromyces lactis]

Seq. No. 45630

Seq. ID jC-gmf102220055d12d1

Method BLASTN
NCBI GI g1438878
BLAST score 208
E value 1.0e-113
Match length 312
% identity 92

NCBI Description Glycine max choline kinase GmCK1p mRNA, complete cds

Seq. No. 45631

Seq. ID jC-gmf102220055g01a1

Method BLASTX
NCBI GI g2618705
BLAST score 149
E value 1.0e-19



```
Match length
% identity
                  66
                  (AC002510) putative ABC transporter, 5' partial
NCBI Description
                  [Arabidopsis thaliana]
                  45632
Seq. No.
                  jC-gmfl02220056c02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q421955
BLAST score
                  164
E value
                  2.0e-14
Match length
                  62
                  65
% identity
                  hypothetical protein 4 - potato transposon Tst1
NCBI Description
                  >gi 21434 emb_CAA36616 (X52387) ORF4 [Solanum tuberosum]
Seq. No.
                  45633
Seq. ID
                  jC-qmf102220056d02a1
Method
                  BLASTX
NCBI GI
                  q4406777
BLAST score
                  234
E value
                  2.0e-19
Match length
                  76
                  58
% identity
                  (AC006532) putative zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  45634
Seq. No.
                  jC-qmf102220056d04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3790587
BLAST score
                  417
E value
                  5.0e-41
Match length
                  92
% identity
                  78
                  (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
NCBI Description
                   thaliana]
                   45635
Seq. No.
                   jC-gmf102220056e02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4079809
BLAST score
                   144
                  7.0e-09
E value
Match length
                  155
                   5
% identity
NCBI Description (AF071172) HERC2 [Homo sapiens]
                   45636
Seq. No.
                   jC-gmf102220057b12d1
Seq. ID
Method
                   BLASTN
                   g21004
NCBI GI
BLAST score
                   92
                   3.0e-44
E value
                   176
Match length
```

NCBI Description French Bean mRNA for plastid-located glutamine synthetase

94

% identity



(EC 6.3.1.2)

Seq. No. 45637

Seq. ID jC-gmf102220057c08a1

Method BLASTN
NCBI GI g303900
BLAST score 147
E value 3.0e-77
Match length 239
% identity 29

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 45638

Seq. ID jC-gmf102220057d08a1

Method BLASTX
NCBI GI g2244833
BLAST score 293
E value 2.0e-26
Match length 123
% identity 50

NCBI Description (Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No. 45639

Seq. ID jC-gmfl02220057e01a1

Method BLASTX
NCBI GI g1708376
BLAST score 142
E value 4.0e-17
Match length 96
% identity 46

NCBI Description INDOLEACETAMIDE HYDROLASE (IAH) (INDOLE-3-ACETAMIDE

HYDROLASE) >gi_1073076_pir__B53376 indoleacetamide

hydrolase - Pseudomonas syringae pv. syringae >gi 472561

(U04358) IAH [Pseudomonas syringae]

Seq. No. 45640

Seq. ID jC-gmfl02220057e06a1

Method BLASTX
NCBI GI g4417271
BLAST score 498
E value 1.0e-50
Match length 102
% identity 92

NCBI Description (AC007019) putative cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 45641

Seq. ID jC-gmf102220057h01a1

Method BLASTX
NCBI GI g3128186
BLAST score 189
E value 3.0e-14
Match length 148
% identity 36

NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45642



jC-qmf102220057h03a1 Seq. ID Method BLASTX q4510377 NCBI GI 256 BLAST score 2.0e-34 E value Match length 148 53 % identity (AC007017) putative RNA helicase A [Arabidopsis thaliana] NCBI Description Seq. No. 45643 jC-gmf102220060g12a1 Seq. ID Method BLASTN g986968 NCBI GI BLAST score 437 0.0e+00E value 445 Match length 100 % identity Glycine max TGACG-motif binding protein (STGA1) mRNA, NCBI Description complete cds Seq. No. 45644 jC-gmf102220060h12d1 Seq. ID Method BLASTX g3420057 NCBI GI BLAST score 518 E value 1.0e-52 166 Match length % identity 35 NCBI Description (AC004680) putative ABC transporter [Arabidopsis thaliana] 45645 Seq. No. jC-gmf102220061c08d1 Seq. ID Method BLASTX NCBI GI q3925223 165 BLAST score E value 2.0e-11 Match length 58 59 % identity (AF037029) 6-phosphogluconate dehydrogenase isoenzyme A NCBI Description [Zea mays] 45646 Seq. No. Seq. ID jC-gmf102220061c10d1 Method BLASTX NCBI GI q1346261 BLAST score 151 E value 8.0e-10 Match length 45 % identity GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) NCBI Description >gi_1015319_dbj_BAA11091_ (D67088) glutamyl-tRNA reductase [Cucumis sativus] 45647 Seq. No.

Seq. ID jC-gmf102220061d07a1

Method BLASTX NCBI GI g2529677



BLAST score 227 E value 1.0e-18 Match length 87 % identity 51

NCBI Description (AC002535) kinesin-like protein, heavy chain [Arabidopsis

thaliana]

Seq. No. 45648

Seq. ID jC-gmfl02220061d12a1

Method BLASTX
NCBI GI g2828284
BLAST score 157
E value 2.0e-10
Match length 129
% identity 34

NCBI Description (AL021687) hypothetical protein [Arabidopsis thaliana]

>gi_2832637_emb_CAA16766_ (AL021711) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 45649

Seq. ID jC-gmf102220061e02d1

Method BLASTN
NCBI GI g18644
BLAST score 38
E value 3.0e-12
Match length 70
% identity 89

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 45650

Seq. ID jC-gmf102220061e07a1

Method BLASTX
NCBI GI g2341024
BLAST score 598
E value 3.0e-62
Match length 138
% identity 55

NCBI Description (AC000104) F19P19.1 [Arabidopsis thaliana]

Seq. No. 45651

Seq. ID jC-gmfl02220061f04d1

Method BLASTX
NCBI GI g3757529
BLAST score 258
E value 2.0e-22
Match length 87
% identity 56

NCBI Description (AC005167) tetracycline transporter-like protein

[Arabidopsis thaliana]

Seq. No. 45652

Seq. ID jC-gmfl02220061f05a1

Method BLASTX
NCBI GI g3687297
BLAST score 158
E value 2.0e-10
Match length 68

% identity (AJ005588) 5-epi-aristolochene synthase [Capsicum annuum] NCBI Description Seq. No. 45653 Seq. ID jC-qmfl02220061f05d1 Method BLASTX NCBI GI q4508070 BLAST score 186 7.0e-14 E value Match length 79 % identity 52 (AC005882) 24349 [Arabidopsis thaliana] NCBI Description Seq. No. 45654 Seq. ID jC-gmf102220061f06a1 Method BLASTN q2654107 NCBI GI BLAST score 137 E value 4.0e-71 Match length 277 % identity 87 Pisum sativum cytosine-5 DNA methyltransferase mRNA, NCBI Description complete cds Seq. No. 45655 Seq. ID jC-gmf102220061f11a1 Method BLASTX

Method BLASTX
NCBI GI g3875740
BLAST score 388
E value 2.0e-37
Match length 150
% identity 53

NCBI Description (Z81497) similar to mannosyl-oligosaccharide alpha-1, 2-mannosidase; cDNA EST EMBL:D67155 comes from this gene;

cDNA EST EMBL:D64219 comes from this gene; cDNA EST

yk260e12.3 comes from this gene; cDNA EST yk260e12.5 comes

from

Seq. No. 45656

Seq. ID jC-gmf102220061g09a1

Method BLASTX
NCBI GI g1619300
BLAST score 281
E value 4.0e-25
Match length 69
% identity 75

NCBI Description (X95269) LRR protein [Lycopersicon esculentum]

Seq. No. 45657

Seq. ID jC-gmfl02220062a06a1

Method BLASTX
NCBI GI g2982452
BLAST score 513
E value 4.0e-52
Match length 169
% identity 9

NCBI Description (AL022223) receptor protein kinase-like protein

Seq. No.

Seq. ID

45663

jC-gmf102220063a07a1



[Arabidopsis thaliana]

```
45658
Seq. No.
                  jC-gmf102220062a10a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2342427
BLAST score
                  149
                  2.0e-09
E value
                  102
Match length
% identity
                  38
                  (AB000799) NPK1-related protein kinase 3 [Arabidopsis
NCBI Description
                  thaliana]
                  45659
Seq. No.
                  jC-qmf102220062b11a1
Seq. ID
Method
                  BLASTX
                  q4558666
NCBI GI
                  172
BLAST score
                   4.0e-12
E value
                  108
Match length
% identity
                  33
                   (AC007063) putative Na/H antiporter isolog [Arabidopsis
NCBI Description
                  thaliana]
                   45660
Seq. No.
                   jC-gmf102220062g09a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3894385
BLAST score
                   178
                  7.0e-13
E value
Match length
                  143
% identity
                  (AF053994) Hcr2-OA [Lycopersicon esculentum]
NCBI Description
                   45661
Seq. No.
                   jC-gmf102220063a01d1
Seq. ID
                   BLASTX
Method
                   g3600043
NCBI GI
BLAST score
                   199
                   2.0e-15
E value
Match length
                   54
                   80
% identity
                  (AF080119) No definition line found [Arabidopsis thaliana]
NCBI Description
                   45662
Seq. No.
                   jC-gmf102220063a03d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2769642
BLAST score
                   275
                   3.0e-24
E value
Match length
                   67
% identity
                   81
                  (297215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon
NCBI Description
                   esculentum]
```



BLASTX Method g3377507 NCBI GI BLAST score 167 8.0e-12 E value Match length 66 48 % identity (AF056026) auxin transport protein EIR1 [Arabidopsis NCBI Description

thaliana] >qi 3661620 (AF093241) putative auxin efflux carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459) $\verb"polar-auxin-transport" efflux component \verb"AGRAVITROPIC" 1$ [Arabidopsis thaliana] >gi_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

Seq. No. 45664

jC-gmf102220063a07d1 Seq. ID

Method BLASTX q3377509 NCBI GI 308 BLAST score 4.0e-28 E value Match length 91 % identity

(AF056027) auxin transport protein REH1 [Oryza sativa] NCBI Description

45665 Seq. No.

jC-gmf102220063b08a1 Seq. ID

Method BLASTX g4558671 NCBI GI BLAST score 370 E value 2.0e-35 112 Match length % identity 66

(AC007063) hypothetical protein [Arabidopsis thaliana] NCBI Description

45666 Seq. No.

jC-gmf102220063b08d1 Seq. ID

Method BLASTX g4263722 NCBI GI BLAST score 249 2.0e-28 E value Match length 77 73 % identity

(AC006223) putative glucan synthase [Arabidopsis thaliana] NCBI Description

45667 Seq. No.

jC-gmf102220063c09a1 Seq. ID

Method BLASTX q639722 NCBI GI BLAST score 346 E value 1.0e-32 Match length 79

% identity 78

(L27484) calcium-dependent protein kinase [Zea mays] NCBI Description

45668 Seq. No.

jC-gmf102220063e03a1 Seq. ID

Method BLASTN NCBI GI g310581



```
BLAST score
                  1.0e-114
E value
Match length
                  237
                  97
% identity
NCBI Description Glycine max protein kinase 3 (SPK-3) mRNA, complete cds
                  45669
Seq. No.
Seq. ID
                  jC-gmf102220063e06d1
                  BLASTX
Method
                  g132935
NCBI GI
BLAST score
                  144
                  5.0e-09
E value
                  47
Match length
% identity
                  53
                  60S RIBOSOMAL PROTEIN L37A (YL37) (RP47)
NCBI Description
                  >gi_101568_pir__S18431 ribosomal protein L35a.e.c16 - yeast
                  (Saccharomyces cerevisiae) >gi_4392_emb_CAA41035_ (X57969)
                  ribosomal protein L37a [Saccharomyces cerevisiae]
                  >gi 1244773 (U43703) Lpi4p [Saccharomyces cerevisiae]
                  >gi 1370305 emb CAA97847 (Z73499) ORF YPL143w
                  [Saccharomyces cerevisiae]
Seq. No.
                  45670
                  jC-gmf102220063g08d1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2738982
BLAST score
                  181
E value
                  1.0e-13
Match length
                  59
                  59
% identity
NCBI Description (AF022157) CYP71A10 [Glycine max]
                  45671
Seq. No.
                  jC-gmf102220064a04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1402883
BLAST score
                  163
E value
                  3.0e-11
Match length
                  138
% identity
                  30
NCBI Description
                  (X98130) unknown [Arabidopsis thaliana]
                  >gi 1495263 emb CAA66119 (X97487) orf09 [Arabidopsis
                  thaliana]
                  45672
Seq. No.
                  jC-gmf102220064h05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2341042
BLAST score
                  194
```

E value

2.0e-16

Match length % identity

76 63

NCBI Description (AC000104) F19P19.26 [Arabidopsis thaliana]

Seq. No.

45673

Seq. ID

jC-gmf102220065a08a1

Method

BLASTX



```
q419760
NCBI GI
BLAST score
                  425
E value
                  6.0e-59
                  133
Match length
                  47
% identity
                  P-glycoprotein atpgpl - Arabidopsis thaliana
NCBI Description
                  >gi 3849833_emb_CAA43646_ (X61370) P-glycoprotein
                  [Arabidopsis thaliana]
                  45674
Seq. No.
                  jC-gmf102220065d02d1
Seq. ID
                  BLASTX
Method
                  g4467152
NCBI GI
BLAST score
                  164
                  2.0e-11
E value
Match length
                  55
% identity
                  53
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  45675
Seq. No.
                  jC-gmf102220065d07a1
Seq. ID
                  {\tt BLASTX}
Method
                  g4262225
NCBI GI
                  261
BLAST score
                  5.0e-37
E value
                  120
Match length
% identity
                  63
                  (AC006200) putative phosphatidic acid phosphatase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  45676
                  jC-qmf102220065f06d1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3249098
                  178
BLAST score
                  3.0e-13
E value
                  51
Match length
                  71
% identity
                  (AC003114) ESTs gb_T04610, gb_N38459, gb_T45174, gb_R30481
NCBI Description
                  and gb N64971 come from this gene. [Arabidopsis thaliana]
                  45677
Seq. No.
                   jC-gmf102220065g11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4038035
BLAST score
                  289
E value
                   6.0e-26
Match length
                  123
% identity
                   46
                  (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
```

jC-gmf102220067f08a1 Seq. ID

Method BLASTN NCBI GI g515691 BLAST score 286

Match length

% identity

63



```
1.0e-160
E value
                   286
Match length
                   100
% identity
NCBI Description Glycine max Forrest beta-tubulin (tubB3) mRNA, partial cds
                   45679
Seq. No.
                   jC-gmf102220067h09a1
Seq. ID
                   BLASTX
Method
                   g1495483
NCBI GI
                   325
BLAST score
                   4.0e-30
E value
                   148
Match length
                   45
% identity
NCBI Description
                   (X97795) RAD54 [Homo sapiens]
                   >gi_4506397_ref_NP_003570.1_pRAD54L_ RAD54
                   (S.cerevisiae) - like
                   45680
Seq. No.
                   jC-qmf102220068a07a1
Seq. ID
                   BLASTX
Method
                   g2842424
NCBI GI
                   550
BLAST score
                   1.0e-56
E value
                   147
Match length
                   65
% identity
                   (AJ223948) RNA helicase [Homo sapiens]
NCBI Description
                   45681
Seq. No.
                   jC-gmf102220068b03d1
Seq. ID
                   BLASTX
Method
                   g2924776
NCBI GI
                   222
BLAST score
                   3.0e-18
E value
                   59
Match length
                   73
% identity
                   (AC002334) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45682
Seq. No.
                   jC-gmf102220068b11a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2347100
                   667
BLAST score
                   3.0e-70
E value
                   141
Match length
                   92
% identity
                   (U76846) ubiquitin-specific protease [Arabidopsis thaliana]
NCBI Description
                   >gi 4567196 gb AAD23612.1_AC007168_3 (AC007168) putative
                   ubiquitin-specific protease [Arabidopsis thaliana]
                   45683
Seq. No.
                   jC-qmf102220068d05d1
 Seq. ID
                   BLASTX
Method
                   a2500354
NCBI GI
                   256
BLAST score
                   4.0e-22
E value
```



```
NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_
(AB001891) QM family protein [Solanum melongena]

Seq. No. 45684
Seq. ID jC-gmf102220068d06a1
```

Seq. ID jC-gmf1022
Method BLASTX
NCBI GI g4455191
BLAST score 151
E value 5.0e-10
Match length 97
% identity 11

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 45685

Seq. ID jC-gmf102220068d12a1

Method BLASTX
NCBI GI g2911533
BLAST score 614
E value 4.0e-64
Match length 128
% identity 88

NCBI Description (X83620) Petunia Shaggy kinase 6 [Petunia x hybrida]

Seq. No. 45686

Seq. ID jC-gmf102220068e09a1

Method BLASTX
NCBI GI g3152592
BLAST score 200
E value 1.0e-15
Match length 95
% identity 25

NCBI Description (AC002986) Contains similarity to 8A-2V protein gb_Y10496

from Mus musculus. [Arabidopsis thaliana]

Seq. No. 45687

Seq. ID jC-gmfl02220069c03d1

Method BLASTX
NCBI GI g4218120
BLAST score 201
E value 8.0e-16
Match length 44
% identity 82

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 45688

Seq. ID jC-gmf102220069e04d1

Method BLASTX
NCBI GI g2293358
BLAST score 196
E value 4.0e-15
Match length 98
% identity 49

NCBI Description (D87669) polyphenol oxidase [Malus domestica]

Seq. No. 45689

Seq. ID jC-gmf102220069e05a1

Method

NCBI GI

E value

BLAST score

BLASTX g3450842

1.0e-16



```
BLASTX
Method
NCBI GI
                  q2347199
                  239
BLAST score
                   4.0e-20
E value
Match length
                  84
                  61
% identity
                  (AC002338) protein kinase isolog [Arabidopsis thaliana]
NCBI Description
                  45690
Seq. No.
                   jC-gmf102220069f02d1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g170043
BLAST score
                  122
                   4.0e-62
E value
                   339
Match length
                   90
% identity
NCBI Description Soybean phytoene desaturase mRNA, complete cds
Seq. No.
                   45691
                   jC-gmf102220070c01d1
Seq. ID
Method
                   BLASTX
                   g1497987
NCBI GI
BLAST score
                   158
E value
                   6.0e-11
Match length
                   61
% identity
                   52
                  (U62798) SCARECROW [Arabidopsis thaliana]
NCBI Description
                   45692
Seq. No.
                   jC-gmf102220070e01d1
Seq. ID
                   BLASTN
Method
                   g556687
NCBI GI
                   75
BLAST score
E value
                   5.0e - 34
Match length
                   170
% identity
                   24
NCBI Description H.annuus mRNA for seed tetraubiquitin
Seq. No.
                   45693
Seq. ID
                   jC-qmf102220070g01a1
Method
                   BLASTX
NCBI GI
                   g3023637
BLAST score
                   177
E value
                   6.0e-13
Match length
                   75
                   48
% identity
                   PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN
NCBI Description
                   8) >qi 1362899 pir A56236 probable RNA helicase 1 - human
                   >gi 807817 dbj BAA09078 (D50487) RNA helicase (HRH1) [Homo
                   sapiens]
                   45694
Seq. No.
Seq. ID
                   jC-gmf102220070g05a1
```



```
Match length
                   49
% identity
                   71
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
                   45695
Seq. No.
                   jC-gmf102220070h02a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1053215
BLAST score
                   401
                   0.0e+00
E value
                   409
Match length
                   100
% identity
                   Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                   nuclear gene encoding chloroplast protein, complete cds
Seq. No.
                   45696
                   jC-gmf102220070h06d1
Seq. ID
                   BLASTN
Method
                   q1332578
NCBI GI
                   67
BLAST score
E value
                   3.0e-29
                   164
Match length
                   11
% identity
NCBI Description P.sylvestris mRNA for polyubiquitin
                   45697
Seq. No.
Seq. ID
                   jC-qmf102220070h07d1
                   BLASTX
Method
NCBI GI
                   q1842158
BLAST score
                   356
                   9.0e-34
E value
Match length
                   77
                   81
% identity
                   (D83260) HXC-26 [Homo sapiens] >gi 1842163 dbj_BAA11907_
NCBI Description
                   (D83389) HXC-26 [Homo sapiens]
                   45698
Seq. No.
                   jC-gmfl02220071b04a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g459961
                   185
BLAST score
                   1.0e-99
E value
                   279
Match length
                   92
% identity
                   Glycine max proplastid omega-6 desaturase mRNA, complete
NCBI Description
                   cds
                   45699
Seq. No.
                   jC-gmf102220071b10d1
Seq. ID
                   BLASTX
Method
                   g3695392
NCBI GI
```

Method BLASTX
NCBI GI g3695392
BLAST score 265
E value 4.0e-23
Match length 98
% identity 57

NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]

NCBI Description



```
45700
Seq. No.
                  jC-gmf102220071c03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q120777
BLAST score
                  545
                  8.0e-56
E value
                  183
Match length
% identity
                  SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)
NCBI Description
                  >gi_147901 (M88334) succinic semialdehyde dehydrogenase
                   [Escherichia coli] >gi_1789015 (AE000351)
                   succinate-semialdehyde dehydrogenase, NADP-dependent
                   activity [Escherichia coli]
Seq. No.
                   45701
                   jC-qmf102220071c10a1
Seq. ID
Method
                  BLASTX
                   q1171429
NCBI GI
                   214
BLAST score
                   4.0e-17
E value
Match length
                   118
% identity
                  (U44028) CKC [Arabidopsis thaliana]
NCBI Description
                   45702
Seq. No.
Seq. ID
                   jC-gmf102220071d10a1
                   BLASTX
Method
                   q2129918
NCBI GI
BLAST score
                   175
                   1.0e-12
E value
                   50
Match length
% identity
                   62
                   BPF-1 protein - parsley >gi_396197_emb_CAA48413_ (X68337)
NCBI Description
                   BPF-1 [Petroselinum crispum] >gi_441310_emb_CAA44518_
                   (X62653) BPF-1 [Petroselinum crispum]
                   45703
Seq. No.
                   jC-gmf102220072a06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3451075
                   350
BLAST score
E value
                   3.0e - 33
                   101
Match length
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45704
                   jC-gmf102220072a07a1
Seq. ID
                   BLASTX
Method
                   q2982452
NCBI GI
                   189
BLAST score
                   2.0e-14
E value
Match length
                   52
                   60
% identity
```

7336

[Arabidopsis thaliana]

(AL022223) receptor protein kinase-like protein



Seq. ID

45705

BLASTX

jC-gmf102220072c03a1

```
Method
                   g2652938
NCBI GI
                   283
BLAST score
                   1.0e-25
E value
Match length
                   68
% identity
                   57
NCBI Description
                   (Z47554) orf [Zea mays]
                   45706
Seq. No.
                   jC-gmf102220072e06a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4519191
BLAST score
                   58
                   9.0e-24
E value
Match length
                   404
                   82
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K9P8, complete sequence
Seq. No.
                   45707
                   jC-gmf102220072g01a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g439856
BLAST score
                    44
                    1.0e-15
E value
Match length
                    80
                    89
% identity
                   Glycine max Williams 82 lipoxygenase mRNA, complete cds
NCBI Description
                    45708
Seq. No.
                    jC-gmf102220072g03a1
Seq. ID
                    BLASTX
Method
                    g2065531
NCBI GI
BLAST score
                    214
                    9.0e-18
E value
                    60
Match length
                    67
% identity
                    (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
                    45709
Seq. No.
                    jC-gmfl02220072h04a1
Seq. ID
                    BLASTX
Method
                    g3287835
NCBI GI
BLAST score
                    216
                    2.0e-17
E value
                    87
Match length
                    51
% identity
                    (+)-DELTA-CADINENE SYNTHASE ISOZYME A (D-CADINENE SYNTHASE)
NCBI Description
                    >gi_1002523 (U27535) (+)-delta-cadinene synthase isozyme A
[Gossypium arboreum] >gi_1217956_emb_CAA65289_ (X96429)
                    (+)-delta-cadinene synthase [Gossypium arboreum]
                    45710
Seq. No.
                    jC-gmf102220073a09a1
Seq. ID
```



```
BLASTX
Method
                  g807957
NCBI GI
BLAST score
                  164
                  3.0e-11
E value
Match length
                  94
% identity
                  37
                  (249259) unknown [Saccharomyces cerevisiae]
NCBI Description
                   45711
Seq. No.
                   jC-gmf102220073b02d1
Seq. ID
                   BLASTN
Method
                   g3603400
NCBI GI
BLAST score
                   187
                   1.0e-101
E value
                   359
Match length
% identity
                   88
                  Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCad1)
NCBI Description
                   mRNA, complete cds
                   45712
Seq. No.
                   jC-gmf102220073f02a1
Seq. ID
                   BLASTX
Method
                   q2739370
NCBI GI
BLAST score
                   458
                   9.0e-46
E value
                   142
Match length
% identity
                   58
                  (AC002505) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   45713
Seq. No.
                   jC-qmf102220073f10a1
Seq. ID
                   BLASTX
Method
                   q4455338
NCBI GI
                   497
BLAST score
                   2.0e-50
E value
                   139
Match length
% identity
                   65
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                   45714
 Seq. No.
                   jC-gmf102220073g01d1
 Seq. ID
                   BLASTX
Method
                   q1502430
NCBI GI
                   351
BLAST score
                   4.0e-33
 E value
                   79
Match length
                   84
 % identity
                   (U62331) phosphate transporter [Arabidopsis thaliana]
 NCBI Description
                   >gi 2564661 (AF022872) phosphate transporter [Arabidopsis
                   thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate
                   Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                   phosphate transporter, AtPT2 [Arabidopsis thaliana]
                    45715
 Seq. No.
                   jC-gmf102220073g02d1
 Seq. ID
```

7338

BLASTX

g4220485

Method

NCBI GI

Match length

% identity



```
BLAST score
                  1.0e-29
E value
Match length
                  98
                  62
% identity
                  (AC006069) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
                  45716
Seq. No.
                  jC-qmf102220073g05a1
Seq. ID
Method
                  BLASTN
                  g3288846
NCBI GI
BLAST score
                  60
                  5.0e-25
E value
Match length
                  60
                  100
% identity
                  Trifolium repens 18S ribosomal RNA gene, partial sequence
NCBI Description
                  45717
Seq. No.
                  jC-qmf102220073g06d1
Seq. ID
                  BLASTX
Method
                  q4335719
NCBI GI
BLAST score
                  174
                  1.0e-12
E value
                   48
Match length
                   50
% identity
                   (AC006248) putative RING-H2 finger protein RHG1a
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   45718
                   jC-gmf102220073h12a1
Seq. ID
                   BLASTX
Method
                   g2462931
NCBI GI
                   360
BLAST score
                   9.0e-44
E value
                   126
Match length
                   73
% identity
                  (Z83833) UDP-glucose:sterol glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   45719
Seq. No.
                   jC-gmf102220075d09a1
Seg. ID
Method
                   BLASTX
                   q2459428
NCBI GI
                   171
BLAST score
                   4.0e-12
E value
                   53
Match length
% identity
                  (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                   45720
Seq. No.
                   jC-gmf102220075e09d1
Seq. ID
                   BLASTN
Method
                   g303900
NCBI GI
                   70
BLAST score
                   2.0e-31
E value
                   177
```





```
NCBI Description Soybean gene for ubiquitin, complete cds
                  45721
Seq. No.
                  jC-gmf102220076a07a1
Seq. ID
                  BLASTX
Method
                  g2980641
NCBI GI
                  143
BLAST score
                   9.0e-09
E value
                   54
Match length
                   50
% identity
                  (Y11250) multi resistance protein [Arabidopsis thaliana]
NCBI Description
                   45722
Seq. No.
                   jC-gmf102220076a07d1
Seq. ID
Method
                   BLASTN
                   g4544435
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
                   52
Match length
                   92
% identity
                   Arabidopsis thaliana chromosome II BAC F14M13 genomic
NCBI Description
                   sequence, complete sequence
                   45723
Seq. No.
                   jC-gmf102220076c06a1
Seq. ID
Method
                   BLASTX
                   q3176659
NCBI GI
BLAST score
                   222
                   4.0e-18
E value
                   92
Match length
                   57
% identity
                   (AC004393) Strong similarity to receptor kinase gb_M80238
NCBI Description
                   from A. thaliana. [Arabidopsis thaliana]
                   45724
Seq. No.
                   jC-gmf102220076g04a1
Seq. ID
                   BLASTX
Method
                   g4103324
NCBI GI
                   613
BLAST score
                   6.0e-64
E value
                   148
Match length
                   90
% identity
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                   tuberosum]
                   45725
Seq. No.
                   jC-gmf102220076h02d1
Seq. ID
                   BLASTX
Method
                   q2583128
NCBI GI
                   149
BLAST score
                   2.0e-09
E value
Match length
                   34
                   79
 % identity
                   (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

7340

45726

jC-gmf102220076h05a1

Seq. No.

Seq. ID



```
BLASTX
Method
                  q1255448
NCBI GI
BLAST score
                  204
                  6.0e-16
E value
Match length
                  46
% identity
                  80
NCBI Description (D50468) mitogen-activated protein kinase [Arabidopsis
                  thaliana]
                  45727
Seq. No.
                  jC-gmf102220077a02a1
Seq. ID
                  BLASTX
Method
                  g4510383
NCBI GI
BLAST score
                  380
                  8.0e-41
E value
Match length
                  157
% identity
                   59
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
                   45728
Seq. No.
                   jC-qmf102220077c07d1
Seq. ID
Method
                   BLASTN
                   g1763233
NCBI GI
BLAST score
                   50
                   5.0e-19
E value
                   74
Match length
% identity
                   92
                  Camptotheca acuminata 3-hydroxy-3-methylglutaryl coenzyme A
NCBI Description
                   reductase gene, complete cds
                   45729
Seq. No.
                   jC-gmf102220077d02a1
Seq. ID
                   BLASTX
Method
                   g4539390
NCBI GI
                   357
BLAST score
                   5.0e-34
E value
Match length
                   90
                   76
% identity
                   (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   45730
                   jC-qmf102220077h12d1
 Seq. ID
                   BLASTX
Method
                   q4091804
NCBI GI
                   222
BLAST score
                   3.0e-18
E value
                   56
Match length
                   80
 % identity
                   (AF052584) CONSTANS-like protein 1 [Malus domestica]
 NCBI Description
 Seq. No.
                   45731
                   jC-gmf102220078a10a1
 Seq. ID
                   BLASTX
 Method
                   g2792302
 NCBI GI
```

353

2.0e-33

BLAST score

E value



```
Match length
                   72
% identity
                  (AF039895) putative aldehyde oxidase [Arabidopsis thaliana]
NCBI Description
                   45732
Seq. No.
                   jC-gmf102220078d11a1
Seq. ID
                   BLASTX
Method
                   q2462826
NCBI GI
                   261
BLAST score
                   9.0e-23
E value
                   123
Match length
                   46
% identity
                  (AF000657) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45733
                   jC-gmf102220078g10a1
Seq. ID
                   BLASTX
Method
                   g4539452
NCBI GI
                   179
BLAST score
                   5.0e-13
E value
Match length
                   52
% identity
                   69
                   (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   45734
                   jC-gmf102220079a11a1
Seq. ID
Method
                   BLASTX
                   g3036807
NCBI GI
                   381
BLAST score
                   8.0e-37
E value
Match length
                   118
% identity
                   66
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                   45735
Seq. No.
                   jC-gmf102220079e08d1
Seq. ID
                   BLASTX
Method
                   g2191135
NCBI GI
BLAST score
                   162
                   9.0e-14
E value
                   95
Match length
% identity
                   48
                   (AF007269) A IG002N01.14 gene product [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. ID jC-gmf102220079f04d1

Method BLASTN
NCBI GI g347452
BLAST score 41
E value 5.0e-14
Match length 161
% identity 84

NCBI Description Soybean hydroxyproline-rich glycoprotein (sbHRGP3) mRNA,

partial cds



```
45737
Seq. No.
                  jC-gmf102220079f07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3024020
                  324
BLAST score
                  5.0e-43
E value
                  105
Match length
                  83
% identity
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >qi 2225881 dbj_BAA20877_ (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
                   45738
Seq. No.
                   jC-gmf102220079g09a1
Seq. ID
                  BLASTX
Method
                   g857395
NCBI GI
BLAST score
                   146
                   4.0e-09
E value
                   89
Match length
% identity
                  (D50869) mitotic cyclin a2-type [Glycine max]
NCBI Description
                   45739
Seq. No.
                   jC-gmf102220079g12d1
Seq. ID
                   BLASTX
Method
                   g3377819
NCBI GI
BLAST score
                   155
                   2.0e-10
E value
                   46
Match length
% identity
                   61
                   (AF076275) No definition line found [Arabidopsis thaliana]
NCBI Description
                   45740
Seq. No.
                   jC-gmf102220080b02d1
Sea. ID
                   BLASTX
Method
                   g1297050
NCBI GI
                   202
BLAST score
                   8.0e-16
E value
                   47
Match length
                   70
% identity
                   (X90558) C-terminal processing protease of the D1 protein
NCBI Description
                   [Spinacia oleracea]
                   45741
Seq. No.
                   jC-gmf102220080e03a1
Seq. ID
                   BLASTX
Method
                   g3540199
NCBI GI
                   397
BLAST score
                   7.0e-39
E value
                   99
Match length
                   73
 % identity
                   (AC004260) Putative monosaccharide transport protein
NCBI Description
                   [Arabidopsis thaliana]
```

45742

BLASTX

jC-qmf102220080g04a1

Seq. No.

Seq. ID Method



```
g2244818
NCBI GI
                  270
BLAST score
                  4.0e-24
E value
                  88
Match length
% identity
                  67
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  45743
Seq. No.
                  jC-gmf102220080h10a1
Seq. ID
                  BLASTN
Method
                  g1236948
NCBI GI
                  79
BLAST score
                  5.0e-37
E value
                  123
Match length
% identity
                  91
NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds
                   45744
Seq. No.
                   jC-gmf102220081c07d1
Seq. ID
                   BLASTX
Method
                   q3335359
NCBI GI
BLAST score
                   307
                   4.0e-28
E value
                   91
Match length
% identity
                   (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   45745
Seq. No.
                   jC-gmf102220081d01d1
Seq. ID
                   BLASTX
Method
                   q1845561
NCBI GI
BLAST score
                   241
                   2.0e-20
E value
                   74
Match length
                   61
% identity
                   (D89432) cytochrome P450 [Glycyrrhiza echinata]
NCBI Description
                   45746
Seq. No.
                   jC-gmf102220081d04a1
Seq. ID
                   BLASTX
Method
                   g3785980
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
                   139
Match length
                   38
% identity
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45747
Seq. No.
                   jC-gmf102220081f11a1
Seq. ID
                   BLASTX
Method
                   q4191789
NCBI GI
BLAST score
                   530
                   3.0e-54
E value
                   131
Match length
                   85
 % identity
                   (AC005917) putative transmembrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
```



```
45748
Seq. No.
                  jC-gmf102220081g10d1
Seq. ID
Method
                  BLASTX
                  q3885334
NCBI GI
                  169
BLAST score
                  7.0e-12
E value
                  39
Match length
% identity
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
                   45749
Seq. No.
                   jC-gmf102220081h02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3402672
BLAST score
                   507
                   1.0e-51
E value
                   136
Match length
                   71
% identity
                   (AC004697) putative white protein [Arabidopsis thaliana]
NCBI Description
                   45750
Seq. No.
                   jC-gmfl02220081h06a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2244797
BLAST score
                   253
                   1.0e-21
E value
                   101
Match length
                   50
% identity
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45751
Seq. No.
                   jC-gmf102220081h11a1
Seq. ID
                   BLASTX
Method
                   g1237086
NCBI GI
BLAST score
                   166
                   2.0e-17
E value
                   81
Match length
                   65
% identity
                   (X96766) ADP-glucose pyrophosphorylase [Pisum sativum]
NCBI Description
                   45752
Seq. No.
                   jC-gmf102220082g03d1
Seq. ID
                   BLASTX
Method
                   g4432846
NCBI GI
                   386
BLAST score
                   2.0e-37
E value
                   103
Match length
                   72
% identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                    45753
 Seq. No.
                    jC-gmf102220083c11d1
 Seq. ID
                   BLASTX
 Method
                    g4490309
 NCBI GI
```

379

BLAST score



```
E value 2.0e-36
Match length 101
% identity 72
```

NCBI Description (AL035678) peroxidase ATP17a-like protein [Arabidopsis

thaliana]

Seq. No. Seq. ID

45754 jC-qmf102220084a11d1

Method BLASTX
NCBI GI g3445209

BLAST score 303 E value 1.0e-27 Match length 75 % identity 71

NCBI Description (AC004786) putative serine carboxypeptidase I [Arabidopsis

thaliana]

Seq. No.

45755

Seq. ID jC-gmf102220084b02a1 Method BLASTX NCBI GI g2499553

 NCBI GI
 g2499553

 BLAST score
 397

 E value
 1.0e-38

 Match length
 102

 % identity
 72

NCBI Description CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)

>gi 629524_pir__S39058 probable deoxyribodipyrimidine

photo-lyase (EC 4.1.99.3) - Arabidopsis thaliana >gi_442529_bbs_139743 (S66907) flavin-type blue-light photoreceptor, HY4=DNA photolyase/tropomyosin A homolog [Arabidopsis thaliana, ecotype Columbia, Peptide, 681 aa]

[Arabidopsis thaliana]

Seq. No. 45756

Seq. ID jC-gmf102220084c11d1

Method BLASTX
NCBI GI g1076334
BLAST score 175
E value 2.0e-12
Match length 50
% identity 60

NCBI Description hypothetical protein HYP1 - Arabidopsis thaliana

>gi 499168_emb_CAA56145_ (X79707) HYP1 [Arabidopsis

thaliana]

Seq. No. 45757

Seq. ID jC-gmfl02220084d03a1

Method BLASTX
NCBI GI g2213590
BLAST score 334
E value 3.0e-31
Match length 128
% identity 50

NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 45758

Seq. ID jC-gmf102220085d01a1



Method BLASTX
NCBI GI g3850588
BLAST score 422
E value 9.0e-42
Match length 102
% identity 75

NCBI Description (AC005278) Contains similarity to gb_AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF 00168. ESTs gb_AA585988 and gb_T04384 come

from this gene. [Arabidopsis thaliana]

Seq. No. 45759

Seq. ID jC-gmf102220085g09a1

Method BLASTX
NCBI GI g4558666
BLAST score 327
E value 2.0e-30
Match length 157
% identity 38

NCBI Description (AC007063) putative Na/H antiporter isolog [Arabidopsis

thaliana]

Seq. No. 45760

Seq. ID jC-gmf102220085g10d1

Method BLASTX
NCBI GI g1771162
BLAST score 205
E value 2.0e-16
Match length 49
% identity 78

NCBI Description (X98930) SBT2 [Lycopersicon esculentum]

>qi 3687307 emb CAA07000 (AJ006379) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 45761

Seq. ID jC-gmfl02220085h07a1

Method BLASTX
NCBI GI g1174718
BLAST score 146
E value 3.0e-09
Match length 122
% identity 21

NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR

>gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC
2.7.1.-) precursor - Arabidopsis thaliana >gi_166888

(L00670) protein kinase [Arabidopsis thaliana]

Seq. No. 45762

Seq. ID jC-gmf102220086a06a1

Method BLASTN
NCBI GI g1808591
BLAST score 64
E value 1.0e-27
Match length 172
% identity 84

NCBI Description C.arietinum mRNA for SAM-synthetase

Seq. ID Method



```
45763
Seq. No.
                  jC-gmf102220086a07d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2935342
BLAST score
                  265
                  3.0e-23
E value
Match length
                  56
% identity
                  84
                  (AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1
NCBI Description
                   [Arabidopsis thaliana]
                  45764
Seq. No.
                  jC-gmf102220086b04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3367520
BLAST score
                  428
                  3.0e-42
E value
                  155
Match length
% identity
                  54
                   (AC004392) Similar to protein kinase APK1A,
NCBI Description
                   tyrosine-serine-threonine kinase gb_D12522 from A.
                  thaliana. [Arabidopsis thaliana]
                   45765
Seq. No.
                   jC-gmf102220086c06d1
Seq. ID
Method
                  BLASTN
                   g3452136
NCBI GI
BLAST score
                   239
E value
                   1.0e-132
                   255
Match length
                   99
% identity
                  Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                  partial
                   45766
Seq. No.
                   jC-gmf102220086d01a1
Seq. ID
                   BLASTX
Method
                   g3367576
NCBI GI
BLAST score
                   154
                   1.0e-10
E value
                   52
Match length
                   58
% identity
                  (ALO31135) NAM / CUC2 -like protein [Arabidopsis thaliana]
NCBI Description
                   45767
Seq. No.
                   jC-gmf102220086d08d1
Seq. ID
                   BLASTX
Method
                   g1946358
NCBI GI
                   186
BLAST score
E value
                   3.0e-14
Match length
                   43
% identity
                   72
                  (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
                   45768
```

jC-gmf102220086f06a1

BLASTX

Match length

% identity

63

43



```
q2668744
NCBI GI
                  162
BLAST score
                  2.0e-11
E value
                  39
Match length
                  79
% identity
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                  45769
Seq. No.
                  jC-gmf102220086f10d1
Seq. ID
                  BLASTN
Method
                  g3033373
NCBI GI
                  44
BLAST score
                  1.0e-15
E value
Match length
                  92
% identity
                  87
                  Arabidopsis thaliana chromosome II BAC F19I3 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  45770
Seq. No.
                  jC-gmf102220088b03a1
Seq. ID
                  BLASTN
Method
                  g2769671
NCBI GI
BLAST score
                  186
                  1.0e-100
E value
                  496
Match length
                  89
% identity
                  Glycine max alternative oxidase (Aox2) mRNA, nuclear gene
NCBI Description
                  encoding mitochondrial protein, complete cds
                   45771
Seq. No.
                   jC-gmf102220088e05a1
Seq. ID
                  BLASTN
Method
                  g1122324
NCBI GI
                  244
BLAST score
E value
                  1.0e-135
                   408
Match length
                   90
% identity
NCBI Description P.sativum mRNA for SecA protein
                   45772
Seq. No.
                   jC-gmf102220088f02a1
Seq. ID
Method
                   BLASTX
                   g1707007
NCBI GI
BLAST score
                   261
E value
                   1.0e-22
Match length
                   125
% identity
                  (U78721) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45773
                   jC-gmf102220089d11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2501516
BLAST score
                   143
                   5.0e-09
E value
```

Seq. ID

45779

jC-gmfl02220090f05a1



```
SYNTAXIN BINDING PROTEIN 2 (UNC-18 HOMOLOG 2) (UNC-18B)
NCBI Description
                   (UNC18-2) >gi 2143861 pir A57022 Munc18-2 - rat
                   >gi 1022681 (\overline{U}20283) \overline{M}unc\overline{18}-2 [Rattus norvegicus]
                   45774
Seq. No.
                   jC-gmf102220089e09a1
Seq. ID
                   BLASTX
Method
                   g2275211
NCBI GI
                   177
BLAST score
                   7.0e-13
E value
                   39
Match length
                   85
% identity
NCBI Description (AC002337) RNA helicase isolog [Arabidopsis thaliana]
                   45775
Seq. No.
                   jC-gmf102220089f11d1
Seq. ID
                   BLASTX
Method
                   g629849
NCBI GI
                   221
BLAST score
                   5.0e-18
E value
                   100
Match length
                   49
% identity
                   pectate lyase (EC 4.2.2.2) - maize >gi 405535 (L20140)
NCBI Description
                   homology with pectate lyase [Zea mays]
                   45776
Seq. No.
                   jC-gmf102220089g07a1
Seq. ID
                   BLASTX
Method
                   g2245378
NCBI GI
                   408
BLAST score
                   5.0e-40
E value
                   118
Match length
                   65
% identity
                   (U83245) auxin response factor 1 [Arabidopsis thaliana]
NCBI Description
                   45777
Seq. No.
                   jC-qmf102220090c02d1
Seq. ID
                   BLASTX
Method
                   q2569940
NCBI GI
BLAST score
                   207
                   3.0e-16
E value
                   145
Match length
% identity
                   (Y15194) GRS protein [Arabidopsis thaliana]
NCBI Description
                   45778
Seq. No.
                   jC-qmf102220090d06a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3643608
                   249
BLAST score
E value
                   3.0e-21
                   68
Match length
% identity
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Method

NCBI GI

BLASTX g2642443



```
BLASTN
Method
                  g1262439
NCBI GI
                  373
BLAST score
E value
                  0.0e + 00
                  429
Match length
                  97
% identity
                  Glycine max lipoxygenase (vlxC) mRNA, complete cds
NCBI Description
                  45780
Sea. No.
                  jC-gmf102220090f11a1
Seq. ID
                  BLASTX
Method
                  g4220535
NCBI GI
BLAST score
                   498
                  2.0e-50
E value
Match length
                  121
% identity
                   83
                   (AL035356) clathrin coat assembly like protein [Arabidopsis
NCBI Description
                   thaliana]
                   45781
Seq. No.
                   jC-gmf102220090f12a1
Seq. ID
Method
                   BLASTX
                   q2500542
NCBI GI
BLAST score
                   396
                   2.0e-38
E value
Match length
                   141
% identity
                   51
                   PUTATIVE ATP-DEPENDENT RNA HELICASE YMR128W
NCBI Description
                   >gi 1078577 pir__S53058 probable membrane protein YMR128w -
                   yeast (Saccharomyces cerevisiae) >gi_728667_emb_CAA88553_
                   (Z48622) unknown [Saccharomyces cerevisiae]
                   45782
Seq. No.
                   jC-gmf102220090g04a1
Seq. ID
                   BLASTX
Method
                   g1786142
NCBI GI
                   254
BLAST score
                   8.0e-22
E value
Match length
                   149
                   33
% identity
                  (AB000455) PEThy; ZPT4-1 [Petunia x hybrida]
NCBI Description
                   45783
Seq. No.
                   jC-gmf102220091a11d1
Seq. ID
                   BLASTX
Method
                   g4335729
NCBI GI
BLAST score
                   164
                   3.0e-11
E value
                   117
Match length
% identity
                   (ACO06248) putative salt-inducible protein [Arabidopsis
NCBI Description
                   thaliana]
                   45784
Seq. No.
                   jC-qmf102220091b05a1
Seq. ID
```



```
BLAST score
                  5.0e-13
E value
Match length
                  60
                  58
% identity
                  (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  45785
Seq. No.
                  jC-gmf102220091c09d1
Seq. ID
                  BLASTN
Method
                  g169056
NCBI GI
                  33
BLAST score
                  4.0e-09
E value
                  89
Match length
                  84
% identity
NCBI Description P.sativum carbonic anhydrase mRNA, complete cds
                   45786
Seq. No.
                   jC-gmf102220091f09d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539662
                   140
BLAST score
                   1.0e-08
E value
                   49
Match length
                   55
% identity
                  (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                   45787
Seq. No.
                   jC-gmf102220091g02d1
Seq. ID
                   BLASTX
Method
                   g2459424
NCBI GI
BLAST score
                   334
                   3.0e-31
E value
                   121
Match length
                   60
% identity
                   (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                   45788
Seq. No.
                   jC-gmf102220091h02d1
Seq. ID
                   BLASTX
Method
                   g1350512
NCBI GI
BLAST score
                   145
                   5.0e-09
E value
                   112
Match length
                   29
% identity
                  (L47671) embryo-abundant protein [Picea glauca]
NCBI Description
                   45789
Seq. No.
                   jC-gmf102220092b05d1
Seq. ID
Method
                   BLASTX
                   q4056506
NCBI GI
BLAST score
                   150
E value
                   2.0e-09
Match length
                   87
                   43
% identity
                   (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
```

7352

45790

Seq. No.



```
jC-gmf102220092d11a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3927838
                  142
BLAST score
                  9.0e-09
E value
                  70
Match length
                  49
% identity
                  (AC005727) unknown protein [Arabidopsis thaliana]
NCBI Description
                  45791
Seq. No.
                  jC-gmf102220092e06d1
Seq. ID
                  BLASTX
Method
                  g4469008
NCBI GI
BLAST score
                  176
                  1.0e-12
E value
Match length
                  95
                  39
% identity
                  (AL035602) UDP rhamnose--anthocyanidin-3-glucoside
NCBI Description
                  rhamnosyltransferase-like protein [Arabidopsis thaliana]
                  45792
Seq. No.
                  jC-gmf102220092f11a1
Seq. ID
                  BLASTX
Method
                  g3559816
NCBI GI
BLAST score
                  520
                  6.0e-53
E value
Match length
                  144
% identity
                  76
NCBI Description (Y15782) transketolase 2 [Capsicum annuum]
                  45793
Seq. No.
                   jC-gmf102220092g01d1
Seq. ID
                  BLASTN
Method
                  g2765092
NCBI GI
BLAST score
                  102
                   4.0e-50
E value
                  262
Match length
                   85
% identity
                  Glycine max mRNA for cytochrome P450-like protein, clone
NCBI Description
                   45794
Seq. No.
                   jC-gmf102220093e06a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1786114
BLAST score
                   213
E value
                   1.0e-116
Match length
                   402
                   88
% identity
                  Vigna unguiculata phosphoinositide-specific phospholipase C
NCBI Description
                  mRNA, complete cds
                   45795
Seq. No.
Seq. ID
                   jC-gmfl02220094d02a1
```

Method BLASTN NCBI GI g1262439 BLAST score 447



E value 0.0e+00 Match length 447 % identity 100

NCBI Description Glycine max lipoxygenase (vlxC) mRNA, complete cds

Seq. No. 45796

Seq. ID jC-gmf102220094f03a1

Method BLASTX
NCBI GI g2828296
BLAST score 557
E value 2.0e-57
Match length 146
% identity 46

NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No. 45797

Seq. ID jC-gmfl02220096d10a1
Method BLASTX
NCBI GI g4218011
BLAST score 635
E value 2.0e-66

E value 2.0 Match length 148 % identity 82

NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]

>gi 4309721 gb_AAD15491 (AC006439) putative

serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 45798

Seq. ID jC-gmfl02220097d02a1

Method BLASTX

NCBI GI g3080389

BLAST score 219

E value 9.0e-18

Match length 112

% identity 52

NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No. 45799

Seq. ID jC-gmf102220097d10a1

Method BLASTX
NCBI GI g3522943
BLAST score 425
E value 6.0e-42
Match length 128
% identity 32

NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No. 45800

Seq. ID jC-gmf102220097f03a1

Method BLASTX
NCBI GI g4102600
BLAST score 267
E value 3.0e-23
Match length 76
% identity 75

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]



Seq. ID jC-gmfl02220097f06a1

Method BLASTX
NCBI GI g2102691
BLAST score 146
E value 4.0e-09
Match length 75
% identity 43

NCBI Description (U64817) fructokinase [Lycopersicon esculentum]

Seq. No. 45802

Seq. ID jC-gmf102220097g03d1

Method BLASTN
NCBI GI g1142620
BLAST score 148
E value 1.0e-77
Match length 236
% identity 91

NCBI Description Phaseolus vulgaris phaseolin G-box binding protein PG2

(PG2) mRNA, partial cds

Seq. No. 45803

Seq. ID jC-gmf102220097g05a1

Method BLASTX
NCBI GI g1800147
BLAST score 208
E value 2.0e-16
Match length 82
% identity 60

NCBI Description (U83655) membrane associated protein [Arabidopsis thaliana]

Seq. No. 45804

Seq. ID jC-gmf102220098a07d1

Method BLASTN
NCBI GI g1332578
BLAST score 40
E value 3.0e-13
Match length 74
% identity 13

NCBI Description P.sylvestris mRNA for polyubiquitin

Seq. No. 45805

Seq. ID jC-gmf102220098f02d1

Method BLASTX
NCBI GI g4467139
BLAST score 176
E value 1.0e-12
Match length 57
% identity 63

NCBI Description (AL035540) putative protein phosphatase-2c [Arabidopsis

thaliana]

Seq. No. 45806

Seq. ID jC-gmfl02220098g04d1

Method BLASTX NCBI GI g3080389



BLAST score 240 E value 3.0e-20 Match length 64 % identity 73

NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No. 45807

Seq. ID jC-gmf102220100c08a1

Method BLASTX
NCBI GI g3335372
BLAST score 238
E value 4.0e-20
Match length 103
% identity 44

NCBI Description (AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No. 45808

Seq. ID jC-gmfl02220101a08a1

Method BLASTX
NCBI GI g886130
BLAST score 200
E value 1.0e-15
Match length 52
% identity 67

NCBI Description (U28148) putative pectinesterase [Medicago sativa]

Seq. No. 45809

Seq. ID jC-gmf102220101b09a1

Method BLASTX
NCBI GI g3892045
BLAST score 236
E value 8.0e-20
Match length 52
% identity 87

NCBI Description (AC002330) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 45810

Seq. ID jC-gmfl02220101b11d1

Method BLASTN
NCBI GI g3334662
BLAST score 387
E value 0.0e+00
Match length 391
% identity 100

NCBI Description G.max mRNA for putative cytochrome P450, clone CP4

Seq. No. 45811

Seq. ID jC-gmfl02220101c10a1

Method BLASTX
NCBI GI g4006831
BLAST score 264
E value 5.0e-23
Match length 138
% identity 35

NCBI Description (AC005970) putative reverse transcriptase [Arabidopsis



thaliana]

Seq. No. 45812 Seq. ID jC-gmfl02220101f08a1 Method BLASTX NCBI GI g1684851 BLAST score 145 E value 4.0e-09 Match length 75 % identity 44 NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris] 45813 Seq. No. Seq. ID jC-gmf102220102a01a1 Method BLASTN NCBI GI g4159706 BLAST score 36 E value 1.0e-10 Match length 127 % identity 86 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MGL6, complete sequence [Arabidopsis thaliana] Seq. No. 45814 Seq. ID jC-gmf102220102e04a1 Method BLASTX NCBI GI g3367596 BLAST score 345 E value 2.0e-32 95 Match length % identity 69 NCBI Description (AL031135) putative protein [Arabidopsis thaliana] Seq. No. 45815 jC-gmfl02220102f12a1 Seq. ID Method BLASTX NCBI GI g4115386 BLAST score 261 1.0e-22 E value Match length 105 % identity 58 NCBI Description (AC005967) unknown protein [Arabidopsis thaliana] 45816 Seq. No. Seq. ID jC-gmf102220103b11d1 Method BLASTX NCBI GI g4115357 BLAST score 157 E value 2.0e-10 Match length 62 % identity 42 NCBI Description (AC005957) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45817

Seq. ID jC-gmfl02220103c04a1

Method BLASTX NCBI GI g1946368



BLAST score E value 6.0e-21 Match length 109 47 % identity NCBI Description 45818 Seq. No. Seq. ID

(U93215) unknown protein [Arabidopsis thaliana]

jC-gmf102220103d04a1

Method BLASTX NCBI GI g3913366 BLAST score 363 7.0e-35 E value Match length 113 % identity 70

PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR NCBI Description >gi 1597723 (U67422) CRINKLY4 precursor [Zea mays]

45819 Seq. No.

Seq. ID jC-gmf102220103d08a1

Method BLASTX NCBI GI g4510401 BLAST score 555 4.0e-57 E value Match length 139 % identity 71

(AC006587) putative general negative regulator of NCBI Description

transcription [Arabidopsis thaliana]

45820 Seq. No.

jC-gmf102220103e09a1 Seq. ID

Method BLASTX g3559805 NCBI GI 370 BLAST score E value 2.0e-35 76 Match length % identity 83

NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis

thalianal

Seq. No. 45821

Seq. ID jC-gmf102220103g04a1

Method BLASTX NCBI GI g2829910 BLAST score 429 E value 2.0e-42 Match length 110 % identity 33

(AC002291) Unknown protein, contains regulator of NCBI Description

chromosome condensation motifs [Arabidopsis thaliana]

Seq. No. 45822

jC-qmf102220103g07a1 Seq. ID

Method BLASTX g4512663 NCBI GI BLAST score 193 8.0e-15 E value Match length 122



```
% identity
                  (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >qi 4544470 gb AAD22377.1 AC006580 9 (AC006580)
                  hypothetical protein [Arabidopsis thaliana]
                  45823
Seq. No.
                  jC-qmf102220103h07a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3293030
BLAST score
                  34
                  1.0e-09
E value
Match length
                  66
                  88
% identity
                  Ricinus communis mRNA for amino acid carrier
NCBI Description
Seq. No.
                  45824
                  jC-gmf102220104d07d1
Seq. ID
                  BLASTN
Method
                  q169920
NCBI GI
BLAST score
                  82
                  3.0e-38
E value
                  159
Match length
% identity
                  91
                  Soybean auxin-regulated protein (Aux28) mRNA, complete cds
NCBI Description
Seq. No.
                  45825
                  jC-gmf102220104h06d1
Seq. ID
Method
                  BLASTX
                  q3367596
NCBI GI
                  195
BLAST score
                  7.0e-15
E value
                  69
Match length
                  46
% identity
                  (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  45826
                  jC-gmf102220106a02a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2494143
BLAST score
                  535
E value
                  7.0e-55
Match length
                  132
                  73
% identity
NCBI Description
                  (AC002329) Mlo-like protein [Arabidopsis thaliana]
Seq. No.
                  45827
                  jC-gmf102220106f04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097587
                  221
BLAST score
```

E value 6.0e-18 Match length 64 58 % identity

NCBI Description (U64926) NTGP5 [Nicotiana tabacum]

Seq. No. 45828

jC-qmf102220106g02a1 Seq. ID



```
BLASTX
Method
NCBI GI
                  q4559356
BLAST score
                  333
                  3.0e-31
E value
Match length
                  110
                  13
% identity
NCBI Description
                  (AC006585) hypothetical protein [Arabidopsis thaliana]
                  45829
Seq. No.
                  jC-gmf102220106h02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g516853
BLAST score
                  231
                  1.0e-127
E value
Match length
                  307
                  29
% identity
NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.
                  45830
                  jC-gmf102220108b03d1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1575724
BLAST score
                  41
E value
                  6.0e-14
Match length
                  193
% identity
                  88
                  Glycine max 14-3-3 related protein SGF14A mRNA, complete
NCBI Description
                  45831
Seq. No.
                   jC-gmf102220108b10a1
Seq. ID
Method
                  BLASTX
                  q1621467
NCBI GI
BLAST score
                   553
                   9.0e-72
E value
Match length
                  164
% identity
                  81
NCBI Description
                  (U73106) laccase [Liriodendron tulipifera]
Seq. No.
                   45832
                   jC-qmf102220108b11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2330649
BLAST score
                  238
E value
                  2.0e-30
Match length
                   157
% identity
NCBI Description
                  (Y14558) topoisomerase I [Pisum sativum]
Seq. No.
                   45833
                   jC-qmf102220108c01a1
Seq. ID
Method
                  BLASTX
                   q3859602
NCBI GI
```

NCBI GI g3859602
BLAST score 293
E value 8.0e-27
Match length 80
% identity 64



NCBI Description (AF104919) contains similarity to human

DHHC-domain-containing cysteine-rich protein (GB:U90653) and several S. cerevisiae probable membrane proteins (GB:U20865, Z48758, U43491) [Arabidopsis thaliana]

Seq. No. 45834

Seq. ID jC-gmf102220108c05a1

Method BLASTN
NCBI GI g945086
BLAST score 47
E value 2.0e-17
Match length 59
% identity 95

NCBI Description Glycine max transcription factor TFIIB mRNA, complete cds

Seq. No. 45835

Seq. ID jC-gmf102220108c10a1

Method BLASTN
NCBI GI g2924653
BLAST score 49
E value 2.0e-18
Match length 57
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDA7, complete sequence [Arabidopsis thaliana]

Seq. No. 45836

Seq. ID jC-gmfl02220108d02a1

Method BLASTX
NCBI GI g3063455
BLAST score 263
E value 8.0e-25
Match length 124
% identity 55

NCBI Description (AC003981) F22013.17 [Arabidopsis thaliana]

Seq. No. 45837

Seq. ID jC-gmfl02220108g06a1

Method BLASTX
NCBI GI g2191150
BLAST score 290
E value 1.0e-26
Match length 73
% identity 46

NCBI Description (AF007269) similar to mitochondrial carrier family

[Arabidopsis thaliana]

Seq. No. 45838

Seq. ID jC-gmf102220112e12a1

Method BLASTX
NCBI GI g1052973
BLAST score 213
E value 4.0e-17
Match length 54
% identity 80

NCBI Description (U37838) fructokinase [Beta vulgaris]



Seq. ID jC-gmf102220112f12d1

Method BLASTX
NCBI GI g1345933
BLAST score 155
E value 2.0e-10
Match length 51
% identity 59

NCBI Description CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS)

>gi_1084323_pir__S53007 citrate synthase - cucurbit
>gi_975633_dbj_BAA07328_ (D38132) glyoxysomal citrate

synthase [Cucurbita sp.]

Seq. No. 45840

Seq. ID jC-gmf102220112h12a1

Method BLASTX
NCBI GI g2213594
BLAST score 290
E value 5.0e-26
Match length 97
% identity 49

NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No. 45841

Seq. ID jC-gmfl02220114a03a1

Method BLASTX

NCBI GI g3193327

BLAST score 241

E value 1.0e-20

Match length 82
% identity 57

NCBI Description (AF069299) No definition line found [Arabidopsis thaliana]

Seq. No. 45842

Seq. ID jC-gmfl02220114c02a1

Method BLASTX
NCBI GI g2804278
BLAST score 508
E value 1.0e-51
Match length 140
% identity 69

NCBI Description (AB003516) squalene epoxidase [Panax ginseng]

Seq. No. 45843

Seq. ID jC-gmf102220114c04a1

Method BLASTX
NCBI GI g2244918
BLAST score 143
E value 8.0e-09
Match length 57
% identity 49

NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 45844

Seq. ID jC-gmf102220114d04a1

Method BLASTX NCBI GI g3894385



```
BLAST score
E value
                  2.0e-22
Match length
                  157
                  5
% identity
                  (AF053994) Hcr2-OA [Lycopersicon esculentum]
NCBI Description
                  45845
Seq. No.
                  jC-gmfl02220114f06d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2398531
BLAST score
                  306
                  7.0e-28
E value
Match length
                  82
% identity
                  77
                  (Y13726) Transcription factor [Arabidopsis thaliana]
NCBI Description
                  45846
Seq. No.
                  jC-gmf102220114h09d1
Seq. ID
Method
                  BLASTX
                  q4262222
NCBI GI
BLAST score
                  203
                  6.0e-16
E value
                  91
Match length
                  33
% identity
                  (AC006200) putative RNA helicase A, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                  45847
Seq. No.
                   jC-qmf102220115a03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3075398
BLAST score
                  321
                   4.0e-30
E value
Match length
                  89
% identity
                   65
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45848
                   jC-gmf102220115b02a1
Seq. ID
Method
                  BLASTN
                  q3452136
NCBI GI
                   239
BLAST score
                   1.0e-132
E value
                   255
Match length
% identity
                   99
                  Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                  partial
Seq. No.
                   45849
Seq. ID
                   jC-qmf102220115b11a1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1345132
BLAST score 638
E value 7.0e-67
Match length 134
% identity 17

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

NCBI Description



>gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
protein kinase, ERECTA [Arabidopsis thaliana]

45850 Seq. No. jC-gmf102220115c01a1 Seq. ID BLASTX Method NCBI GI g2392021 BLAST score 241 3.0e-20E value 69 Match length 62 % identity (D63425) phopholipid hydroperoxide glutathione NCBI Description peroxidase-like protein [Spinacia oleracea] 45851 Seq. No. jC-gmf102220115g02a1 Seq. ID Method BLASTX NCBI GI g2213592 392 BLAST score 3.0e-38 E value 109 Match length 33 % identity (AC000348) T7N9.12 [Arabidopsis thaliana] NCBI Description 45852 Seq. No. jC-gmf102220115g09a1 Seq. ID BLASTN Method q410285 NCBI GI BLAST score 104 3.0e-51 E value 188 Match length 89 % identity NCBI Description Pisum sativum rho (ras-related) GTP-binding protein mRNA, complete cds 45853 Seq. No. jC-gmf102220125b03d1 Seq. ID BLASTX Method NCBI GI q3927836 BLAST score 148 E value 2.0e-09 50 Match length 52 % identity NCBI Description (AC005727) unknown protein [Arabidopsis thaliana] 45854 Seq. No. jC-qmf102220125e04a1 Seq. ID Method BLASTX NCBI GI q3482967 BLAST score 269 7.0e-24 E value Match length 62 % identity 82

protein phosphatase 2C [Arabidopsis thaliana]

(AL031369) Protein phosphatase 2C-like protein [Arabidopsis

thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)

NCBI GI

BLAST score

g266567

205



```
Seq. No.
                  45855
                  jC-gmf102220125e07a1
Seq. ID
Method
                  BLASTX
                  g4454039
NCBI GI
                  149
BLAST score
                  9.0e-10
E value
Match length
                  90
% identity
                  32
NCBI Description
                  (AL035394) putative Na+/H+-exchanging protein [Arabidopsis
                  thaliana]
Seq. No.
                  45856
Seq. ID
                  jC-gmf102220125f07d1
Method
                  BLASTX
NCBI GI
                  q4512671
BLAST score
                  165
E value
                  1.0e-11
Match length
                  46
                  70
% identity
NCBI Description
                  (AC006931) unknown protein [Arabidopsis thaliana]
                  45857
Seq. No.
Seq. ID
                  jC-gmf102220125h10d1
Method
                  BLASTX
NCBI GI
                  g3201635
BLAST score
                  147
E value
                  1.0e-09
Match length
                  37
% identity
                  78
NCBI Description
                  (AC004669) hypothetical protein [Arabidopsis thaliana]
                  45858
Seq. No.
Seq. ID
                  jC-gmf102220126g06a1
Method
                  BLASTX
NCBI GI
                  g1350677
BLAST score
                  176
                  2.0e-13
E value
Match length
                  58
% identity
                  62
NCBI Description
                  60S RIBOSOMAL PROTEIN L19
Seq. No.
                  45859
Seq. ID
                  jC-gmf102220127b04d1
Method
                  BLASTX
NCBI GI
                  q4415929
BLAST score
                  174
E value
                  2.0e-12
Match length
                  88
% identity
                  36
NCBI Description
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
                  45860
Seq. No.
Seq. ID
                  jC-gmf102220127e04d1
Method
                  BLASTX
```

7365



4.0e-16 E value Match length 58 67 % identity

MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR NCBI Description

(ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi_421956_pir__S23558 mitochondrial processing peptidase
(EC 3.4.99.41) alpha chain precursor - potato

>gi_21493_emb_CAA46990_ (X66284) mitochondrial processing

peptidase [Solanum tuberosum]

45861 Seq. No.

jC-gmf102220127e09a1 Seq. ID

Method BLASTX g2894607 NCBI GI 153 BLAST score 3.0e-10 E value 53 Match length 51 % identity

(AL021889) NAM (no apical meristem) - like protein NCBI Description

[Arabidopsis thaliana]

45862 Seq. No.

jC-gmf102220127e10d1 Seq. ID

Method BLASTX g480314 NCBI GI BLAST score 156 2.0e-10 E value Match length 52 58 % identity

NCBI Description UDP rhamnose--anthocyanidin-3-glucoside

rhamnosyltransferase - garden petunia (fragment) >gi 397567 emb CAA81057 (Z25802) UDP rhamnose:

anthocyanidin-3-glucoside rhamnosyltransferase [Petunia x

hybrida]

45863 Seq. No.

Seq. ID jC-qmf102220127h05d1

BLASTX Method g1652057 NCBI GI BLAST score 167 2.0e-11 E value Match length 54 % identity 59

(D90902) hypothetical protein [Synechocystis sp.] NCBI Description

Seq. No. 45864

jC-gmf102220130d10a1 Seq. ID

BLASTN Method NCBI GI q169974 BLAST score 164 E value 3.0e-87 304 Match length % identity

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 45865

Seq. ID jC-gmf102220130f11a1



```
BLASTX
Method
NCBI GI
                  q1663545
BLAST score
                  157
                  2.0e-10
E value
Match length
                  71
% identity
                  46
                  (U55807) disease resistance protein homolog [Glycine max]
NCBI Description
Seq. No.
                  45866
                  jC-gmf102220130h09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402697
BLAST score
                  647
E value
                  8.0e-68
Match length
                  174
                  72
% identity
                  (AC004261) putative phosphatidylinositol-4-phosphate
NCBI Description
                  5-kinase [Arabidopsis thaliana]
                  45867
Seq. No.
                  jC-gmf102220130h09d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3894201
BLAST score
                  155
E value
                  3.0e-10
Match length
                  33
                  85
% identity
                  (AC005662) phosphatidylinositol-4-phosphate-5-kinase, 5'
NCBI Description
                  partial [Arabidopsis thaliana]
Seq. No.
                  45868
Seq. ID
                  jC-gmf102220131a09d1
Method
                  BLASTX
NCBI GI
                  q3738325
BLAST score
                  198
E value
                   3.0e-15
Match length
                  75
% identity
                   61
                   (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                   thaliana]
                  45869
Seq. No.
                  jC-gmfl02220131b01d1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g758643
BLAST score
                  175
E value
                  1.0e-93
Match length
                  247
% identity
                   93
NCBI Description P.sativum mRNA for nucleoside diphosphate kinase II
```

Seq. ID jC-gmf102220131b04d1

Method BLASTX
NCBI GI g459009
BLAST score 187
E value 3.0e-14

Match length % identity 43 (U00037) similar to multifunctional aminoacyl-tRNA NCBI Description synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans] Seq. No. 45871 jC-gmf102220131e12a1 Seq. ID Method BLASTX NCBI GI g4567279 BLAST score 166 E value 2.0e-11 Match length 166 % identity 31 (AC006841) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] Seq. No. 45872 jC-gmf102220131g03d1 Seq. ID Method BLASTX g4140026 NCBI GI BLAST score 245 E value 9.0e-21 Match length 78 % identity 59 (AB009370) flavonoid 3-O-galactosyl transferase [Vigna NCBI Description mungo] 45873 Seq. No.

Seq. ID jC-gmfl02220131h02d1

Method BLASTX
NCBI GI g112564
BLAST score 161
E value 2.0e-11
Match length 51
% identity 61

NCBI Description beta-glucosidase (EC 3.2.1.21) - cassava

>gi 249262 bbs 101989 (S35175) linamarase=beta-glucosidase

[Manihot esculenta=cassava, Cranz, Peptide, 531 aa]

[Manihot esculenta]

Seq. No. 45874

Seq. ID jC-gmf102220132aa09a1

Method BLASTX
NCBI GI g2654868
BLAST score 178
E value 6.0e-13
Match length 57
% identity 74

NCBI Description (AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No. 45875

Seq. ID jC-gmfl02220132af04a1

Method BLASTX
NCBI GI g3776581
BLAST score 392
E value 5.0e-38



Match length 109 % identity 70

NCBI Description (AC005388) Similar to Beta integral membrane protein

homolog gb U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 45876

Seq. ID jC-gmf102220132ah12a1

Method BLASTX
NCBI GI g2642433
BLAST score 165
E value 2.0e-11
Match length 139
% identity 36

NCBI Description (AC002391) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 45877

Seq. ID jC-gmfl02220133f08a1

Method BLASTX
NCBI GI g833835
BLAST score 293
E value 2.0e-26
Match length 109
% identity 54

NCBI Description (U26025) amygdalin hydrolase isoform AH I precursor [Prunus

serotina]

Seq. No. 45878

Seq. ID jC-gmf102220136d03d1

Method BLASTN
NCBI GI g3885514
BLAST score 121
E value 2.0e-61
Match length 268
% identity 87

NCBI Description Medicago sativa clone MS56 unknown mRNA

Seq. No. 45879

Seq. ID jC-gmfl02220136g06a1

Method BLASTX
NCBI GI g1916290
BLAST score 172
E value 3.0e-12
Match length 77
% identity 47

NCBI Description (U89876) ALY [Mus musculus]

Seq. No. 45880

Seq. ID jC-gmf102220138a10a1

Method BLASTX
NCBI GI g3258569
BLAST score 207
E value 2.0e-16
Match length 51
% identity 73

NCBI Description (U89959) Similar to yeast general negative regulator of

transcription subunit 1 [Arabidopsis thaliana]



```
Seq. No.
                   45881
                   jC-gmf102220138b02d1
Seq. ID
Method
                   BLASTN
                   g1732362
NCBI GI
BLAST score
                   45
E value
                   4.0e-16
Match length
                   97
                   87
% identity
NCBI Description Malus domestica pAFD103 mRNA, partial cds
                   45882
Seq. No.
                   jC-gmf102220138b03d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4376203
BLAST score
                   275
                   3.0e-24
E value
                   99
Match length
                   51
% identity
                   (U35226) putative cytochrome P-450 [Nicotiana
NCBI Description
                   plumbaginifolia]
                   45883
Seq. No.
                   jC-gmf102220138c06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g399356
BLAST score
                   249
E value
                   3.0e-21
Match length
                   124
% identity
                   47
                   PSEUDOURIDYLATE SYNTHASE 3 (PSEUDOURIDINE SYNTHASE 3)
NCBI Description
                   (DEPRESSED GROWTH-RATE PROTEIN DEG1) >gi_82981_pir__S14145
                   depressed growth-rate protein DEG1 - yeast (Saccharomyces cerevisiae) >gi_836755_dbj_BAA09239_ (D50617) depressed
                   growth-rate protein [Saccharomyces cerevisiae]
                   >gi_870819_dbj_BAA08034_ (D44600) DEPRESSED GROWTH-RATE
                   PROTEIN DEG1 [Saccharomyces cerevisiae]
                   45884
Seq. No.
Seq. ID
                   jC-qmf102220138d06a1
Method
                   BLASTN
NCBI GI
                   q456567
BLAST score
                   76
E value
                   1.0e-34
Match length
                   202
                   87
% identity
NCBI Description
                   Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
Seq. No.
                   45885
Seq. ID
                   jC-qmf102220138e04a1
```

Method BLASTN
NCBI GI g18761
BLAST score 312
E value 1.0e-175
Match length 376
% identity 96



```
NCBI Description Soybean stem mRNA for 31 kD glycoprotein
                  45886
Seq. No.
                  jC-gmf102220138e11a1
Seq. ID
                  BLASTX
Method
                  g3341443
NCBI GI
                  201
BLAST score
                  5.0e-16
E value
                  73
Match length
                  58
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                  45887
Seq. No.
                  jC-gmf102220138f04d1
Seq. ID
Method
                  BLASTX
                  g3258569
NCBI GI
BLAST score
                  179
                  3.0e-13
E value
                  58
Match length
                  62
% identity
                  (U89959) Similar to yeast general negative regulator of
NCBI Description
                  transcription subunit 1 [Arabidopsis thaliana]
                  45888
Seq. No.
                  jC-gmf102220138g01d1
Seq. ID
Method
                  BLASTX
                  g2583123
NCBI GI
                  160
BLAST score
                  5.0e-11
E value
                  51
Match length
                  59
% identity
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                  thaliana]
                  45889
Seq. No.
                  jC-gmf102220138g08a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3947733
                   233
BLAST score
                   3.0e-19
E value
Match length
                  132
                   41
% identity
                  (AJ009719) NL25 [Solanum tuberosum]
NCBI Description
Seq. No.
                   45890
                   jC-gmf102220139b11a1
Seq. ID
                   BLASTX
Method
```

q2116552 NCBI GI BLAST score 164 1.0e-17 E value Match length 111 43 % identity

(AB000113) cationic amino acid transporter 3 [Rattus NCBI Description

norvegicus]

45891 Seq. No.

jC-gmf102220139f11a1 Seq. ID



```
BLASTN
Method
NCBI GI
                  q556835
BLAST score
                  122
                   3.0e-62
E value
                   240
Match length
                   89
% identity
NCBI Description P.vulgaris mRNA for profilin
                   45892
Seq. No.
                   jC-gmf102220139g11d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g629592
BLAST score
                   290
E value
                   6.0e-26
                   122
Match length
                   49
% identity
NCBI Description hypothetical protein - rape
Seq. No.
                   45893
                   jC-gmf102220139h01a1
Seq. ID
Method
                   BLASTN
                   g497119
NCBI GI
BLAST score
                   134
E value
                   2.0e-69
Match length
                   234
% identity
                   89
                  Pisum sativum monodehydroascorbate reductase mRNA, complete
NCBI Description
                   45894
Seq. No.
                   jC-gmf102220141a01d1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2961335
BLAST score
                   34
                   1.0e-09
E value
Match length
                   58
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20
NCBI Description
                   (ESSAII project)
                   45895
Seq. No.
Seq. ID
                   jC-qmf102220141e06d1
Method
                   BLASTX
NCBI GI
                   g3608133
BLAST score
                   155
E value
                   3.0e-10
Match length
                   42
                   64
% identity
                  (AC005314) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45896
                   jC-qmf102220142a03d1
Seq. ID
Method
                   BLASTN
                   g2149954
NCBI GI
BLAST score
                   43
```

4.0e-15

79

E value Match length



% identity Phaseolus vulgaris putative aquaporin-1 (Mip-1) mRNA, NCBI Description complete cds 45897 Seq. No. jC-gmf102220142b06a1 Seq. ID BLASTX Method q3176660 NCBI GI 246 BLAST score 4.0e-21 E value 102 Match length

% identity 48 (AC004393) Similar to ERECTA receptor protein kinase NCBI Description gb U47029 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 45898

jC-gmf102220142c03d1 Seq. ID

BLASTX Method q548746 NCBI GI 159 BLAST score E value 6.0e-11 Match length 39 79 % identity

50S RIBOSOMAL PROTEIN L12, CHLOROPLAST PRECURSOR (CL12) NCBI Description

>gi_478604_pir__S21111 ribosomal protein L12 precursor, chloroplast - wood tobacco >gi_248303_bbs_93167 (S93166) ribosomal protein L12, CL12 [Nicotiana sylvestris=tobacco, leaf, Peptide Chloroplast, 186 aa] [Nicotiana sylvestris]

45899 Seq. No.

jC-qmf102220142d01d1 Seq. ID

Method BLASTX q633890 NCBI GI 325 BLAST score 3.0e-30 E value 111 Match length % identity

(S72926) glucose and ribitol dehydrogenase homolog [Hordeum NCBI Description

vulgare]

45900 Seq. No.

jC-gmf102220142f03d1 Seq. ID

BLASTN Method q56539 NCBI GI 103 BLAST score 8.0e-51 E value Match length 284 100 % identity

R.norvegicus gene encoding prolactin, exon 5 NCBI Description

>gi 206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

45901 Seq. No.

jC-qmf102220142f10d1 Seq. ID

BLASTX Method NCBI GI g2146731 239 BLAST score



```
2.0e-20
E value
Match length
                   86
% identity
                   20
                  FK506-binding protein - Arabidopsis thaliana >gi_1354207
NCBI Description
                   (U49453) rof1 [Arabidopsis thaliana]
                   45902
Seq. No.
                   jC-gmfl02220142g12a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2961352
BLAST score
                   221
                   5.0e-18
E value
Match length
                   94
                   47
% identity
                   (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45903
                   jC-gmf102220143a12a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g14311
BLAST score
                   40
                   2.0e-13
E value
Match length
                   67
% identity
                   97
                   G.max chloroplast gene rps19 and flanking regions
NCBI Description
                   45904
Seq. No.
                   jC-gmf102220143b12d1
Seq. ID
Method
                   BLASTX
                   g2347208
NCBI GI
BLAST score
                   157
                   2.0e-10
E value
                   94
Match length
                   33
% identity
                   (AC002338) APG protein isolog [Arabidopsis thaliana]
NCBI Description
                   45905
Seq. No.
                   jC-gmf102220143c08d1
Seq. ID
                   {\tt BLASTX}
Method
                   g3335359
NCBI GI
                   411
BLAST score
                   4.0e-40
E value
                   94
Match length
                   82
% identity
                   (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   45906
Seq. No.
                   jC-gmf102220143d01d1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g169980
BLAST score
                   217
E value
                   1.0e-118
                   386
Match length
                   93
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
```



```
jC-gmf102220143d12d1
Seq. ID
                  BLASTX
Method
                   g4432844
NCBI GI
BLAST score
                   194
                   9.0e-15
E value
                   79
Match length
                   43
% identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   45908
Seq. No.
                   jC-gmf102220143e09d1
Seq. ID
                   BLASTX
Method
                   g4234955
NCBI GI
BLAST score
                   200
                   2.0e-15
E value
Match length
                   59
% identity
                   63
                   (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
NCBI Description
                   45909
Seq. No.
                   jC-gmf102220144a02a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1173641
BLAST score
                   257
                   1.0e-142
E value
                   511
Match length
% identity
                   96
                   Glycine max lipoxygenase (lox7) mRNA, complete cds
NCBI Description
                   45910
Seq. No.
                   jC-gmf102220144a07a1
Seq. ID
                   BLASTX
Method
                   q2335096
NCBI GI
                   368
BLAST score
                   4.0e-35
E value
                   170
Match length
% identity
                   51
                   (AC002339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45911
 Seq. No.
                   jC-gmf102220144b03a1
 Seq. ID
                   BLASTN
Method
                   q348717
NCBI GI
                   241
BLAST score
                   1.0e-133
E value
                   481
Match length
                   88
 % identity
                   Medicago truncatula protochlorophyllide reductase homolgue
 NCBI Description
                   protein mRNA, complete cds
                    45912
 Seq. No.
                    jC-gmf102220144f01a1
 Seq. ID
                   BLASTX
 Method
                   g3337351
 NCBI GI
                   192
 BLAST score
```

2.0e-14

96

E value

Match length

NCBI Description



```
% identity
                 (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  45913
Seq. No.
                  jC-gmf102220145d09a1
Seq. ID
Method
                  BLASTX
                  q2352492
NCBI GI
                  166
BLAST score
                  4.0e-12
E value
                  55
Match length
% identity
                  51
                  (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                  thaliana] >gi 2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
Seq. No.
                  45914
Seq. ID
                  jC-qmf102220145e11a1
Method
                  BLASTX
                  g2244996
NCBI GI
                  501
BLAST score
                   9.0e-51
E value
Match length
                   159
                   65
% identity
                  (Z97341) similarity to a membrane-associated salt-inducible
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                   45915
                   jC-gmf102220146e12a1
Seq. ID
                   BLASTN
Method
                   g517257
NCBI GI
BLAST score
                   70
                   7.0e-31
E value
                   118
Match length
                   90
% identity
                   Z.mays MNB1a mRNA for DNA-binding protein
NCBI Description
                   45916
Seq. No.
                   jC-gmf102220148a04a1
Seq. ID
                   BLASTX
Method
                   q3915039
NCBI GI
BLAST score
                   324
E value
                   5.0e-30
                   112
Match length
                   58
% identity
                   SUGAR CARRIER PROTEIN C >gi_169718 (L08196) sugar carrier
NCBI Description
                   protein [Ricinus communis]
                   45917
 Seq. No.
                   jC-gmf102220148b07a1
 Seq. ID
                   BLASTX
Method
                   g2760326
NCBI GI
                   230
 BLAST score
                   4.0e-19
 E value
                   124
 Match length
                   31
 % identity
```

(AC002130) F1N21.11 [Arabidopsis thaliana]



```
45918
Seq. No.
Seq. ID
                  jC-qmf102220148b09a1
                  BLASTN
Method
                  g1663548
NCBI GI
BLAST score
                  74
E value
                  2.0e-33
                  142
Match length
                  88
% identity
                  Glycine max clone RLG6 disease resistance protein homolog
NCBI Description
                  gene, partial cds
                  45919
Seq. No.
                  jC-gmf102220148f08a1
Seq. ID
                  BLASTX
Method
                  g3176874
NCBI GI
BLAST score
                  282
E value
                   4.0e-25
Match length
                  117
                   52
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                  thaliana]
                   45920
Seq. No.
                   jC-gmf102220148g04a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q730456
BLAST score
                   171
                   1.0e-12
E value
                   44
Match length
% identity
                   70
NCBI Description
                  40S RIBOSOMAL PROTEIN S19
Seq. No.
                   45921
                   jC-qmf102220148g06a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2661020
BLAST score
                   266
E value
                   1.0e-148
Match length
                   306
% identity
                   97
NCBI Description Glycine max catalase (cat4) mRNA, complete cds
Seq. No.
                   45922
                   jC-gmle01810002a12d1
Seq. ID
                   BLASTN
Method
                   g1711035
NCBI GI
                   71
BLAST score
                   1.0e-31
E value
                   105
Match length
                   96
% identity
                   Pisum sativum hydroxyproline rich glycoprotein PsHRGP1
NCBI Description
                   mRNA, partial cds
```

Seq. ID jC-gmle01810002g02a1

Method BLASTX NCBI GI g3128174



```
BLAST score
                  1.0e-09
E value
                  48
Match length
% identity
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  45924
Seq. No.
Seq. ID
                  jC-qmle01810003d02a1
                  BLASTN
Method
                  q1326160
NCBI GI
BLAST score
                  58
                  5.0e-24
E value
                  168
Match length
                  95
% identity
NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds
Seq. No.
                   45925
                  jC-qmle01810004a02a1
Seq. ID
                  BLASTX
Method
                   q1082359
NCBI GI
                  110
BLAST score
                   1.0e-10
E value
                   95
Match length
                   43
% identity
                  excision repair protein ERCC5 - human >gi_306742 (L20046)
NCBI Description
                   excision repair protein [Homo sapiens]
                   45926
Seq. No.
                   jC-gmle01810004a05d1
Seq. ID
Method
                   BLASTN
                   q3452136
NCBI GI
                   239
BLAST score
E value
                   1.0e-132
                   255
Match length
% identity
                   99
                  Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                   partial
                   45927
Seq. No.
                   jC-gmle01810004a08a1
Seq. ID
Method
                   BLASTX
                   g128284
NCBI GI
BLAST score
                   153
E value
                   5.0e-10
Match length
                   126
                   35
% identity
                  PYRUVATE-FLAVODOXIN OXIDOREDUCTASE >gi_43821 emb_CAA31665_
NCBI Description
                   (X13303) nifJ protein (AA 1-1171) [Klebsiella pneumoniae]
                   45928
Seq. No.
                   jC-gmle01810004b03a1
Seq. ID
                   BLASTX
Method
                   g309673
NCBI GI
BLAST score
                   424
                   6.0e-42
E value
                   104
Match length
```

7378

84

% identity



```
NCBI Description (L19651) light harvesting protein [Pisum sativum]
                   45929
Seq. No.
                   jC-qmle01810004c05a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q161207
                   182
BLAST score
                   8.0e-98
E value
                   314
Match length
                   89
% identity
NCBI Description P.polycephalum actin (Ppa35) mRNA, complete cds
                   45930
Seq. No.
                   jC-qmle01810004c08d1
Seq. ID
                   BLASTN
Method
                   g2052028
NCBI GI
BLAST score
                   100
                   2.0e-49
E value
                   120
Match length
                   95
% identity
NCBI Description G.max mRNA for glutathione transferase
                   45931
Seq. No.
                   jC-gmle01810004c12a1
Seq. ID
                   BLASTX
Method
                   q4107343
NCBI GI
BLAST score
                   354
                   1.0e-33
E value
                   101
Match length
                   71
% identity
NCBI Description (AJ224922) ATP citrate lyase [Sordaria macrospora]
                   45932
Seq. No.
                   jC-gmle01810004c12d1
Seq. ID
                   BLASTX
Method
                   g4107343
NCBI GI
BLAST score
                   195
E value
                   4.0e-15
                   54
Match length
                   74
% identity
NCBI Description (AJ224922) ATP citrate lyase [Sordaria macrospora]
Seq. No.
                   45933
                   jC-gmle01810004d09a1
Seq. ID
                   BLASTN
Method
                   g3452136
NCBI GI
                   214
BLAST score
E value
                   1.0e-117
                   230
Match length
                   99
 % identity
NCBI Description Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
                   partial
                   45934
 Seq. No.
                   jC-gmle01810004e08d1
 Seq. ID
```

7379

BLASTX

g115813

Method

NCBI GI



```
BLAST score
                  3.0e-13
E value
Match length
                  51
                  73
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
NCBI Description
                  (CAB-8) >gi 19182 emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  45935
Seq. No.
                  jC-gmle01810004e12a1
Seq. ID
                  BLASTX
Method
                  g4249386
NCBI GI
                  327
BLAST score
                  3.0e-54
E value
                  134
Match length
                  81
% identity
                  (AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1
NCBI Description
                  from Arabidopsis thaliana. EST gb_H37393 comes from this
                  gene. [Arabidopsis thaliana]
                  45936
Seq. No.
                  jC-gmle01810004h07d1
Seq. ID
                  BLASTX
Method
                  g2760331
NCBI GI
                  224
BLAST score
                  2.0e-18
E value
                  129
Match length
                  34
% identity
NCBI Description (AC002130) F1N21.16 [Arabidopsis thaliana]
                  45937
Seq. No.
                  jC-qmle01810005a11a1
Seq. ID
                  BLASTX
Method
                  q1345837
NCBI GI
                   505
BLAST score
                   2.0e-51
E value
                   129
Match length
% identity
                   71
                  PHYTOENE DEHYDROGENASE (PHYTOENE DESATURASE) >gi 433145
NCBI Description
                   (U03903) phytoene dehydrogenase [Cercospora nicotianae]
                   45938
Seq. No.
                   jC-gmle01810005a11d1
Seq. ID
Method
                   BLASTX
                   g2505955
NCBI GI
                   174
BLAST score
                   2.0e-12
E value
Match length
                   51
% identity
                   67
                  (Y15007) phytoene desaturase [Phaffia rhodozyma]
NCBI Description
                   45939
Seq. No.
                   jC-gmle01810005e12a1
Seq. ID
```

Method BLASTX
NCBI GI g3176671
BLAST score 274
E value 3.0e-24



```
Match length
% identity
                  (AC004393) Contains similarity to hypothetical gene B0495.7
NCBI Description
                  gb_687822 from C. elegans cosmid gb_U21317. [Arabidopsis
                  thaliana]
                  45940
Seq. No.
                  jC-gmle01810005g10a1
Seq. ID
                  BLASTX
Method
                  g2244831
NCBI GI
                  237
BLAST score
                  6.0e-20
E value
                  116
Match length
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45941
Seq. No.
Seq. ID
                   jC-gmle01810005h11a1
                   BLASTN
Method
                   q984307
NCBI GI
                   233
BLAST score
                   1.0e-128
E value
                   323
Match length
% identity
                   Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                   cds, beta-carboxyltransferase (accD), photosystem I
                   component (psaI), ORF 202 protein (ORF 203), ORF 151
                   protein (ORF 151), ORF 103 protein (ORF 103), ORF 229
                   precurso
                   45942
Seq. No.
                   jC-qmle01810006a07a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3033389
BLAST score
                   162
                   6.0e-11
E value
                   112
Match length
% identity
                   7
                  (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
NCBI Description
                   45943
Seq. No.
                   jC-gmle01810006b02d1
Seq. ID
Method
                   BLASTX
                   g1652892
NCBI GI
BLAST score
                   210
                   1.0e-16
E value
                   107
Match length
                   42
 % identity
                   (D90909) ABC transporter [Synechocystis sp.]
NCBI Description
                    45944
 Seq. No.
                    jC-gmle01810006b11a1
 Seq. ID
```

 Seq. No.
 45944

 Seq. ID
 jC-gmle01810006b11a1

 Method
 BLASTX

 NCBI GI
 g3935168

 BLAST score
 346

9.0e-33

Match length 94

E value



```
% identity
                  (AC004557) F17L21.11 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  45945
                  jC-qmle01810006c05d1
Seq. ID
                  BLASTX
Method
                  q4490317
NCBI GI
                  233
BLAST score
                  2.0e-19
E value
Match length
                  95
                  52
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                  45946
Seq. No.
                  jC-gmle01810006e11a1
Seq. ID
Method
                  BLASTN
                  q1053215
NCBI GI
                  401
BLAST score
                  0.0e + 00
E value
                   409
Match length
% identity
                  100
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
                   45947
Seq. No.
                   jC-gmle01810006f06a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3758890
BLAST score
                   365
                   2.0e-43
E value
                   166
Match length
% identity
                   38
                  (Y14317) catalase/peroxidase [Streptomyces reticuli]
NCBI Description
                   45948
Seq. No.
                   jC-gmle01810006h09d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g488434
BLAST score
                   163
                   2.0e-11
E value
                   46
Match length
                   70
% identity
                  (U06259) catalase [Mycobacterium tuberculosis]
NCBI Description
                   45949
Seq. No.
                   jC-gmle01810007b02a1
Seq. ID
                   BLASTN
Method
                   q4406529
NCBI GI
BLAST score
                   187
                   1.0e-101
E value
Match length
                   415
% identity
                   Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
NCBI Description
                   encoding chloroplast protein, complete cds
```

45950 jC-gmle01810007b06a1 Seq. ID

Seq. No.



```
BLASTN
Method
                  g1055367
NCBI GI
BLAST score
                   476
E value
                  0.0e + 00
Match length
                   480
% identity
                   100
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                   45951
                   jC-gmle01810008b06d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4432851
BLAST score
                   259
                   2.0e-22
E value
Match length
                   71
% identity
                   (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4567239_gb_AAD23653.1_AC007070 2 (AC007070)
                   hypothetical protein [Arabidopsis Thaliana]
Seq. No.
                   45952
                   jC-qmle01810008b10d1
Seq. ID
                   BLASTN
Method
                   g1850543
NCBI GI
BLAST score
                   99
E value
                   2.0e-48
                   151
Match length
                   96
% identity
                  Alternaria alternata hsp70 mRNA, partial cds
NCBI Description
Seq. No.
                   45953
                   jC-gmle01810008e03d1
Seq. ID
                   BLASTX
Method
                   q1710055
NCBI GI
                   226
BLAST score
                   7.0e-19
E value
Match length
                   84
% identity
                   48
                   RDS1 PROTEIN >gi_1363621_pir__S58477 rds1 protein - fission
NCBI Description
                   yeast (Schizosaccharomyces pombe) >gi_1184029_emb_CAA54544_
                   (X77328) rds1 [Schizosaccharomyces pombe]
                   45954
Seq. No.
                   jC-qmle01810009a01a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3435305
                   43
BLAST score
                   7.0e-15
E value
```

99 Match length % identity

Medicago sativa glycolate oxidase mRNA, partial cds NCBI Description

45955 Seq. No.

jC-gmle01810009a04d1 Seq. ID

BLASTX Method NCBI GI g951449



```
BLAST score
                  3.0e-13
E value
                  56
Match length
                  57
% identity
                  (L46681) aspartic protease precursor [Lycopersicon
NCBI Description
                  esculentum]
                  45956
Seq. No.
                  jC-qmle01810009b03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3695019
BLAST score
                  237
                  8.0e-20
E value
                  97
Match length
% identity
                  (AF055848) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
                   45957
Seq. No.
                   jC-gmle01810009c07a1
Seq. ID
                  BLASTX
Method
                   q3242720
NCBI GI
BLAST score
                   178
                   3.0e-13
E value
                   71
Match length
% identity
                   (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
NCBI Description
                   thaliana]
                   45958
Seq. No.
Seq. ID
                   jC-qmle01810009c11a1
                   BLASTX
Method
                   q4455276
NCBI GI
BLAST score
                   245
                   7.0e-21
E value
Match length
                   78
                   65
% identity
                   (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   45959
Seq. No.
                   jC-gmle01810009c12a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3281870
                   192
BLAST score
                   1.0e-14
E value
Match length
                   124
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   45960
Seq. No.
                   jC-gmle01810009e12a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2832680
                   190
BLAST score
                   2.0e-14
E value
```

52

47

Match length

% identity



```
NCBI Description
                 (AL021712) putative protein [Arabidopsis thaliana]
```

Seq. ID jC-qmle01810009h07a1

Method BLASTX NCBI GI q3123310 BLAST score 187 E value 3.0e-14 Match length 61 % identity 59

NCBI Description PUTATIVE FLAVOPROTEIN C26F1.14C

Seq. No.

jC-gmle01810010b11d1 Seq. ID

45962

Method BLASTX NCBI GI g4097880 BLAST score 269 5.0e-24E value Match length 65 % identity 83

NCBI Description (U70866) polyprotein [Bean pod mottle virus]

Seq. No.

45963

jC-gmle01810010b12a1 Seq. ID

Method BLASTX g729443 NCBI GI BLAST score 281 E value 5.0e-25 Match length 104 % identity 25

PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR NCBI Description

>gi_109464_pir__S19656 protein disulfide-isomerase homolog
P5 precursor - golden hamster >gi_49645_emb_CAA44550_

(X62678) P5 [Mesocricetus auratus]

Seq. No. 45964

Seq. ID jC-gmle01810010e10a1

Method BLASTX NCBI GI g2160138 BLAST score 184 1.0e-13 E value Match length 107 % identity 19

NCBI Description (AC000375) No definition line found [Arabidopsis thaliana]

Seq. No. 45965

Seq. ID jC-gmle01810010h04a1

Method BLASTX NCBI GI g2190540 BLAST score 256 E value 4.0e-22 Match length 80 % identity 60

NCBI Description (ACO01229) Similar to Arabidopsis TFL1 (gb U77674).

[Arabidopsis thaliana]

45966 Seq. No.



```
jC-gmle01810010h11d1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g984307
BLAST score
                  200
E value
                  1.0e-109
Match length
                  272
                  93
% identity
                  Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                  cds, beta-carboxyltransferase (accD), photosystem I
                  component (psaI), ORF 202 protein (ORF 203), ORF 151
                  protein (ORF 151), ORF 103 protein (ORF 103), ORF 229
                  precurso
                  45967
Seq. No.
                  jC-gmle01810011a02d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2194117
BLAST score
                  171
                   4.0e-12
E value
                   49
Match length
% identity
                   63
                   (AC002062) Strong similarity to Arabidopsis receptor
NCBI Description
                  protein kinase PR5K (gb_ATU48698). [Arabidopsis thaliana]
                   45968
Seq. No.
                   jC-gmle01810011b08a1
Seq. ID
Method
                   BLASTX
                   g3393062
NCBI GI
BLAST score
                   305
E value
                   8.0e-28
                   72
Match length
                   74
% identity
                  (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
                   45969
Seq. No.
                   jC-gmle01810011c04a1
Seq. ID
                   BLASTX
Method
                   g2126641
NCBI GI
                   148
BLAST score
                   3.0e-09
E value
Match length
                   146
                   32
% identity
                   polysaccharide synthase homolog - Streptococcus pneumoniae
NCBI Description
                   >gi_1586509_prf__2204223E cellubiuronic acid synthase
                   [Streptococcus pneumoniae]
                   45970
Seq. No.
                   jC-gmle01810011e01a1
Seq. ID
                   BLASTN
```

Method g161207 NCBI GI 265 BLAST score 1.0e-147 E value Match length 449 90 % identity

P.polycephalum actin (Ppa35) mRNA, complete cds NCBI Description

45971 Seq. No.



```
jC-gmle01810011e02d1
Seq. ID
                  BLASTX
Method
                  q3292823
NCBI GI
BLAST score
                  156
E value
                   3.0e-10
Match length
                  53
% identity
                   62
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   45972
                   jC-gmle01810011g08a1
Seq. ID
Method
                  BLASTX
                   q20729
NCBI GI
BLAST score
                   478
E value
                   4.0e-48
Match length
                   113
% identity
                   86
                  (X15190) precursor (AA -68 to 337) [Pisum sativum]
NCBI Description
                   45973
Seq. No.
Seq. ID
                   jC-gmle01810011g10a1
Method
                   BLASTN
NCBI GI
                   g986966
BLAST score
                   290
E value
                   1.0e-162
Match length
                   294
% identity
                   100
                  Glycine max TGACG-motif binding factor (STF2) mRNA,
NCBI Description
                   complete cds
                   45974
Seq. No.
Seq. ID
                   jC-gmle01810011h06a1
                   BLASTN
Method
                   g496493
NCBI GI
                   116
BLAST score
                   2.0e-58
E value
Match length
                   266
                   89
% identity
                   P.sativum (Rosakrone) mRNA for nonphosphorylating,
NCBI Description
                   NADP-specific, glyceraldehyde-3-phosphate dehydrogenase
Seq. No.
                   45975
                   jC-gmle01810011h09a1
Seq. ID
                   BLASTN
Method
                   q56539
NCBI GI
                   75
BLAST score
                   4.0e-34
E value
                   251
Match length
% identity
                   92
                  R.norvegicus gene encoding prolactin, exon 5
NCBI Description
                   >gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene
                   : exon v and flanks
                   45976
```

jC-gmle01810012g03d1 Seq. ID

BLASTX Method NCBI GI g418854



```
BLAST score
                  492
                  1.0e-49
E value
Match length
                  98
                  18
% identity
                  ubiquitin precursor - parsley >gi_288112_emb_CAA45621_
NCBI Description
                   (X64344) polyubiquitin [Petroselinum crispum]
                  >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                   [Petroselinum crispum]
                   45977
Seq. No.
Seq. ID
                  jC-gmle01810013b10d1
                  BLASTX
Method
                  q2494144
NCBI GI
                  189
BLAST score
                   3.0e-14
E value
Match length
                  72
% identity
                   (AC002329) predicted leucine-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                   45978
Seq. No.
                   jC-qmle01810013d11d1
Seq. ID
                   BLASTX
Method
                   g2129575
NCBI GI
                   189
BLAST score
                   3.0e-14
E value
Match length
                   53
                   72
% identity
                  DNA repair protein homolog XPBara - Arabidopsis thaliana
NCBI Description
                   45979
Seq. No.
Seq. ID
                   jC-gmle01810013g01a1
Method
                   BLASTX
NCBI GI
                   g3023267
                   292
BLAST score
                   3.0e-26
E value
Match length
                   146
                   43
% identity
                   ALPHA-GLUCOSIDASE PRECURSOR (MALTASE)
NCBI Description
                   >gi 2645160 dbj BAA23616_ (D45356) alpha-glucosidase
                   [Aspergillus niger]
                   45980
Seq. No.
                   jC-gmle01810015a12d1
Seq. ID
                   BLASTX
Method
                   g3864
NCBI GI
                   471
BLAST score
                   2.0e-47
E value
                   109
Match length
                   78
% identity
                  (X56259) lysine--tRNA ligase [Saccharomyces cerevisiae]
NCBI Description
```

Seq. ID jC-gmle01810015e02d1

Method BLASTX
NCBI GI g3776557
BLAST score 232

Match length

NCBI Description

% identity

161

33



```
1.0e-19
E value
                  87
Match length
                  47
% identity
                   (AC005388) Contains similarity to gi_2924495 hypothetical
NCBI Description
                  protein Rv1920 from Mycobacterium tuberculosis genome
                  gb_AL022020. [Arabidopsis thaliana]
Seq. No.
                   jC-gmle01810015e07d1
Seq. ID
                  BLASTX
Method
                  g2335096
NCBI GI
BLAST score
                  142
                   1.0e-08
E value
                   40
Match length
% identity
                  (AC002339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45983
Seq. No.
                   jC-gmle01810015g12d1
Seq. ID
                   BLASTX
Method
                   g3075393
NCBI GI
                   148
BLAST score
                   2.0e-09
E value
                   49
Match length
% identity
                  (AC004484) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45984
Seq. No.
                   jC-gmle01810017c06a2
Seq. ID
                   BLASTN
Method
NCBI GI
                   q473216
BLAST score
                   48
                   2.0e-18
E value
Match length
                   64
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
                   45985
Seq. No.
                   jC-qmle01810017d03a2
Seq. ID
                   BLASTX
Method
                   q3128174
NCBI GI
BLAST score
                   141
E value
                   5.0e-09
Match length
                   63
% identity
                   (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   45986
Seq. No.
                   jC-gmle01810018d04a2
Seq. ID
Method
                   BLASTX
                   q3193293
NCBI GI
                   163
BLAST score
E value
                   4.0e-11
```

(AF069298) contains a short region of similarity to another

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)



[Arabidopsis thaliana]

```
Seq. No.
                  45987
Seq. ID
                  jC-qmle01810019c04a2
Method
                  BLASTX
NCBI GI
                  q4262186
BLAST score
                  529
                   4.0e-54
E value
                  131
Match length
% identity
                   (AC005508) Highly similar to cullin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   45988
Seq. No.
Seq. ID
                   jC-gmle01810019d02a2
Method
                  BLASTN
NCBI GI
                   g1326160
BLAST score
                   43
                   6.0e-15
E value
                   157
Match length
% identity
                  Phaseolus vulgaris dehydrin mRNA, complete cds
NCBI Description
                   45989
Seq. No.
                   jC-gmle01810019e08a2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1055367
                   310
BLAST score
                   1.0e-174
E value
Match length
                   389
                   95
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   45990
                   jC-gmle01810019g10a2
Seq. ID
Method
                   BLASTX
                   g479413
NCBI GI
BLAST score
                   354
                   3.0e-66
E value
Match length
                   150
% identity
                   86
NCBI Description myosin-like protein - Arabidopsis thaliana
                   45991
Seq. No.
                   jC-qmle01810019h04a2
Seq. ID
                   BLASTN
Method
                   g1235570
NCBI GI
                   166
BLAST score
                   2.0e-88
E value
                   278
Match length
                   90
% identity
NCBI Description P.anserina sul2 gene
```

Seq. No. 45992

Seq. ID jC-gmle01810020b11a1

Method BLASTX



```
q2897875
NCBI GI
                  391
BLAST score
                  8.0e-38
E value
                  163
Match length
                  47
% identity
                  (U90274) histone acetyltransferase HAT B [Zea mays]
NCBI Description
                  45993
Seq. No.
                  jC-qmle01810020d07a1
Seq. ID
                  BLASTX
Method
                  q3025189
NCBI GI
                  263
BLAST score
                  6.0e-42
E value
                  147
Match length
                  60
% identity
                  HYPOTHETICAL 67.1 KD PROTEIN SLL1770
NCBI Description
                  >gi 1652753 dbj_BAA17672 (D90908) ABC1-like [Synechocystis
                  sp.]
                  45994
Seq. No.
Seq. ID
                  jC-qmle01810020e03d1
                  BLASTX
Method
NCBI GI
                  q115813
                  197
BLAST score
                  2.0e-15
E value
                  50
Match length
                  78
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE III PRECURSOR
NCBI Description
                   (CAB-8) >gi_19182_emb CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   45995
Seq. No.
Seq. ID
                   jC-qmle01810020g07a1
                   BLASTX
Method
                   g82080
NCBI GI
BLAST score
                   506
                   2.0e-51
E value
Match length
                   100
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872_prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   45996
Seq. No.
                   jC-gmle01810021a09a1
Sea. ID
Method
                   BLASTX
                   g2465923
NCBI GI
BLAST score
                   190
                   6.0e-18
E value
Match length
                   107
% identity
                   30
                   (AF024648) receptor-like serine/threonine kinase
NCBI Description
```

[Arabidopsis thaliana]

Seq. No. 45997

Seq. ID jC-gmle01810021c11d1

Method BLASTN

Match length

% identity

95

45



```
NCBI GI
                   g2739045
BLAST score
                   78
E value
                  7.0e-36
Match length
                  190
% identity
                  85
NCBI Description
                  Glycine max polyphosphoinositide binding protein Ssh2p
                   (SSH2) mRNA, complete cds
Seq. No.
                  45998
                  jC-gmle01810021e07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4102839
BLAST score
                  249
E value
                  3.0e-21
Match length
                  117
% identity
                  46
NCBI Description
                  (AF016713) LeOPT1 [Lycopersicon esculentum]
Seq. No.
                  45999
Seq. ID
                  jC-gmle01810021f03a1
Method
                  BLASTX
NCBI GI
                  q3894197
BLAST score
                  328
E value
                  2.0e-30
Match length
                  79
% identity
                  72
NCBI Description
                  (AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  46000
                  jC-gmle01810022a09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406530
BLAST score
                  519
E value
                  8.0e-53
Match length
                  145
% identity
                  74
NCBI Description
                  (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  46001
Seq. ID
                  jC-gmle01810022b03a1
Method
                  BLASTX
NCBI GI
                  g1839578
BLAST score
                  398
E value
                  9.0e-39
Match length
                  123
% identity
                  61
NCBI Description
                  vacuolar invertase 1, GIN1 [Vitis vinifera=grape berries,
                  Sultana, berries, Peptide, 642 aa]
Seq. No.
                  46002
Seq. ID
                  jC-gmle01810022g05d1
Method
                  BLASTX
NCBI GI
                  g2197048
BLAST score
                  207
E value
                  3.0e-16
```



```
NCBI Description
                  (AF001032) amino acid permease [Neurospora crassa]
Seq. No.
                   46003
Seq. ID
                   jC-gmle01810023b02a1
Method
                  BLASTN
NCBI GI
                  g20892
BLAST score
                  98
E value
                  1.0e-47
Match length
                  150
% identity
                  92
NCBI Description Pea U2 snRNA (clone pPSU2.1)
Seq. No.
                  46004
                  jC-gmle01810023g04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3006179
BLAST score
                  373
E value
                  9.0e-36
Match length
                  149
% identity
                  50
NCBI Description (AL022304) putative long-chain-fatty-acid--coa ligase
                  [Schizosaccharomyces pombe]
Seq. No.
                  46005
Seq. ID
                  jC-gmle01810024a03a1
Method
                  BLASTX
NCBI GI
                  q4115938
BLAST score
                  299
E value
                  1.0e-32
Match length
                  117
% identity
                  67
NCBI Description
                  (AF118223) contains similarity several bacterial
                  glutathione-regulated potassium efflux system proteins
                  [Arabidopsis thaliana]
Seq. No.
                  46006
Seq. ID
                  jC-gmle01810024a07d1
Method
                  BLASTX
NCBI GI
                  q4469019
BLAST score
                  322
E value
                  9.0e-30
Match length
                  110
% identity
NCBI Description
                  (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                  46007
                  jC-gmle01810024b03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006922
BLAST score
                  192
E value
                  6.0e-15
Match length
                  69
```

NCBI Description

% identity

Seq. No.

46008

thaliana]

7393

(Z99708) cytochrome P450 like protein [Arabidopsis



```
Seq. ID
                   jC-gmle01810024d01a1
Method
                   BLASTX
NCBI GI
                   q4263790
BLAST score
                   213
E value
                   2.0e-17
Match length
                  92
% identity
                  52
NCBI Description
                 (AC006068) putative ch-TOG protein [Arabidopsis thaliana]
Seq. No.
                  46009
Seq. ID
                  jC-gmle01810024h10a1
Method
                  BLASTX
NCBI GI
                  g416760
BLAST score
                  380
E value
                  1.0e-36
Match length
                  134
% identity
                  54
NCBI Description
                  CELL DIVISION CONTROL PROTEIN 11 >gi_482158 pir S40911
                  cell division control protein CDC11 - yeast (Saccharomyces
                  cerevisiae) >gi_295594 (L16550) cell division cycle protein
                   [Saccharomyces cerevisiae] >gi_1015762 emb_CAA89604
                   (Z49576) ORF YJR076c [Saccharomyces cerevisiae] >gi 1019697
                   (L47993) ORF YJR076c [Saccharomyces cerevisiae]
Seq. No.
                  46010
Seq. ID
                  jC-gmle01810025a04d1
Method
                  BLASTN
NCBI GI
                  g2661022
BLAST score
                  313
E value
                  1.0e-176
Match length
                  388
% identity
                  100
NCBI Description Glycine max catalase (cat5) mRNA, partial cds
Seq. No.
                  46011
Seq. ID
                  jC-gmle01810025b06d1
Method
                  BLASTX
NCBI GI
                  g4115536
BLAST score
                  285
E value
                  2.0e-25
Match length
                  90
% identity
                  59
NCBI Description
                  (AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna
                  mungo]
Seq. No.
                  46012
Seq. ID
                  jC-gmle01810025c01a1
Method
```

BLASTN NCBI GI g1326160 BLAST score 59 E value 2.0e-24 Match length 161 % identity 95

NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No. 46013

Seq. ID jC-gmle01810025f10d1



Method BLASTN
NCBI GI g4185595
BLAST score 81
E value 2.0e-37
Match length 165

NCBI Description Pisum sativum mRNA for precursor for 23-kDa protein of

photosystem II, complete cds

Seq. No. 46014

% identity

Seq. ID jC-qmle01810026a10a1

88

Method BLASTN
NCBI GI g1055367
BLAST score 144
E value 2.0e-75
Match length 172
% identity 96

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 46015

Seq. ID jC-gmle01810026a12d1

Method BLASTN
NCBI GI g3378649
BLAST score 35
E value 4.0e-10
Match length 75
% identity 87

NCBI Description M.sativa mRNA translated from abscisic activated gene

Seq. No. 46016

Seq. ID jC-gmle01810026d03d1

Method BLASTX
NCBI GI g4567095
BLAST score 222
E value 3.0e-18
Match length 53
% identity 74

NCBI Description (AF129516) fertilization-independent endosperm protein

[Arabidopsis thaliana]

Seq. No. 46017

Seq. ID jC-gmle01810026h07a1

Method BLASTX
NCBI GI g3608144
BLAST score 328
E value 1.0e-30
Match length 85
% identity 73

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 46018

Seq. ID jC-gmle01810027a03d1

Method BLASTN
NCBI GI g2738999
BLAST score 193
E value 1.0e-104



Match length 298 % identity 91

NCBI Description Glycine max cytochrome P450 monooxygenase CYP71D10p

(CYP71D10) mRNA, complete cds

Seq. No. 46019

Seq. ID jC-gmle01810027a04d1

Method BLASTX
NCBI GI g3451075
BLAST score 275
E value 2.0e-24
Match length 124
% identity 49

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 46020

Seq. ID jC-gmle01810027b03a1

Method BLASTN
NCBI GI g19156
BLAST score 32
E value 5.0e-09
Match length 72
% identity 86

NCBI Description L.esculentum mRNA for 33kDa precursor protein of

oxygen-evolving complex

Seq. No. 46021

Seq. ID jC-gmle01810028a02d1

Method BLASTX
NCBI GI g140372
BLAST score 160
E value 4.0e-11
Match length 84
% identity 40

NCBI Description HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION

>gi_83159_pir__S19367 hypothetical protein YCL039w - yeast

(Saccharomyces cerevisiae)

Seq. No. 46022

Seq. ID jC-gmle01810028b09a1

Method BLASTX
NCBI GI g548771
BLAST score 526
E value 9.0e-54
Match length 135
% identity 71

NCBI Description 60S RIBOSOMAL PROTEIN L3-2 >gi 101073_pir_ S25592 ribosomal

protein L3 - fission yeast (Schizosaccharomyces pombe) >gi_5059_emb_CAA40901_ (X57734) ribosomal protein L3

[Schizosaccharomyces pombe]

Seq. No. 46023

Seq. ID jC-gmle01810028c09d1

Method BLASTX
NCBI GI g2239089
BLAST score 166
E value 1.0e-11

```
Match length
                   74
% identity
                   41
NCBI Description
                   (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758)
                   anthranilate N-hydroxycinnamoyl/benzoyltransferase
                   [Dianthus caryophyllus]
Seq. No.
                   46024
Seq. ID
                   jC-gmle01810028d04a1
Method
                   BLASTX
NCBI GI
                  g3080438
BLAST score
                   143
E value
                  5.0e-09
Match length
                  71
% identity
                  46
NCBI Description
                  (AL022605) putative protein [Arabidopsis thaliana]
Seq. No.
                  46025
Seq. ID
                  jC-gmle01810028d11a1
Method
                  BLASTX
NCBI GI
                  g1946367
BLAST score
                  251
E value
                  2.0e-21
Match length
                  124
% identity
                  41
NCBI Description
                  (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  46026
Seq. ID
                  jC-gmle01810028g04d1
Method
                  BLASTN
NCBI GI
                  g303852
BLAST score
                  45
E value
                  2.0e-16
Match length
                  57
% identity
                  95
NCBI Description Rice mRNA for ribosomal protein L3, complete cds
Seq. No.
                  46027
Seq. ID
                  jC-gmle01810028g11a1
Method
                  BLASTX
NCBI GI
                  q4335735
BLAST score
                  421
E value
                  2.0e-41
Match length
                  144
% identity
                  55
NCBI Description
                  (AC006248) hypothetical protein [Arabidopsis thaliana]
```

Seq. ID jC-gmle01810029a04a1

Method BLASTN
NCBI GI g1055367
BLAST score 362
E value 0.0e+00
Match length 449
% identity 95

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds



Seq. ID jC-gmle01810029c01a1

Method BLASTX
NCBI GI g3925277
BLAST score 307
E value 5.0e-28
Match length 128
% identity 47

NCBI Description (AL032643) similar to Uncharacterized protein family

UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes

from this gene [Caenorhabditis elegans]

Seq. No. 46030

Seq. ID jC-gmle01810029e08d1

Method BLASTX
NCBI GI g2651310
BLAST score 180
E value 3.0e-13
Match length 70
% identity 53

NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis

thaliana]

Seq. No. 46031

Seq. ID jC-gmle01810029e10d1

Method BLASTX
NCBI GI g3033377
BLAST score 188
E value 4.0e-14
Match length 70
% identity 50

NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis

thaliana]

Seq. No.

46032

Seq. ID jC-gmle01810029f01a1

Method BLASTX
NCBI GI g3785995
BLAST score 495
E value 4.0e-50
Match length 156
% identity 64

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 46033

Seq. ID jC-gmle01810029h10d1

Method BLASTX
NCBI GI g231660
BLAST score 125
E value 2.0e-15
Match length 131
% identity 46

NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No. 46034



```
Seq. ID
                   jC-qmle01810029h12d1
Method
                   BLASTX
NCBI GI
                   g3005931
BLAST score
                   405
E value
                   3.0e-46
Match length
                   137
% identity
                   38
NCBI Description (AJ005016) ABC transporter [Homo sapiens]
Seq. No.
                   46035
Seq. ID
                   jC-gmle01810030a02a2
Method
                  BLASTX
NCBI GI
                  g2492964
BLAST score
                  531
E value
                   2.0e-54
Match length
                  141
% identity
                  72
NCBI Description
                  PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE,
                  TYROSINE-INHIBITED (PHOSPHO-2-KETO-3-DEOXYHEPTONATE
                  ALDOLASE) (DAHP SYNTHETASE)
                   (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE)
                  >qi 1854641 (U53216)
                  3-deoxy-D-arabinoheptulosonate-7-phosphate synthase
                   [Candida albicans]
Seq. No.
                  46036
Seq. ID
                  jC-qmle01810030a04a2
Method
                  BLASTX
NCBI GI
                  g3023999
BLAST score
                  421
E value
                  2.0e-41
Match length
                  131
% identity
                  63
NCBI Description
                  ISOCITRATE DEHYDROGENASE (NADP), MITOCHONDRIAL PRECURSOR
                  (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH)
                  (IDP) >gi_1778636_dbj_BAA19073_ (AB000261) NADP-dependent
                  isocitrate dehydrogenase precursor [Aspergillus niger]
                  >gi_1778638_dbj_BAA19074_ (AB000262) NADP-dependent
                  isocitrate dehydrogenase precursor [Aspergillus niger]
Seq. No.
                  46037
Seq. ID
                  jC-gmle01810030a10a2
Method
                  BLASTX
NCBI GI
                  q3881976
BLAST score
                  186
E value
                  8.0e-26
Match length
                  107
% identity
                  55
```

NCBI Description (AJ012409) hypothetical protein [Homo sapiens]

Seq. No.

Seq. ID

jC-gmle01810030c07a2 Method

46038

BLASTX NCBI GI q3152594 BLAST score 334 E value 1.0e-31 Match length 80



% identity

NCBI Description (AC002986) Contains repeats similar to RECA protein

gb L26100 from Acinetobacter calcoaceticus. [Arabidopsis

thaliana]

Seq. No.

46039

Seq. ID

jC-qmle01810030f06a2

Method NCBI GI BLASTN q984307

BLAST score E value

165 1.0e-87

Match length % identity

189 96

NCBI Description Glycine max ribosomal protein S16 (rps16) gene, partial

cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229

precurso

Seq. No.

46040

Seq. ID

jC-gmle01810030g01d1

Method NCBI GI BLASTX g2062173

BLAST score

235

E value

1.0e-19

Match length % identity

68

NCBI Description

(AC001645) cell division protein FtsH isolog [Arabidopsis

thaliana]

Seq. No.

46041

Seq. ID Method

jC-gmle01810031b08d1

NCBI GI

BLASTX g2055386

BLAST score

174

E value

2.0e-12

Match length

108 42

% identity

NCBI Description (U73681) AlkB [Caulobacter crescentus]

Seq. No.

46042

Seq. ID

jC-gmle01810031c06d1

Method NCBI GI

BLASTX

q2146731

BLAST score

154 9.0e-11

E value Match length

60 37

% identity

NCBI Description FK506-binding protein - Arabidopsis thaliana >gi 1354207

(U49453) rof1 [Arabidopsis thaliana]

Seq. No.

46043

Seq. ID

jC-gmle01810031d04d1

Method NCBI GI BLASTX g2191135

BLAST score

160

7.0e-11 E value



```
55
Match length
                  53
% identity
                  (AF007269) A IG002N01.14 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  46044
Seq. No.
                  jC-gmle01810031e03a2
Seq. ID
                  BLASTX
Method
                  q2809251
NCBI GI
                  343
BLAST score
                  2.0e-32
E value
                  80
Match length
                  78
% identity
NCBI Description (AC002560) F21B7.20 [Arabidopsis thaliana]
                   46045
Seq. No.
                   jC-gmle01810031f03a2
Seq. ID
                  BLASTX
Method
                   g3184188
NCBI GI
                   321
BLAST score
                   1.0e-29
E value
                  105
Match length
                   65
% identity
NCBI Description (AB005742) UMP-CMP kinase [Lentinula edodes]
                   46046
Seq. No.
                   jC-gmle01810031f03d1
Seq. ID
                   BLASTX
Method
                   g3184188
NCBI GI
                   195
BLAST score
                   7.0e-15
E value
Match length
                   54
                   72
% identity
NCBI Description (AB005742) UMP-CMP kinase [Lentinula edodes]
                   46047
Seq. No.
Seq. ID
                   jC-gmle01810032f06a2
                   BLASTX
Method
                   q4263543
NCBI GI
                   243
BLAST score
                   2.0e-20
E value
Match length
                   138
% identity
                  (AC006250) putative Athila retroelement ORF1 protein
NCBI Description
                   [Arabidopsis thaliana]
                   46048
Seq. No.
                   jC-gmle01810033b05a2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2104687
BLAST score
                   149
                   2.0e-09
E value
Match length
                   104
 % identity
                   26
NCBI Description (X97905) RNA- or ssDNA-binding protein [Vicia faba]
```

7401

46049

Seq. No.

```
jC-gmle01810033e02a2
Seq. ID
                  BLASTX
Method
                  g3096949
NCBI GI
BLAST score
                  441
                  1.0e-43
E value
Match length
                  172
% identity
                  49
                  (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                  [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                  nucleotide-gated cation channel [Arabidopsis thaliana]
                  46050
Seq. No.
                  jC-gmle01810033e03a2
Seq. ID
                  BLASTX
Method
                  g2828293
NCBI GI
                  163
BLAST score
                  4.0e-11
E value
                  137
Match length
                  36
% identity
NCBI Description
                  46051
Seq. No.
Seq. ID
                  jC-gmle01810033e06a2
```

(AL021687) putative protein [Arabidopsis thaliana]

BLASTX Method q3287695 NCBI GI 501 BLAST score 1.0e-50 E value 165 Match length % identity 59

(AC003979) Similar to hypothetical protein C34B7.2 NCBI Description

gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis

thaliana]

46052 Seq. No.

jC-gmle01810033g04a2 Seq. ID

BLASTX Method NCBI GI q3600060 BLAST score 157 2.0e-10 E value 167 Match length 33 % identity

(AF080120) contains similarity to protein kinases (Pfam: NCBI Description

pkinase.hmm, score: 24.94) [Arabidopsis thaliana]

46053 Seq. No.

jC-gmle01810033h01a2 Seq. ID

BLASTN Method NCBI GI q3435305 BLAST score 167 8.0e-89 E value 283 Match length 90 % identity

NCBI Description Medicago sativa glycolate oxidase mRNA, partial cds

Seq. No. 46054

jC-qmle01810034b10a2 Seq. ID

Method BLASTX

BLAST score

E value Match length 539 3.0e-55

145



```
NCBI GI
                   q3176715
BLAST score
                   278
                   6.0e-42
E value
Match length
                   129
                   64
% identity
NCBI Description
                  (AC002392) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   46055
Seq. ID
                   jC-qmle01810034d07a2
Method
                   BLASTN
NCBI GI
                   g1055367
BLAST score
                   473
E value
                   0.0e + 00
Match length
                   481
                   100
% identity
NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small
                   subunit mRNA, complete cds
                   46056
Seq. No.
Seq. ID
                   jC-gmle01810034h11a2
                   BLASTX
Method
NCBI GI
                   g1783355
BLAST score
                   604
E value
                   9.0e-63
Match length
                  136
% identity
NCBI Description (Y10421) delta-9 fatty acid desaturase [Cryptococcus
                   curvatus]
Seq. No.
                   46057
Seq. ID
                   jC-qmle01810035a07a2
Method
                   BLASTX
NCBI GI
                   g3309117
BLAST score
                   293
                   2.0e-35
E value
Match length
                   157
% identity
                   45
NCBI Description (AF051899) 1,8-cineole synthase [Salvia officinalis]
Seq. No.
                   46058
                   jC-gmle01810035b02d1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g310560
BLAST score
                   163
E value
                   1.0e-86
Match length
                   263
                   90
% identity
NCBI Description Soybean ascorbate peroxidase mRNA, complete cds
Seq. No. Seq. ID
                   46059
                   jC-gmle01810035b08a2
Method
                   BLASTX
NCBI GI
                   g1171978
```

% identity

NCBI Description

pombe]



% identity POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) NCBI Description (PABP 2) >gi 304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi 2911051 emb CAA17561 (AL021961) poly(A)-binding protein [Arabidopsis thaliana] 46060 Seq. No. jC-qmle01810035c01a2 Seq. ID Method BLASTX NCBI GI q4490736 561 BLAST score 6.0e-58 E value Match length 126 87 % identity (AL035708) putative protein [Arabidopsis thaliana] NCBI Description 46061 Seq. No. jC-gmle01810035c04a2 Seq. ID BLASTN Method NCBI GI g2661020 84 BLAST score 6.0e-40 E value Match length 120 93 % identity NCBI Description Glycine max catalase (cat4) mRNA, complete cds 46062 Seq. No. jC-gmle01810035d01a2 Seq. ID BLASTX Method NCBI GI g4204295 BLAST score 164 3.0e-11 E value 109 Match length 38 % identity NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana] 46063 Seq. No. jC-gmle01810035d07d1 Seq. ID BLASTN Method g303741 NCBI GI 96 BLAST score 1.0e-46 E value 188 Match length 88 % identity NCBI Description Pea mRNA for GTP-binding protein, complete cds 46064 Seq. No. jC-gmle01810035e12a2 Seq. ID BLASTX Method q3184098 NCBI GI 316 BLAST score 4.0e-29 E value 91 Match length

(AL023777) coenzyme a synthetase [Schizosaccharomyces



46065

Seq. No.

```
Seq. ID
                   jC-qmle01810035f03a2
Method
                   BLASTX
                 g1657382
NCBI GI
BLAST score
                   445
E value
                   1.0e-56
Match length
                   115
% identity
NCBI Description (Y09101) cholinephosphate cytidylyltransferase [Pisum
                   sativum]
Seq. No.
                   46066
Seq. ID
                   jC-qmle01810035f04a2
                   BLASTX
Method
NCBI GI
                   g2599104
BLAST score
                   110
                   3.0e-09
E value
Match length
                   64
                   53
% identity
NCBI Description (AF028833) 60S ribosomal protein [Dunaliella salina]
                   46067
Seq. No.
Seq. ID
                   jC-gmle01810035f04d1
Method
                   BLASTX
NCBI GI
                   q3915826
BLAST score
                   207
E value
                   2.0e-16
Match length
                   92
% identity
                   45
NCBI Description 60S RIBOSOMAL PROTEIN L5
                   46068
Seq. No.
                   jC-gmle01810035h08a2
Seq. ID
Method
                   BLASTX
                   g113954
NCBI GI
BLAST score
                   199
E value
                   3.0e-15
Match length
                   133
% identity
                   18
NCBI Description ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT
                   PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL
                   1,2-CYCLIC PHOSPHATE 2-PHOSPHOHYDROLASE)
                   >gi_71765_pir__LUHU3 annexin III - human
                   >gi_1942126_pdb_1AII_ Annexin Iii Co-Crystallized With
                   Inositol-2-Phosphate >gi 178697 (M63310)
                   1,2-cyclic-inositol-phosphate phosphodiesterase [Homo
                   sapiens] >gi_307115 (M20560) lipocortin-III [Homo sapiens]
>gi_410202 (L20591) annexin III [Homo sapiens]
                   46069
Seq. No.
Seq. ID
                   jC-qmle01810036b04d1
                   BLASTX
Method
NCBI GI
                   g3695412
BLAST score
                   323
```

7.0e-30

102

E value Match length



% identity 61 NCBI Description (A

(AF096373) contains similarity to group 1 glycosyl

transferases (Pfam: PF00534, E=2.1e-11) [Arabidopsis

thaliana]

Seq. No. 46070

Seq. ID jC-gmle01810036e01d1

Method BLASTX
NCBI GI g126120
BLAST score 170
E value 5.0e-12
Match length 78
% identity 50

NCBI Description AGGLUTININ ALPHA CHAIN (MPA) >gi_81437_pir__\$15825

agglutinin alpha chain - Osage orange

>gi 4139497 pdb 1JOT A Chain A, Structure Of The Lectin Mpa

Complexed With T-Antigen Disaccharide

Seq. No. 46071

Seq. ID jC-gmle01810036e08d1

Method BLASTN
NCBI GI g2463568
BLAST score 115
E value 7.0e-58
Match length 347
% identity 91

NCBI Description Glycine max mRNA for squalene synthase, complete cds

Seq. No. 46072

Seq. ID jC-gmle01810036g10a2

Method BLASTX
NCBI GI g586919
BLAST score 263
E value 7.0e-23
Match length 114
% identity 43

NCBI Description YSA1 PROTEIN >gi 1078606 pir S48276 YSA1 protein - yeast

(Saccharomyces cerevisiae) >gi_476067_emb_CAA55614_ (X78993) hyp. protein [Saccharomyces cerevisiae] >gi 536466 emb CAA85068 (Z35980) ORF YBR111c

[Saccharomyces cerevisiae]

Seq. No. 46073

Seq. ID jC-gmle01810036g10d1

Method BLASTX
NCBI GI g2398587
BLAST score 243
E value 1.0e-20
Match length 75
% identity 59

NCBI Description (Y11598) MnSOD [Candida sp.]

Seq. No. 46074

Seq. ID jC-gmle01810037a08a2

Method BLASTX
NCBI GI g1666299
BLAST score 145



```
6.0e-09
E value
                  79
Match length
                  42
% identity
                  (X92980) RNA-binding protein [Anabaena variabilis]
NCBI Description
                  46075
Seq. No.
                  jC-gmle01810037d01a2
Seq. ID
                  BLASTN
Method
                  g467614
NCBI GI
                  162
BLAST score
                  7.0e-86
E value
                  398
Match length
                  85
% identity
NCBI Description A.alternata AltA2 mRNA for aldehyde dehydrogenase
                   46076
Seq. No.
                   jC-gmle01810037g06a2
Seq. ID
                   BLASTX
Method
                   g3746059
NCBI GI
BLAST score
                   211
                   2.0e-17
E value
Match length
                   51
                   76
% identity
                  (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative
                   cysteinyl-tRNA synthetase [Arabidopsis thaliana]
                   46077
Seq. No.
                   jC-gmle01810037h08a2
Seq. ID
                   BLASTX
Method
                   g3925779
NCBI GI
                   190
BLAST score
                   3.0e-14
E value
                   152
Match length
% identity
                   34
NCBI Description (AL034353) putative major facilitator family multi-drug
                   resistance protein [Schizosaccharomyces pombe]
                   46078
Seq. No.
                   jC-gmle01810037h09a2
Seq. ID
                   BLASTX
Method
                   g2244987
NCBI GI
                   250
BLAST score
                   9.0e-22
E value
                   77
Match length
 % identity
NCBI Description (Z97340) similarity to protein kinase - slime mold
                    (Dictyostelium) [Arabidopsis thaliana]
                   46079
 Seq. No.
                   jC-gmle01810038a05d1
 Seq. ID
                   BLASTX
 Method
                   q3927836
 NCBI GI
 BLAST score
                   165
 E value
                    1.0e-11
```

75

44

Match length

% identity



NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Seq. No. 46080

Seq. ID jC-gmle01810040a11d1

Method BLASTN
NCBI GI g2463568
BLAST score 177
E value 8.0e-95
Match length 432
% identity 92

NCBI Description Glycine max mRNA for squalene synthase, complete cds

Seq. No. 46081

Seq. ID jC-gmle01810040e06a1

Method BLASTN
NCBI GI g4324966
BLAST score 155
E value 6.0e-82
Match length 163
% identity 99

NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No. 46082

Seq. ID jC-gmle01810040e06d1

Method BLASTN
NCBI GI g4324966
BLAST score 54
E value 1.0e-21
Match length 169
% identity 82

NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No. 46083

Seq. ID jC-gmle01810040h03a1

Method BLASTX
NCBI GI g1723558
BLAST score 272
E value 6.0e-24
Match length 110
% identity 54

NCBI Description HYPOTHETICAL 57.2 KD PROTEIN C12B10.16C IN CHROMOSOME I

>gi 1262429 emb CAA94706 (Z70721) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 46084

Seq. ID jC-gmle01810040h07a1

Method BLASTX
NCBI GI g1134882
BLAST score 301
E value 2.0e-27
Match length 106
% identity 57

NCBI Description (Z68291) cysteine protease [Pisum sativum]

Seq. No. 46085

Seq. ID jC-gmle01810041a10a1

Method BLASTN



```
q4097879
NCBI GI
BLAST score
                  130
                  7.0e-67
E value
                  339
Match length
                  85
% identity
NCBI Description Bean pod mottle virus complete segment RNA1 polyprotein
                  gene, complete cds
                  46086
Seq. No.
                  jC-gmle01810041b11a1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1175406
BLAST score 230
E value 5.0e-19
Match length 122
% identity 40

NCBI Description HYPOTHETICAL 65.9 KD PROTEIN C31A2.12 IN CHROMOSOME I

>gi_2130423_pir__S58106 hypothetical protein SPAC31A2.12 -

fission yeast (Schizosaccharomyces pombe) >gi_914890_emb_CAA90470_ (Z50113) unknown

[Schizosaccharomyces pombe]

Seq. No. 46087

Seq. ID jC-gmle01810042b11d1

Method BLASTX
NCBI GI g1175406
BLAST score 158
E value 1.0e-10
Match length 133
% identity 34

NCBI Description HYPOTHETICAL 65.9 KD PROTEIN C31A2.12 IN CHROMOSOME I

>gi 2130423 pir S58106 hypothetical protein SPAC31A2.12 -

fission yeast (Schizosaccharomyces pombe) >gi_914890_emb_CAA90470_ (Z50113) unknown

[Schizosaccharomyces pombe]

Seq. No. 46088

Seq. ID jC-gmle01810041d08a1

Method BLASTN
NCBI GI g1304226
BLAST score 74
E value 2.0e-33
Match length 248
% identity 90

NCBI Description Soybean mRNA for epoxide hydrolase, complete cds

Seq. No. 46089

Seq. ID jC-gmle01810041e10a1

Method BLASTX
NCBI GI g2655098
BLAST score 238
E value 5.0e-20
Match length 118
% identity 39

NCBI Description (AF023472) peptide transporter [Hordeum vulgare]

Seq. No. 46090



```
jC-gmle01810041e11a1
Seq. ID
                  BLASTX
Method
                  q4510348
NCBI GI
                  255
BLAST score
E value
                   4.0e-22
Match length
                  111
% identity
                   47
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                   jC-qmle01810041e11d1
Method
                   BLASTX
                   g4510348
NCBI GI
                  268
BLAST score
                   2.0e-23
E value
Match length
                   92
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46092
Seq. No.
                   jC-qmle01810042a03a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1351714
                   238 .
BLAST score
                   7.0e-20
E value
                   111
Match length
                   41
% identity
                   PUTATIVE TRANSPORTER C11D3.18C >gi 1107907 emb CAA92319
NCBI Description
                   (Z68166) unknown [Schizosaccharomyces pombe]
                   46093
Seq. No.
Seq. ID
                   jC-qmle01810042a11d1
Method
                   BLASTX
NCBI GI
                   q12688
BLAST score
                   218
                   9.0e-18
E value
                   101
Match length
% identity
                   47
                  (V00650) URF 1 [Emericella nidulans]
NCBI Description
Seq. No.
                   46094
Seq. ID
                   jC-gmle01810042b07d1
Method
                   BLASTX
                   g2827651
NCBI GI
                   230
BLAST score
                   4.0e-19
E value
Match length
                   74
                   27
% identity
                  (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
                   46095
Seq. No.
                   jC-gmle01810042c11a1
Seq. ID
Method
                   BLASTX
                   g3193284
NCBI GI
                   208
BLAST score
```

2.0e-16

130

E value

Match length



```
% identity
NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]
                  46096
Seq. No.
                  jC-gmle01810042d02d1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g349158
BLAST score
                  37
E value
                  2.0e-11
Match length
                  132
                  89
% identity
NCBI Description Vigna aconitifolia AIR carboxylase (purE) mRNA, partial cds
                  46097
Seq. No.
                  jC-gmle01810042d06a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2851658
BLAST score
                  282
E value
                  5.0e-25
Match length
                  159
% identity
                  38
NCBI Description HYPOTHETICAL 77.3 KD PROTEIN IN GLNA-RBN INTERGENIC REGION
                  >qi 2367323 (AE000463) putative glycosidase [Escherichia
                  coli]
                  46098
Seq. No.
                  jC-gmle01810042d09a1
Seq. ID
Method
                  BLASTX
                  g3482933
NCBI GI
BLAST score
                  562
                  7.0e-58
E value
Match length
                  158
                  66
% identity
NCBI Description
                  (AC003970) Similar to cdc2 protein kinases [Arabidopsis
                  thaliana]
Seq. No.
                  46099
Seq. ID
                  jC-gmle01810042d11a1
Method
                  BLASTX
                  g4406530
NCBI GI
                  255
BLAST score
                  3.0e-22
E value
Match length
                  82
% identity
                  63
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  46100
Seq. ID
                  jC-qmle01810042e07a1
Method
                  BLASTX
NCBI GI
                  g4455192
```

NCBI GI 94455192
BLAST score 332
E value 5.0e-31
Match length 129
% identity 29

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 46101

Method

NCBI GI

BLASTX

g2894606



```
Seq. ID
                  jC-gmle01810042f12d1
                  BLASTN
Method
NCBI GI
                  q18741
                  95
BLAST score
                   4.0e-46
E value
                  255
Match length
                  84
% identity
                  Glycine max gene encoding ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase small subunit
Seq. No.
                  46102
Seq. ID
                  jC-gmle01810042h09a1
Method
                  BLASTN
NCBI GI
                  q4097879
BLAST score
                  84
                  1.0e-39
E value
                  252
Match length
% identity
                  84
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                   46103
Seq. No.
Seq. ID
                   jC-gmle01810043a09a1
                  BLASTX
Method
NCBI GI
                  q3264834
BLAST score
                  254
E value
                  8.0e-22
Match length
                  152
% identity
                  (AF072541) xylitol dehydrogenase; XDH [Galactocandida
NCBI Description
                  mastotermitis]
                   46104
Seq. No.
                   jC-gmle01810043b12d1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2952433
BLAST score
                  177
                   7.0e-13
E value
Match length
                   64
% identity
                   56
NCBI Description
                   (AF051135) putative ubiquitin activating enzyme E1
                   [Arabidopsis thaliana]
Seq. No.
                   46105
Seq. ID
                   jC-gmle01810043c09a1
Method
                  BLASTN
NCBI GI
                  g14311
BLAST score
                  85
E value
                  2.0e-40
Match length
                  161
% identity
NCBI Description
                  G.max chloroplast gene rps19 and flanking regions
Seq. No.
                   46106
                   jC-qmle01810043d02d1
Seq. ID
```



```
BLAST score
                  2.0e-13
E value
                  61
Match length
                  72
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  46107
                   jC-gmle01810043d11d1
Seq. ID
                  BLASTX
Method
                  g2529682
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
                  89
Match length
                   30
% identity
                  (AC002535) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46108
Seq. No.
Seq. ID
                   jC-gmle01810043g02d1
Method
                   BLASTX
                   g3928085
NCBI GI
BLAST score
                   379
                   1.0e-36
E value
                   101
Match length
% identity
                   71
                  (AC005770) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46109
Seq. No.
Seq. ID
                   jC-gmle01810043h04d1
                   BLASTX
Method
NCBI GI
                   g3212863
BLAST score
                   200
                   2.0e-15
E value
                   44
Match length
% identity
                   82
                   (AC004005) putative translation initiation factor
NCBI Description
                   [Arabidopsis thaliana]
                   46110
Seq. No.
                   jC-gmle01810043h06a1
Seq. ID
                   BLASTX
Method
                   g541848
NCBI GI
BLAST score
                   232
E value
                   3.0e-19
Match length
                   104
% identity
                   43
                   amino acid transport protein I - Arabidopsis thaliana
NCBI Description
                   >qi 22641 emb CAA47603 (X67124) amino acid permease I
                   [Arabidopsis thaliana] >gi_404019 (L16240) amino acid
                   transporter [Arabidopsis thaliana]
Seq. No.
                   46111
Seq. ID
                   jC-gmle01810044a12a1
Method
                   BLASTX
NCBI GI
                   q1723685
BLAST score
                   462
```

3.0e-46

132

E value Match length



% identity HYPOTHETICAL 38.3 KD PROTEIN IN RPL16B-PDC6 INTERGENIC NCBI Description REGION >gi_2131667_pir__S64381 hypothetical protein YGR086c - yeast (Saccharomyces cerevisiae) >gi_1323125_emb_CAA97088_ (Z72871) ORF YGR086c [Saccharomyces cerevisiae] 46112 Seq. No. jC-gmle01810044e11a1 Seq. ID BLASTX Method NCBI GI q1781299 BLAST score 299 5.0e-27 E value 98 Match length 58 % identity (Y09506) transformer-SR ribonucleoprotein [Nicotiana NCBI Description tabacum] Seq. No. 46113 Seq. ID jC-gmle01810044e12a1 BLASTX Method q3763925 NCBI GI 433 BLAST score 9.0e-43E value 89 Match length 90 % identity NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana] 46114 Seq. No. jC-gmle01810044g04d1 Seq. ID BLASTX Method NCBI GI g2262172 255 BLAST score E value 4.0e-22 59 Match length % identity (AC002329) predicted protein of unknown function NCBI Description [Arabidopsis thaliana] Seq. No. 46115 Seq. ID jC-gmle01810044g05d1 BLASTX Method g4038594 NCBI GI BLAST score 162 E value 4.0e-11 35 Match length % identity (AJ222798) tDET1 protein [Lycopersicon esculentum] NCBI Description >gi 4454332 emb CAA11914 (AJ224356) tDET1 protein [Lycopersicon esculentum] 46116 Seq. No.

Seq. ID jC-gmle01810044h09d1

Method BLASTX
NCBI GI g3860277
BLAST score 330
E value 9.0e-31

E value

Match length

% identity

1.0e-22

99

89



```
Match length
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi 4314394 gb AAD15604 (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  46117
                  jC-gmle01810045a04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432867
BLAST score
                  205
                  3.0e-16
E value
Match length
                  71
                  52
% identity
                  (AC006300) putative dnaJ-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  46118
Seq. No.
Seq. ID
                  jC-gmle01810045a11d1
                  BLASTX
Method
                  g1749486
NCBI GI
                  370
BLAST score
                  1.0e-35
E value
                  89
Match length
                  78
% identity
                  (D89139) similar to Human electron transfer flavoprotein
NCBI Description
                  alpha subunit precursor, SWISS-PROT Accession Number P13804
                   [Schizosaccharomyces pombe]
                   46119
Seq. No.
                   jC-gmle01810045c09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3540206
                   581
BLAST score
                   3.0e-60
E value
                  133
Match length
                   73
% identity
                  (AC004260) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46120
Seq. No.
                   jC-gmle01810045c09d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2642157
BLAST score
                   203
                   7.0e-16
E value
                   67
Match length
% identity
                  (AC003000) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                   46121
Seq. No.
                   jC-gmle01810045c11a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q169988
BLAST score
                   55
```

% identity

NCBI Description



```
Glycine max NADP-specific isocitrate dehydrogenase (idh1)
NCBI Description
                  mRNA, 3' end
                   46122
Seq. No.
                   jC-gmle01810045g07d1
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                   g2980790
                  167
BLAST score
                   1.0e-11
E value
                   43
Match length
% identity
                   (AL022197) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46123
Seq. No.
                   jC-gmle01810045h02a1
Seq. ID
                   BLASTN
Method
                   g20728
NCBI GI
BLAST score
                   102
                   4.0e-50
E value
Match length
                   293
                   89
% identity
                   Pea chloroplast GAPA mRNA encoding
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit A
                   (EC 1.2.1.13)
                   46124
Seq. No.
                   jC-gmle01810046c01a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g169127
BLAST score
                   44
                   4.0e-16
E value
                   108
Match length
                   85
% identity
                   Pisum sativum (clone pCLp) nuclear encoded precursor to
NCBI Description
                   chloroplast protein mRNA, complete cds
                   46125
Seq. No.
Seq. ID
                   jC-gmle01810046c09d1
Method
                   BLASTX
NCBI GI
                   g2500139
BLAST score
                   156
E value
                   3.0e-10
                   68
Match length
                   49
% identity
                   PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)
NCBI Description
                   >gi_1653916_dbj_BAA18826_ (D90917) peptide chain release
                   factor [Synechocystis sp.]
                   46126
Seq. No.
                   jC-gmle01810046d03a1
Seq. ID
                   BLASTX
Method
                   q2224933
NCBI GI
                   328
BLAST score
E value
                   9.0e-31
Match length
                   103
```

(AF004216) ethylene-insensitive3 [Arabidopsis thaliana]



>gi_2224935 (AF004217) ethylene-insensitive3 [Arabidopsis
thaliana]

Seq. No. 46127

Seq. ID jC-gmle01810046e08d1

Method BLASTN
NCBI GI g2765092
BLAST score 88
E value 7.0e-42
Match length 140
% identity 91

NCBI Description Glycine max mRNA for cytochrome P450-like protein, clone

CPG

Seq. No. 46128

Seq. ID jC-gmle01810046e09a1

Method BLASTN
NCBI GI g1055367
BLAST score 353
E value 0.0e+00
Match length 384
% identity 99

NCBI Description Glycine max ribulose-1,5-bisphosphate carboxylase small

subunit mRNA, complete cds

Seq. No. 46129

Seq. ID jC-gmle01810046f01a1

Method BLASTX
NCBI GI g4467359
BLAST score 277
E value 1.0e-24
Match length 90
% identity 66

NCBI Description (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis

thaliana]

Seq. No. 46130

Seq. ID jC-gmle01810046f12a1

Method BLASTX
NCBI GI g4512675
BLAST score 292
E value 3.0e-41
Match length 115
% identity 73

NCBI Description (AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No. 46131

Seq. ID jC-gmle01810047a11a1

Method BLASTN
NCBI GI g3869069
BLAST score 34
E value 1.0e-09
Match length 122
% identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Match length

NCBI Description

% identity

52

69



```
Seq. No.
Seq. ID
                  jC-gmle01810047b01a1
                  BLASTX
Method
                  g2245096
NCBI GI
BLAST score
                  334
E value
                  3.0e-31
                  99
Match length
                  68
% identity
                  (Z97343) inositol 2-dehydrogenase homolog [Arabidopsis
NCBI Description
                  thaliana]
                  46133
Seq. No.
                  jC-gmle01810047e07d1
Seq. ID
                  BLASTX
Method
                  g3522946
NCBI GI
BLAST score
                  162
                  4.0e-11
E value
Match length
                  135
% identity
                 (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  46134
Seq. No.
                   jC-qmle01810047e09a1
Seq. ID
                  BLASTX
Method
                  q4204469
NCBI GI
                  274
BLAST score
E value
                   3.0e-24
                   82
Match length
% identity
NCBI Description
                  (AF090120) cystathionine beta-synthetase; CBS [Fugu
                  rubripes]
Seq. No.
                   46135
                   jC-qmle01810047f03d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g400890
BLAST score
                   200
                   4.0e-16
E value
Match length
                   56
% identity
                   38
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR
NCBI Description
                   >gi_282837_pir_ S26953 photosystem II 22K protein precursor
                   - spinach >gi 21307 emb CAA48557 (X68552) 22kD-protein of
                   PSII [Spinacia oleracea] >gi_260917_bbs 119338 (S49864)
                   photosystem II 22 kda polypeptide [spinach, Peptide, 274
                   aa] [Spinacia oleracea]
Seq. No.
                   46136
                   jC-gmle01810048d02d1
Seq. ID
                   BLASTX
Method
                   q3080369
NCBI GI
BLAST score
                   175
E value
                   1.0e-12
```

(AL022580) putative protein [Arabidopsis thaliana]



Seq. No. 46137 Seq. ID jC-gm

jC-gmle01810048e01a1

Method BLASTX
NCBI GI g3776005
BLAST score 384
E value 4.0e-37
Match length 112
% identity 88

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.

46138

Seq. ID jC-gmle01810048g01d1

Method BLASTX
NCBI GI g3914019
BLAST score 154
E value 2.0e-10
Match length 48
% identity 62

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_2305014

(AF004317) S-adenosyl-L-methionine synthetase homolog [Musa

acuminata]

Seq. No. 46139

Seq. ID jC-gmle01810048h02a1

Method BLASTX
NCBI GI g2392895
BLAST score 326
E value 2.0e-30
Match length 115
% identity 61

NCBI Description (AF017056) brassinosteroid insensitive 1 [Arabidopsis

thaliana]

Seq. No. 46140

Seq. ID jC-gmle01810048h03a1

Method BLASTX
NCBI GI g1170681
BLAST score 397
E value 1.0e-38
Match length 102
% identity 75

NCBI Description GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA

(CELL DIVISION CYCLE 2-LIKE 1) (CLK-1) (P58 CLK-1)

Seq. No. 46141

Seq. ID jC-gmle01810049a12a1

Method BLASTX
NCBI GI g4102839
BLAST score 174
E value 1.0e-12
Match length 42
% identity 74

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 46142

Seq. ID jC-gmle01810049b12a1

NCBI GI

E value Match length

BLAST score



```
BLASTN
Method
NCBI GI
                  q3449321
BLAST score
                  33
                  5.0e-09
E value
Match length
                  53
% identity
                  91
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTG10, complete sequence [Arabidopsis thaliana]
                  46143
Seq. No.
Seq. ID
                  jC-gmle01810049d12a1
                  BLASTX
Method
                  g4559351
NCBI GI
                  183
BLAST score
                  1.0e-13
E value
Match length
                  109
% identity
                   40
                  (AC006585) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46144
Seq. No.
                   jC-gmle01810049f10a1
Seq. ID
Method
                   BLASTX
                   q3063464
NCBI GI
                   137
BLAST score
                   2.0e-17
E value
                   58
Match length
                   81
% identity
                  (AC003981) F22013.26 [Arabidopsis thaliana]
NCBI Description
                   46145
Seq. No.
Seq. ID
                   jC-gmle01810050d03a1
                   BLASTN
Method
NCBI GI
                   g2293111
BLAST score
                   60
                   1.0e-25
E value
                   144
Match length
                   86
% identity
NCBI Description V.faba mRNA for potassium channel
                   46146
Seq. No.
Seq. ID
                   jC-gmle01810051a06a1
                   BLASTX
Method
NCBI GI
                   g2073541
BLAST score
                   274
E value
                   8.0e-36
                   130
Match length
                   66
% identity
                   (L19437) transaldolase [Homo sapiens] >gi_2612879
NCBI Description
                   (AF010400) transaldolase-related protein [Homo sapiens]
Seq. No.
                   46147
                   jC-gmle01810051b05a1
Seq. ID
Method
                   BLASTX
```

g3033392 257

3.0e-22

68



```
% identity
                  (AC004238) putative translation initiation factor
NCBI Description
                  EIF-2B-epsilon subunit [Arabidopsis thaliana]
Seq. No.
                  46148
                  jC-qmle01810051d12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g984307
BLAST score
                  160
E value
                  7.0e-85
Match length
                  262
% identity
                  92
                  Glycine max ribosomal protein S16 (rps16) gene, partial
NCBI Description
                  cds, beta-carboxyltransferase (accD), photosystem I
                  component (psaI), ORF 202 protein (ORF 203), ORF 151
                  protein (ORF 151), ORF 103 protein (ORF 103), ORF 229
                  precurso
                  46149
Seq. No.
Seq. ID
                  jC-qmle0181Q052a09a1
Method
                  BLASTX
NCBI GI
                  q2827649
BLAST score
                  180
E value
                  4.0e-13
Match length
                  142
                  35
% identity
                  (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
                  46150
Seq. No.
                  jC-qmle01810052e06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q421955
BLAST score
                  340
                  7.0e-32
E value
Match length
                  151
% identity
                  47
                  hypothetical protein 4 - potato transposon Tst1
NCBI Description
                  >gi 21434 emb CAA36616 (X52387) ORF4 [Solanum tuberosum]
                  46151
Seq. No.
                  jC-gmle01810053b02a1
Seq. ID
                  BLASTX
Method
                  q4574742
NCBI GI
BLAST score
                  451
                  6.0e-45
E value
                  132
Match length
% identity
                  66
                  (AF135270) fragmin A [Physarum polycephalum]
NCBI Description
                  46152
Seq. No.
```

Seq. ID jC-gmle01810053b03a1

Method BLASTX
NCBI GI g128683
BLAST score 571
E value 8.0e-59
Match length 193
% identity 58



NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 NCBI Description >gi 83833 pir_ S02154 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Podospora anserina mitochondrion (SGC3) >gi_13297_emb_CAA32646_ (X14485) ND2 (AA 1 - 556) [Podospora anserina] >gi_14031_emb_CAA38765_ (X55026) NADH-ubiquinone oxidoreductase subunit 2 [Podospora anserina] 46153 Seq. No. jC-gmle01810053f05a1 Seq. ID BLASTX Method q2440002 NCBI GI 174 BLAST score 2.0e-12 E value 162 Match length 25 % identity (AF003692) 8R-lipoxygenase-allene oxide synthase fusion NCBI Description protein [Plexaura homomalla] 46154 Seq. No. jC-gmle01810053g08a1 Seq. ID Method BLASTX g4455367 NCBI GI 295 BLAST score 1.0e-26 E value 144 Match length 48 % identity NCBI Description (AL035524) putative protein [Arabidopsis thaliana] 46155 Seq. No. jC-gmle01810053g10d1 Seq. ID BLASTX Method q132724 NCBI GI BLAST score 152 3.0e-10 E value 46 Match length % identity 63 NCBI Description 50S RIBOSOMAL PROTEIN L18 >gi_71259_pir__R5BS8F ribosomal protein L18 - Bacillus stearothermophilus 46156 Seq. No. jC-gmle01810053h08a1 Seq. ID BLASTX Method NCBI GI q3024689 BLAST score 246 6.0e-21 E value 120 Match length % identity NCBI Description TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100) >gi_1491718_emb_CAA64777 (X95525) hTAFII100 [Homo sapiens] Seq. No. 46157

Seq. ID jC-gmle01810054b09a1

Method BLASTX
NCBI GI g4467095
BLAST score 141



```
6.0e-09
E value
Match length
                  75
                  41
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                  46158
Seq. No.
                  jC-qmle01810054b11d1
Seq. ID
                  BLASTN
Method
                  g1184120
NCBI GI
                  73
BLAST score
                  7.0e-33
E value
                  153
Match length
                  87
% identity
                  Vigna radiata clone MII-3 auxin-induced protein mRNA,
NCBI Description
                  complete cds
                  46159
Seq. No.
                  jC-gmle01810054c08a1
Seq. ID
Method
                  BLASTX
                  g404690
NCBI GI
                  138
BLAST score
                  7.0e-09
E value
                  50
Match length
                  52
% identity
                  (L19075) cytochrome P450 [Catharanthus roseus]
NCBI Description
Seq. No.
                   46160
                   jC-gmle01810054f03a1
Seq. ID
                   BLASTX
Method
                   q4490297
NCBI GI
BLAST score
                   206
E value
                   3.0e-16
Match length
                   123
% identity
                   46
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                   46161
Seq. No.
                   jC-qmle01810054f11a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2104683
BLAST score
                   257
                   2.0e-24
```

E value Match length 127 57 % identity

NCBI Description (X97908) transcription factor [Vicia faba]

46162 Seq. No.

jC-qmle01810054h06a1 Seq. ID

Method BLASTX NCBI GI q3080447 BLAST score 355 1.0e-33 E value Match length 137 % identity 56

(AL022605) putative protein [Arabidopsis thaliana] NCBI Description

46163 Seq. No.



```
jC-gmle01810055c09a1
Seq. ID
                  BLASTN
Method
                  g11768
NCBI GI
                  39
BLAST score
                  3.0e-13
E value
                  103
Match length
                  85
% identity
                  Chloroplast N. tabacum ATPase alpha subunit gene
NCBI Description
                  46164
Seq. No.
                  jC-gmle01810055f02a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3721856
BLAST score
                  763
                  2.0e-81
E value
                  165
Match length
                  79
% identity
                  (AB014057) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
Seq. No.
                  46165
                  jC-gmle01810055f11a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1053215
BLAST score
                  467
E value
                  0.0e + 00
Match length
                  475
% identity
                  100
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
                  46166
Seq. No.
                   jC-gmle01810055g03d1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218327
BLAST score
                   64
E value
                  2.0e-27
Match length
                  132
% identity
                  Vigna angularis mRNA for peroxidase basic isozyme
NCBI Description
                   (monomer), complete cds
                   46167
Seq. No.
                   jC-gmle01810055h02d1
Seq. ID
                   BLASTX
Method
NCBI GI
                  g2827631
BLAST score
                   262
                   7.0e-23
E value
Match length
                  104
% identity
                   55
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

Seq. ID jC-qmle01810055h08a1

46168

Method BLASTX
NCBI GI g1723378
BLAST score 169
E value 7.0e-12



```
Match length
% identity
                  40
                  HYPOTHETICAL 28.1 KD PROTEIN IN CARA-YCF30 INTERGENIC
NCBI Description
                  REGION (ORF238) >gi_2147529_pir__S73123 hypothetical
                  protein 238 - Porphyra purpurea chloroplast >gi 1276668
                  (U38804) ORF238 [Porphyra purpurea]
                  46169
Seq. No.
                  jC-gmle01810055h09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q130582
BLAST score
                  205
E value
                  5.0e-16
                  123
Match length
% identity
                  37
                  RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94
NCBI Description
                  [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
                  >gi_100342_pir__S04273 hypothetical protein - common
                  tobacco >gi 20045 emb CAA32025 (X13777) ORF [Nicotiana
                  tabacum]
                  46170
Seq. No.
Seq. ID
                  jC-gmle01810055h11a1
Method
                  BLASTX
NCBI GI
                  q2315153
BLAST score
                  644
                  1.0e-67
E value
                  137
Match length
% identity
NCBI Description
                  (Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  jC-qmle01810056b06a1
Method
                  BLASTX
NCBI GI
                  q3738298
BLAST score
                  296
E value
                  1.0e-26
Match length
                  107
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 4249394 (AC006072) unknown protein [Arabidopsis
                  thaliana]
                  46172
Seq. No.
Seq. ID
                  jC-gmle01810056b07a1
                  BLASTN
Method
NCBI GI
                  q18741
                  230
BLAST score
E value
                  1.0e-126
```

445 Match length 98 % identity

Glycine max gene encoding ribulose-1,5-bisphosphate NCBI Description

carboxylase small subunit

46173 Seq. No.

Seq. ID jC-gmle01810056e07a1

Method BLASTX



```
NCBI GI
                  q81857
BLAST score
                  344
                  2.0e-32
E value
Match length
                  94
                  72
% identity
                  IgE-dependent histamine-releasing factor homolog - alfalfa
NCBI Description
                  (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally
                  controlled tumor protein [Medicago sativa]
Seq. No.
                  46174
                  jC-gmle01810056g01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760832
BLAST score
                  424
                  1.0e-41
E value
Match length
                  150
                  59
% identity
                  (AC003105) similar to barley ids-4 gene product
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  46175
                  jC-gmle01810056g04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2258125
BLAST score
                  297
E value
                  8.0e-27
Match length
                  162
% identity
                  45
NCBI Description (Z83828) AmMst-1 [Amanita muscaria]
                  46176
Seq. No.
                  jC-gmle01810059c08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173638
BLAST score
                  362
E value
                  1.0e-34
Match length
                  105
% identity
                  59
                  (U35779) 1-aminocyclopropane-1-carboxylate synthase
NCBI Description
                  [Triticum aestivum]
                  46177
Seq. No.
                  jC-gmle01810059d10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3417405
BLAST score
                  275
                  2.0e-24
E value
Match length
                  61
% identity
NCBI Description
                  (Z74233) ORF YDL184w-b [Saccharomyces cerevisiae]
```

Seq. No. 46178

Seq. ID jC-gmle01810059f05a1

Method BLASTN
NCBI GI g1053215
BLAST score 463
E value 0.0e+00



Match length 475 % identity 99

NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 46179

Seq. ID jC-gmle01810059f10a1

Method BLASTX
NCBI GI g3025189
BLAST score 413
E value 2.0e-40
Match length 153
% identity 46

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770

>gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis

sp.]

Seq. No. 46180

Seq. ID jC-gmle01810059h05d1

Method BLASTX
NCBI GI 94580513
BLAST score 230
E value 5.0e-19
Match length 62
% identity 66

NCBI Description (AF036300) scarecrow-like 1 [Arabidopsis thaliana]

Seq. No. 46181

Seq. ID jC-gmle01810060b11d1

Method BLASTX
NCBI GI g2194124
BLAST score 261
E value 1.0e-22
Match length 73
% identity 66

NCBI Description (AC002062) Similar to Glycine metalloendoproteinase

(gb_U63725). [Arabidopsis thaliana]

Seq. No. 46182

Seq. ID jC-gmle01810060d11d1

Method BLASTX
NCBI GI g2213590
BLAST score 173
E value 2.0e-12
Match length 92
% identity 39

NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 46183

Seq. ID jC-gmle01810060e07a1

Method BLASTN
NCBI GI g170073
BLAST score 196
E value 1.0e-106
Match length 247
% identity 95

NCBI Description Soybean calmodulin (SCaM-3) mRNA, complete cds



Seq. No. 46184

jC-gmle01810061f07a1 Seq. ID

Method BLASTX q131384 NCBI GI BLAST score 191 5.0e-15 E value Match length 71 % identity 62

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 81934_pir__S04132

photosystem II oxygen-evolving complex protein 1 precursor - garden pea >gi 20621 emb CAA33408 (X15350) precursor (AA

-81 to 248) [Pisum sativum] >gi 344004 dbj BAA02554 (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >qi 226937 prf 1611461A O2 evolving

complex 33kD protein [Arachis hypogaea]

Seq. No. 46185

Seq. ID jC-gmle01810061h05a1

Method BLASTN NCBI GI g1053215 BLAST score 290 E value 1.0e-162 Match length 426 % identity 92

Glycine max chlorophyll a/b-binding protein (cab3) mRNA, NCBI Description

nuclear gene encoding chloroplast protein, complete cds

Seq. No. 46186

jC-gmle01810062a10a1 Seq. ID

BLASTX Method NCBI GI q1705679 BLAST score 231 4.0e-19 E value Match length 67

% identity 64

CELL DIVISION CONTROL PROTEIN 48 >gi_2118116_pir__S67669 NCBI Description

cell division control protein CDC48 - yeast (Saccharomyces cerevisiae) >gi_1431189_emb_CAA98694_ (Z74174) ORF YDL126c

[Saccharomyces cerevisiae] >gi 1449400 emb CAA40276

(X56956) CDC48p [Saccharomyces cerevisiae]

46187 Seq. No.

jC-gmle01810062a10d1 Seq. ID

Method BLASTX NCBI GI g3337433 BLAST score 176 1.0e-12 E value Match length 53 % identity 60

(AF047037) transitional endoplasmic reticulum ATPase TER94 NCBI Description

[Drosophila melanogaster]

Seq. No. 46188

Seq. ID jC-gmle01810062f12a1



```
BLASTX
Method
NCBI GI
                  g2191168
                  251
BLAST score
E value
                  1.0e-21
                  108
Match length
                  48
% identity
                   (AF007270) contains similarity to myosin heavy chain
NCBI Description
                   [Arabidopsis thaliana]
                  46189
Seq. No.
                  jC-gmle01810062g08a1
Seq. ID
                  BLASTX
Method
                  g2352427
NCBI GI
BLAST score
                  200
E value
                  1.0e-15
Match length
                  115
% identity
                  20
                   (AF004161) peroxisomal Ca-dependent solute carrier
NCBI Description
                   [Oryctolagus cuniculus]
Seq. No.
                   46190
                   jC-gmle01810062g08d1
Seq. ID
Method
                  BLASTX
                   g4107480
NCBI GI
                   229
BLAST score
E value
                   6.0e-19
Match length
                  86
% identity
                   19
                  (AL035085) putative mitochondrial carrier protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   46191
Seq. No.
                   jC-gmle01810062h03a1
Seq. ID
                   BLASTN
Method
                   g1055367
NCBI GI
                   349
BLAST score
                   0.0e+00
E value
Match length
                   432
% identity
                   95
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   46192
Seq. No.
                   jC-gmle01810062h09a1
Seq. ID
                   BLASTX
Method
                   g4510340
NCBI GI
BLAST score
                   145
                   5.0e-09
E value
                   75
Match length
% identity
                   45
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46193
                   jC-qmle01810063a06d1
Seq. ID
```

BLASTN

45

g169036

Method NCBI GI

BLAST score

3.0e-16 E value 97 Match length 87 % identity NCBI Description Pisum sativum L. aldolase gene, 3' end cds 46194 Seg. No. jC-gmle01810063c02a1 Seq. ID BLASTX Method g3510253 NCBI GI BLAST score 381 1.0e-36 E value Match length 107 % identity 70 (AC005310) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 46195 jC-gmle01810063d06d1 Seq. ID BLASTN Method q343022 NCBI GI 135 BLAST score E value 8.0e-70 409 Match length % identity 83 Pea chloroplast photosystem II gene encoding the D2 and NCBI Description 44kd chlorophyll a-binding proteins, complete cds 46196 Seq. No. jC-gmle01810063d08a1 Seq. ID Method BLASTX q531389 NCBI GI BLAST score 145 5.0e-09 E value 119 Match length 34 % identity NCBI Description [Zea mays]

(U12626) copia-like retrotransposon Hopscotch polyprotein

46197 Seq. No.

jC-gmle01810063d09a1 Seq. ID

BLASTX Method NCBI GI g913141 BLAST score 189 E value 2.0e-14 Match length 87 43 % identity

ARK3 product/receptor-like serine/threonine protein kinase NCBI Description

ARK3 [Arabidopsis thaliana, Columbia, Peptide, 851 aa]

46198 Seq. No.

jC-gmle01810063e06a1 Seq. ID

Method BLASTX q3080527 NCBI GI BLAST score 315 6.0e-29 E value 110 Match length % identity 50

(AL022600) putative mannose-1-phosphate gaunyl transferase NCBI Description



[Schizosaccharomyces pombe]

```
46199
Seq. No.
Seq. ID
                  jC-qmle01810063f05a1
Method
                  BLASTX
NCBI GI
                  q2760329
BLAST score
                  231
                  5.0e-19
E value
                  113
Match length
                   49
% identity
                  (AC002130) F1N21.14 [Arabidopsis thaliana]
NCBI Description
                   46200
Seq. No.
                  jC-qmle01810063f09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1053215
BLAST score
                   398
E value
                   0.0e + 00
Match length
                   406
                   100
% identity
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
                   46201
Seq. No.
                   jC-gmle01810063h10a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4210331
BLAST score
                   41
E value
                   1.0e-13
Match length
                   161
% identity
                   81
                  Arabidopsis thaliana mRNA for 2-oxoglutarate dehydrogenase
NCBI Description
                   E2 subunit
                   46202
Seq. No.
                   jC-gmle01810064b05a1
Seq. ID
Method
                   BLASTX
                   g3785975
NCBI GI
BLAST score
                   595
                   1.0e-61
E value
Match length
                   141
% identity
                   82
                  (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46203
                   jC-gmle01810064c02d1
Seq. ID
Method
                   BLASTN
                   g1053215
NCBI GI
                   74
BLAST score
E value
                   8.0e-34
Match length
                   154
% identity
                   86
                   Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                   nuclear gene encoding chloroplast protein, complete cds
```

Seq. No. 46204

Seq. ID jC-gmle01810064c12a1



```
BLASTX
Method
NCBI GI
                  g3850816
BLAST score
                  443
E value
                  5.0e-44
Match length
                  113
% identity
                  70
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
Seq. No.
                  46205
Seq. ID
                  jC-gmle01810064d02a1
Method
                  BLASTX
NCBI GI
                  g2213586
BLAST score
                  182
                  2.0e-13
E value
Match length
                  110
% identity
                  (AC000348) T7N9.6 [Arabidopsis thaliana]
NCBI Description
                  46206
Seq. No.
Seq. ID
                  iC-gmle01810064d05a1
Method
                  BLASTX
NCBI GI
                  q586467
BLAST score
                  184
                  1.0e-13
E value
Match length
                  103
% identity
                  39
                  HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN IN
NCBI Description
                  COQ1-HHF1 INTERGENIC REGION >gi 626789 pir S45858 probable
                  aldehyde dehydrogenase (EC 1.2.1.-) - yeast (Saccharomyces
                  cerevisiae)
                  46207
Seq. No.
                  jC-gmle01810064e03a1
Seq. ID
                  BLASTX
Method
                  q3894391
NCBI GI
BLAST score
                  153
                  6.0e-10
E value
                  144
Match length
% identity
                  (AF053997) Hcr2-5B [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  46208
                  jC-gmle01810064e07a1
Seq. ID
Method
                  BLASTX
                  g2618691
NCBI GI
                  336
BLAST score
                  2.0e-31
E value
                  120
Match length
                  54
% identity
                  (AC002510) putative chloroplast envelope Ca2+-ATPase
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 46209

Seq. ID jC-gmle01810064e10a1

Method BLASTX NCBI GI g2506155



BLAST score 2.0e-11 E value 105 Match length % identity 38

HYPOTHETICAL OXIDOREDUCTASE IN HYBA-EXBD INTERGENIC REGION NCBI Description >gi 882532 (U28377) ORF o294 [Escherichia coli] >gi 1789378

(AE000383) putative oxidoreductase [Escherichia coli]

46210 Seq. No.

jC-gmle01810064e10d1 Seq. ID

BLASTX Method g633890 NCBI GI 191 BLAST score E value 3.0e-20 Match length 92 59 % identity

(S72926) glucose and ribitol dehydrogenase homolog [Hordeum NCBI Description

vulgare]

Seq. No. 46211

jC-gmle01810064f06a1 Seq. ID

Method BLASTX g2511537 NCBI GI BLAST score 623 E value 5.0e-65 Match length 159 % identity 68

(AF014922) protein phosphatase 2B [Paramecium tetraurelia] NCBI Description

46212 Seq. No.

jC-gmle01810065b02a1 Seq. ID

Method BLASTN NCBI GI g4566613 BLAST score 56 E value 1.0e-22 132 Match length % identity 86

Populus alba x Populus tremula actin depolymerizing factor NCBI Description

mRNA, partial cds

Seq. No. 46213

jC-gmle01810065d02a1 Seq. ID

Method BLASTX NCBI GI g3250679 BLAST score 378 2.0e-36 E value Match length 127 % identity 60

(AL024486) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 46214

jC-qmle01810065e09d1 Seq. ID

Method BLASTX NCBI GI g2245099 BLAST score 231 E value 4.0e-19 Match length 58



```
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  46215
                  jC-gmle01810066b10a1
Seq. ID
                  BLASTX
Method
                  g3335516
NCBI GI
BLAST score
                  672
E value
                  8.0e-71
Match length
                  150
% identity
                  49
                  (AF053941) nonphototropic hypocotyl 2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  46216
                  jC-gmle01810066e01d1
Seq. ID
                  BLASTX
Method
                  q1853968
NCBI GI
BLAST score
                  187
                  5.0e-14
E value
Match length
                  77
% identity
                  69
NCBI Description (D88121) CPRD12 protein [Vigna unguiculata]
                  46217
Seq. No.
                  jC-gmle01810066e10a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2598575
BLAST score
                  259
                  2.0e-22
E value
Match length
                  69
                  75
% identity
NCBI Description (Y15293) MtN21 [Medicago truncatula]
                  46218
Seq. No.
                  jC-gmle01810066f10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113449
BLAST score
                  159
E value
                  7.0e-11
Match length
                  86
                  36
% identity
                  PROBABLE ATP-DEPENDENT PERMEASE PRECURSOR
NCBI Description
                  >gi 83202 pir S19421 ATP-dependent permease ADP1 precursor
                  - yeast (Saccharomyces cerevisiae)
                  >gi_1907154_emb_CAA42328_ (X59720) YCR011c, len:1049
                  [Saccharomyces cerevisiae]
                  46219
Seq. No.
                  jC-gmle01810066f10d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q113449
```

Method BLASTX
NCBI GI g113449
BLAST score 196
E value 5.0e-15
Match length 82
% identity 44

NCBI Description PROBABLE ATP-DEPENDENT PERMEASE PRECURSOR

>gi_83202_pir__S19421 ATP-dependent permease ADP1 precursor
- yeast (Saccharomyces cerevisiae)
>gi_1907154_emb_CAA42328_ (X59720) YCR011c, len:1049
[Saccharomyces cerevisiae]

Seq. No. 46220

Seq. ID jC-gmle01810066h12a1

Method BLASTX
NCBI GI g115833
BLAST score 239
E value 5.0e-20
Match length 74
% identity 64

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR

(CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605)

a-binding protein [Lycopersicon esculentum]

Seq. No. 46221

Seq. ID jC-gmle01810067b04a1

Method BLASTX
NCBI GI g3122264
BLAST score 210
E value 1.0e-16
Match length 137
% identity 36

NCBI Description PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA

SUBUNIT (EIF-3 ALPHA) (EIF3 P150) >gi_2281117 (U49332)

150-kD protein [Dictyostelium discoideum]

Seq. No.

Seq. ID jC-gmle01810067c04d1

46222

Method BLASTX
NCBI GI g3413423
BLAST score 172
E value 3.0e-12
Match length 60
% identity 52

NCBI Description (AJ006309) hypothetical protein [Arabidopsis thaliana]

Seq. No. 46223

Seq. ID jC-gmle01810067c07d1

Method BLASTX
NCBI GI g643469
BLAST score 198
E value 2.0e-15
Match length 94
% identity 55

NCBI Description (U19886) unknown [Lycopersicon esculentum]

Seq. No. 46224

Seq. ID jC-gmle01810067d09a1

Method BLASTX
NCBI GI g3341679
BLAST score 475
E value 1.0e-47
Match length 165



% identity (AC003672) dynamin-like protein phragmoplastin 12 NCBI Description [Arabidopsis thaliana] Seq. No. 46225 jC-gmle01810067e05d1 Seq. ID BLASTX Method q3522929 NCBI GI 297 BLAST score 6.0e-27 E value 66 Match length 82 % identity (AC002535) putative dTDP-glucose 4-6-dehydratase NCBI Description [Arabidopsis thaliana] >gi 3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] 46226 Seq. No. jC-qmle01810067f10a1 Seq. ID ${\tt BLASTX}$ Method q115833 NCBI GI 228 BLAST score 6.0e-19 E value 85 Match length 55 % identity CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR NCBI Description (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605) a-binding protein [Lycopersicon esculentum] 46227 Seq. No. jC-gmle01810067g10a1 Seq. ID BLASTX Method g4454051 NCBI GI 265 BLAST score E value 8.0e-38 140 Match length 56 % identity (AL035394) putative polygalacturonase [Arabidopsis NCBI Description thaliana] Seq. No. 46228 jC-gmle01810067g11a1 Seq. ID Method BLASTX NCBI GI g2642450 BLAST score 392

5.0e-38 E value Match length 108 73 % identity

(AC002391) putative metal ion transporter (Nramp) NCBI Description

[Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

46229 Seq. No.

jC-gmle01810068b03d1 Seq. ID

Method BLASTN NCBI GI g1055367 BLAST score 71

E value 3.0e-32 Match length 110 % identity Glycine max ribulose-1,5-bisphosphate carboxylase small NCBI Description subunit mRNA, complete cds 46230 Seq. No. jC-gmle01810068d05d1 Seq. ID Method BLASTX NCBI GI g3859944 BLAST score 160 E value 7.0e-11 Match length 41 % identity 73 (AF084570) FKBP12 interacting protein [Arabidopsis NCBI Description thaliana] Seq. No. 46231 jC-gmle01810068d07a1 Seq. ID Method BLASTX g3892059 NCBI GI BLAST score 148 E value 9.0e-10 Match length 71 % identity 24 (AC002330) predicted protein of unknown function NCBI Description [Arabidopsis thaliana] 46232 Seq. No. jC-gmle01810070b07a1 Seq. ID BLASTX

Method

NCBI GI q3924603 BLAST score 319 E value 1.0e-42 128 Match length % identity 70

NCBI Description (AF069442) putative WD-repeat protein [Arabidopsis

thaliana]

Seq. No. 46233

jC-qmle01810070b12a1 Seq. ID

Method BLASTX NCBI GI g4579913 BLAST score 423 E value 6.0e-46Match length 128 % identity

(AB023423) sulfate transporter [Arabidopsis thaliana] NCBI Description

Seq. No. 46234

jC-qmle01810070c03d1 Seq. ID

Method BLASTX q3808101 NCBI GI BLAST score 161 E value 3.0e-11Match length 53 % identity 64



```
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
                  46235
                  jC-gmle01810070c09d1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g473216
BLAST score
                  138
E value
                  1.0e-71
                  308
Match length
                  89
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
                  46236
Seq. No.
                  jC-gmle01810070d06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1065907
BLAST score
                  266
                  1.0e-148
E value
Match length
                  430
                  90
% identity
NCBI Description Pisum sativum chloroplast processing enzyme mRNA, nuclear
                  gene encoding chloroplast protein, complete cds
                  46237
Seq. No.
                  jC-gmle01810070e02d1
Seq. ID
Method
                  BLASTN
                  g310560
NCBI GI
                  44
BLAST score
                  8.0e-16
E value
Match length
                  84
                  88
% identity
NCBI Description Soybean ascorbate peroxidase mRNA, complete cds
                  46238
Seq. No.
                  jC-gmle01810070f04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g602589
                  33
BLAST score
                  2.0e-09
E value
Match length
                  41
% identity
                  95
NCBI Description P.hybrida mRNA for triosephosphate isomerase
                  46239
Seq. No.
Seq. ID
                  jC-gmle01810071a03d1
                  BLASTX
Method
                  g3355308
NCBI GI
                  192
BLAST score
E value
                  2.0e-14
                  110
Match length
% identity
NCBI Description (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
                   46240
Seq. No.
```

Seq. ID jC-gmle01810071a12a1

Method BLASTX NCBI GI g3355308



```
BLAST score
E value
                  2.0e-43
                  136
Match length
                  62
% identity
                  (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
NCBI Description
                  46241
Seq. No.
                  jC-gmle01810071c01d1
Seq. ID
Method
                  BLASTX
                  g3033389
NCBI GI
BLAST score
                  179
E value
                  6.0e-13
Match length
                  93
% identity
                  42
                  (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
NCBI Description
                  46242
Seq. No.
                  jC-qmle01810071c06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642450
BLAST score
                  201
                  8.0e-16
E value
Match length
                  76
% identity
                  61
NCBI Description
                  (AC002391) putative metal ion transporter (Nramp)
                   [Arabidopsis thaliana] >gi_3169188 (AC004401) putative
                  metal ion transporter (Nramp) [Arabidopsis thaliana]
                  46243
Seq. No.
                  jC-gmle01810071e08d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006920
BLAST score
                  412
E value
                  3.0e-40
                  97
Match length
% identity
                  81
NCBI Description
                  (Z99708) actin interacting protein [Arabidopsis thaliana]
                  46244
Seq. No.
Seq. ID
                   jC-qmle01810071f03a1
Method
                  BLASTX
NCBI GI
                  g3334219
BLAST score
                   142
E value
                   4.0e-16
Match length
                  58
                  73
% identity
                  4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)
NCBI Description
                  >gi 2231615 (U87257) 4-hydroxyphenylpyruvate dioxygenase
                   [Daucus carota]
Seq. No.
                   46245
Seq. ID
                   jC-gmle01810071g04d1
Method
                   BLASTX
NCBI GI
                  g113465
BLAST score
                  543
```

9.0e-56

127

E value Match length



% identity NCBI Description ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_419739_pir__S30259 ADP, ATP carrier protein, mitochondrial - Chlamydomonas reinhardtii >gi_18110_emb_CAA46311_ (X65194) mitochondrial ADP/ATP translocator protein [Chlamydomonas reinhardtii] >gi_446768_prf__1912294A ADP/ATP translocator [Chlamydomonas reinhardtii] 46246 Seq. No. jC-gmle01810071g11d1 Seq. ID Method BLASTX NCBI GI g3005931 BLAST score 146 4.0e-09 E value Match length 37 68 % identity (AJ005016) ABC transporter [Homo sapiens] NCBI Description Seq. No. 46247 jC-gmle01810071h07a1 Seq. ID Method BLASTN NCBI GI g4406529 BLAST score 128 1.0e-65 E value Match length 327 % identity 85 Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene NCBI Description encoding chloroplast protein, complete cds Seq. No. 46248 jC-gmle01810072a11d1 Seq. ID Method BLASTX NCBI GI g629561 BLAST score 199 2.0e-15 E value Match length 71 % identity 56 NCBI Description SRG1 protein - Arabidopsis thaliana >gi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis thalianal Seq. No. 46249 jC-gmle01810072d10d1 Seq. ID Method BLASTX NCBI GI g2244833 BLAST score 181 1.0e-13 E value Match length 67 % identity 51

NCBI Description (Z97337) centromere protein homolog [Arabidopsis thaliana]

46250 Seq. No.

Seq. ID jC-gmle01810072g01a1

Method BLASTX NCBI GI g100424 BLAST score 346



```
E value
                  7.0e - 33
                  89
Match length
                  41
% identity
NCBI Description ADP, ATP carrier protein precursor - potato
                  46251
Seq. No.
                  jC-qmle01810073b12d1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3059094
                  125
BLAST score
                  3.0e-64
E value
                  193
Match length
                  91
% identity
NCBI Description Glycine max mRNA for magnesium chelatase subunit
                  46252
Seq. No.
                  jC-qmle01810073f02d1
Seq. ID
                  BLASTX
Method
                  g3327271
NCBI GI
BLAST score
                  318
                  3.0e-29
E value
                  72
Match length
                  75
% identity
                  (AB016000) PKn2 [Ipomoea nil]
NCBI Description
Seq. No.
                  46253
                  jC-gmle01810073g10a1
Seq. ID
Method
                  BLASTX
                  g3201477
NCBI GI
                  148
BLAST score
                  1.0e-09
E value
Match length
                  60
                  50
% identity
                  (AJ006021) putative PRL1 associated protein [Arabidopsis
NCBI Description
                  thaliana]
                  46254
Seq. No.
                  jC-gmle01810075b06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3021265
                  288
BLAST score
                  5.0e-39
E value
Match length
                  116
                  69
% identity
                  (AL022347) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana] >gi_3292839_emb_CAA19829_ (AL031018) protein
                  kinase - like protein [Arabidopsis thaliana]
                  46255
Seq. No.
                  jC-qmle01810075c05a1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1352956
BLAST score 430
E value 1.0e-42
Match length 127
% identity 65

NCBI Description HYPOTHETICAL 75.5 KD PROTEIN IN CCT3-CCT8 INTERGENIC REGION



>gi_1077794_pir__S56783 hypothetical protein YJL012c yeast (Saccharomyces cerevisiae) >gi_1006727_emb_CAA89303_
(Z49287) ORF YJL012c [Saccharomyces cerevisiae]

Seq. No. 46256

Seq. ID jC-gmle01810075f07a1

Method BLASTN
NCBI GI g409566
BLAST score 95
E value 5.0e-46
Match length 259
% identity 84

NCBI Description Neurospora crassa initiation factor 5a (eIF-5A) mRNA,

complete cds

Seq. No. 46257

Seq. ID jC-gmle01810075g04a1

Method BLASTN
NCBI GI g2598656
BLAST score 50
E value 2.0e-19
Match length 94
% identity 88

NCBI Description Vicia faba mRNA for elongation factor 1-alpha (EF1-a)

Seq. No. 46258

Seq. ID jC-gmle01810075h04a1

Method BLASTX
NCBI GI g586875
BLAST score 167
E value 1.0e-11
Match length 131
% identity 33

NCBI Description HYPOTHETICAL 29.2 KD PROTEIN IN METS-KSGA INTERGENIC REGION

>gi_2127033_pir__S66068 hypothetical protein - Bacillus

subtilis >gi 467428 dbj BAA05274 (D26185) unknown [Bacillus subtilis] >gi 2632306 emb CAB11815 (Z99104) similar to hypothetical proteins [Bacillus subtilis]

Seq. No. 46259

Seq. ID jC-gmle01810075h06a1

Method BLASTX
NCBI GI g3913031
BLAST score 411
E value 1.0e-40
Match length 95
% identity 78

NCBI Description BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE)

>gi 2559006 (AF026217) beta-amylase [Medicago sativa]

Seq. No. 46260

Seq. ID jC-qmle01810077a12d1

Method BLASTN
NCBI GI g20831
BLAST score 46
E value 8.0e-17
Match length 180



% identity NCBI Description P.sativum petC mRNA for chloroplast Rieske FeS protein 46261 Seq. No. jC-gmle01810077b02d1 Seq. ID BLASTX Method g2809262 NCBI GI 167 BLAST score 1.0e-11 E value 80 Match length 45 % identity (AC002560) F21B7.31 [Arabidopsis thaliana] NCBI Description 46262 Seq. No.

jC-gmle01810077f09d1 Seq. ID BLASTX Method g2499967 NCBI GI 174 BLAST score

2.0e-12 E value Match length 43 79 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E NCBI Description

B) >gi 632724_bbs_151002 (S72358) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,

143 aa] [Nicotiana sylvestris]

Seq. No. 46263

jC-gmle01810078c02d1 Seq. ID

BLASTX Method NCBI GI q3023453 BLAST score 159 1.0e-10 E value 76 Match length 46 % identity

NCBI Description CBBY PROTEIN >gi 1825471 (U67781) CbbY [Rhodobacter:

sphaeroides]

46264 Seq. No.

jC-gmle01810078d08a1 Seq. ID

Method BLASTX a3169180 NCBI GI 162 BLAST score 2.0e-11 E value Match length 41 % identity 78

(AC004401) putative casein kinase II catalytic subunit NCBI Description

[Arabidopsis thaliana]

Seq. No. 46265

Seq. ID jC-qmle01810078e01a1

Method BLASTX NCBI GI q3122599 BLAST score 270 1.0e-23 E value Match length 98 % identity 51

NCBI Description PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)



>gi_1653389_dbj_BAA18303_ (D90913) pyridoxamine 5-phosphate oxidase [Synechocystis sp.]

46266 Seq. No.

jC-gmle01810078e08a1 Seq. ID

Method BLASTX NCBI GI q4097880 BLAST score 585 9.0e-61 E value 122 Match length 91 % identity

(U70866) polyprotein [Bean pod mottle virus] NCBI Description

Seq. No. 46267

jC-gmle01810078h04a1 Seq. ID

Method BLASTN g4406529 NCBI GI BLAST score 66 6.0e-29 E value Match length 142 87 % identity

Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene NCBI Description

encoding chloroplast protein, complete cds

Seq. No. 46268

jC-gmle01810078h09a1 Seq. ID

Method BLASTX NCBI GI g1549393 BLAST score 327 E value 2.0e-30 118 Match length 53

% identity

(U68141) XFEN1b [Xenopus laevis] NCBI Description

Seq. No. 46269

jC-gmle01810080f01a1 Seq. ID

Method BLASTX NCBI GI q4220445 193 BLAST score E value 9.0e-15 Match length 132 % identity

(AC006216) Similar to gi 3004555 F19F24.14 salt inducible NCBI Description protein homolog from Arabidopsis thaliana BAC gb_AC003673.

[Arabidopsis thaliana]

46270 Seq. No.

jC-gmle01810080f07a1 Seq. ID

Method BLASTX NCBI GI q1076414 BLAST score 386 E value 2.0e-37 Match length 131 % identity

subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis NCBI Description

thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974)

subtilisin-like protease [Arabidopsis thaliana]



46271 Seq. No. jC-gmle01810080g06a1 Seq. ID Method BLASTN q4097879 NCBI GI 221 BLAST score 1.0e-121 E value 497 Match length 86 % identity Bean pod mottle virus complete segment RNA1 polyprotein NCBI Description gene, complete cds 46272 Seq. No. jC-gmle01810080g07a1 Seq. ID Method BLASTX NCBI GI g4538976 BLAST score 667 3.0e-70E value Match length 155 % identity 80 (AL049487) sucrose-phosphate synthase-like protein NCBI Description [Arabidopsis thaliana] 46273 Seq. No. jC-gmle01810080g12d1 Seq. ID Method BLASTN g2739005 NCBI GI BLAST score 44 7.0e-16 E value Match length 146 84 % identity Glycine max cytochrome P450 monooxygenase CYP93C1p NCBI Description (CYP93C1) mRNA, complete cds 46274 Seq. No. jC-gmle01810080h12a1 Seq. ID BLASTX Method g1346226 NCBI GI 564 BLAST score 3.0e-58 E value 145 Match length 70 % identity NCBI Description EXOGLUCANASE I PRECURSOR (EXOCELLOBIOHYDROLASE I) (1,4-BETA-CELLOBIOHYDROLASE) (BETA-GLUCANCELLOBIOHYDROLASE) >gi_487090_pir__S38794 cellulose 1,4-beta-cellobiosidase
(EC 3.2.1.91) - imperfect fungus (Humicola grisea) >gi 2761 emb CAA35159 (X17258) beta-glucancellobiohydrolase [Humicola grisea] 46275 Seq. No. jC-gmle01810080h12d1 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g542393
BLAST score 174
E value 8.0e-13
Match length 59
% identity 59



```
cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) -
NCBI Description
                  basidiomycete (Phanerochaete chrysosporium)
                  >gi_630435_pir__S44715 cellulose 1,4-beta-cellobiosidase
                  (EC 3.2.1.91) - basidiomycete (Phanerochaete chrysosporium)
                  >gi_453224_emb_CAA82762_ (Z29653) cellulase [Phanerochaete
                  chrysosporium] >gi_511302 (L22656) major cellobiohydrolase
                  [Phanerochaete chrysosporium]
Seq. No.
                  46276
                  jC-gmle01810082b09d1
Seq. ID
                  BLASTX
Method
                  q4220483
NCBI GI
BLAST score
                  319
E value
                  1.0e-29
Match length
                  82
                  74
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  46277
Seq. No.
                  jC-gmle01810082e08d1
Seq. ID
                  BLASTX
Method
                  g1408322
NCBI GI
                  277
BLAST score
                  1.0e-24
E value
                  115
Match length
% identity
                  46
                  (D86351) cytochrome P-450 (CYP93A2) [Glycine max]
NCBI Description
                  46278
Seq. No.
                  jC-gmle01810082h09a1
Seq. ID
                  BLASTX
Method
                  g1749542
NCBI GI
                  325
BLAST score
                  2.0e-30
E value
Match length
                  105
% identity
                  (D89167) similar to Saccharomyces cerevisiae
NCBI Description
                  5-methyltetrahydropteroyltriglutamate-homocysteine
                  s-methyltransferase, SWISS-PROT Accession Number P05694
                  [Schizosaccharomyces pombe]
                  46279
Seq. No.
                  jC-gmle01810083a07a1
Seq. ID
                  BLASTX
                  g4544460
                  165
                  2.0e-11
                  71
                  45
% identity
                  (ACO06592) putative reverse transcriptase [Arabidopsis
```

Method NCBI GI BLAST score E value Match length

NCBI Description

thaliana]

46280 Seq. No.

jC-gmle01810083b03d1 Seq. ID

Method BLASTN NCBI GI g2288979 BLAST score 38



E value 5.0e-12 Match length 74 % identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC T01024 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 46281

Seq. ID jC-gmle01810083c04d1

Method BLASTX
NCBI GI g1346882
BLAST score 330
E value 9.0e-31
Match length 72
% identity 88

NCBI Description PHYTOENE SYNTHASE PRECURSOR (MEL5) >gi_2129505_pir__S56668

geranylgeranyl-diphosphate geranylgeranyltransferase (EC
2.5.1.32) precursor - muskmelon >gi_870985_emb_CAA85775_

(Z37543) phytoene synthase [Cucumis melo]

Seq. No. 46282

Seq. ID jC-gmle01810083c06a1

Method BLASTN
NCBI GI g758249
BLAST score 165
E value 1.0e-87
Match length 305
% identity 89

NCBI Description P.vulgaris mRNA for plasma membrane H+ ATPase

Seq. No. 46283

Seq. ID jC-gmle01810083d09a1

Method BLASTN
NCBI GI g4406529
BLAST score 70
E value 4.0e-31
Match length 186
% identity 84

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 46284

Seq. ID jC-gmle01810083d10a1

Method BLASTX
NCBI GI g3892045
BLAST score 225
E value 5.0e-19
Match length 70
% identity 67

NCBI Description (AC002330) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 46285

Seq. ID jC-gmle01810083e10a1

Method BLASTX
NCBI GI g1708418
BLAST score 349
E value 1.0e-40



Match length 106 % identity 82

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)

>gi_1321961_emb_CAA56772_ (X80796) translation initiation

factor eIF-4A [Schizosaccharomyces pombe] >gi_2222814

(L40627) cell cycle control protein eIF-4A

[Schizosaccharomyces pombe]

Seq. No. 46286

Seq. ID jC-gmle01810083e12a1

Method BLASTX
NCBI GI g1020413
BLAST score 168
E value 1.0e-11
Match length 154
% identity 34

NCBI Description (D63703) isobutene-forming enzyme and benzoate

4-hydroxylase [Rhodotorula minuta]

Seq. No. 46287

Seq. ID jC-gmle01810083e12d1

Method BLASTX
NCBI GI g1020413
BLAST score 160
E value 6.0e-11
Match length 91
% identity 36

NCBI Description (D63703) isobutene-forming enzyme and benzoate

4-hydroxylase [Rhodotorula minuta]

Seq. No. 46288

Seq. ID jC-gmle01810083f01a1

Method BLASTN
NCBI GI g602358
BLAST score 60
E value 2.0e-25
Match length 132
% identity 87

NCBI Description P.sativum mRNA for type II chlorophyll a/b binding protein

Seq. No. 46289

Seq. ID jC-gmle01810083g05a1

Method BLASTN
NCBI GI g303900
BLAST score 410
E value 0.0e+00
Match length 430
% identity 28

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 46290

Seq. ID jC-gmle01810084b09a1

Method BLASTX
NCBI GI g3292824
BLAST score 525
E value 2.0e-53
Match length 167



% identity 63

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.

46291

Seq. ID

jC-gmle01810084c08d1

Method NCBI GI BLASTX q2673909

BLAST score E value

147 3.0e-09

Match length 68 % identity 51

NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.

46292

Seq. ID

jC-gmle01810084d08a1

Method BLASTX
NCBI GI g1235680
BLAST score 335
E value 3.0e-31
Match length 152
% identity 43

NCBI Description

(U48698) receptor serine/threonine kinase PR5K [Arabidopsis

thaliana] >gi_1589714_prf__2211427A receptor protein kinase

[Arabidopsis thaliana]

Seq. No.

46293

Seq. ID

jC-gmle01810084e05a1

Method BLASTX
NCBI GI g2558938
BLAST score 339
E value 8.0e-32
Match length 142
% identity 52

NCBI Description (AF024625) arm repeat containing protein [Brassica napus]

Seq. No.

46294

Seq. ID

jC-gmle01810084g05d1

Method BLASTX
NCBI GI g2245095
BLAST score 350
E value 3.0e-33
Match length 86
% identity 79

NCBI Description (Z97343) formyltransferase purU homolog [Arabidopsis

thaliana]

Seq. No.

46295

Seq. ID

jC-gmle01810084h02a1

Method BLASTN
NCBI GI g2511692
BLAST score 212
E value 1.0e-115
Match length 469
% identity 90

NCBI Description Phaseolus vulgaris Moldavian encoding cysteine proteinase

precursor (clone cp71)

```
Seq. No.
                    46296
                    jC-qmle01810084h07d1
Seq. ID
Method
                   BLASTX
NCBI GI
                    g2498731
BLAST score
                    294
                    1.0e-26
E value
Match length
                    76
                    68
% identity
                   PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                    >gi_1362013_pir__S57611 zeta-crystallin homolog -
                    Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                    zeta-crystallin homologue [Arabidopsis thaliana]
                    46297
Seq. No.
                    jC-qmle01810085a01a1
Seq. ID
                    BLASTX
Method
                    q3434971
NCBI GI
BLAST score
                    312
                    9.0e-29
E value
                    122
Match length
% identity
                    58
                    (AB008105) ethylene responsive element binding factor 3
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    46298
                    jC-gmle01810085a10a1
Seq. ID
                    BLASTX
Method
                    g1730600
NCBI GI
BLAST score
                    227
                    1.0e-18
E value
                    108
Match length
                    48
% identity
NCBI Description
                    >gi_1122760_emb_CAA92525_ (Z68230) unknown [Bacillus
subtilis] >gi_2633885_emb_CAB13387_ (Z99111) alternate gene
                    name: yllC; similar to hypothetical proteins [Bacillus
```

HYPOTHETICAL 35.3 KD PROTEIN IN FTSL 5'REGION (ORFB)

subtilis]

46299 Seq. No.

Seq. ID jC-gmle01810085b02a1

Method BLASTX NCBI GI g2809247 152 BLAST score E value 6.0e-10 Match length 89 % identity 7

NCBI Description (AC002560) F21B7.16 [Arabidopsis thaliana]

Seq. No. 46300

Seq. ID jC-gmle01810085b12a1

Method BLASTN q1778822 NCBI GI 198 BLAST score 1.0e-107 E value 308 Match length 91 % identity

NCBI Description Glycine max early light-induced protein (ELIP) mRNA,



complete cds

Seq. No. 46301 jC-qmle01810085d03a1 Seq. ID Method BLASTX NCBI GI g1169586 BLAST score 318 2.0e-29

E value 95 Match length 85 % identity

NCBI Description FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC

(D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (CY-F1) >gi_542079_pir__S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946)

fructose-1,6-bisphosphatase [Solanum tuberosum]

46302 Seq. No.

Seq. ID jC-gmle01810085d10a1

Method BLASTX NCBI GI q131384 BLAST score 262 9.0e-23 E value Match length 81 % identity 74

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD NCBI Description

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi_81934_pir__S04132

photosystem II oxygen-evolving complex protein 1 precursor

- garden pea >gi_20621_emb_CAA33408_ (X15350) precursor (AA -81 to 248) [Pisum sativum] >gi_344004_dbj_BAA02554_ (D13297) precursor for 33-kDa protein of photosystem II [Pisum sativum] >gi_226937_prf__1611461A O2 evolving

complex 33kD protein [Arachis hypogaea]

Seq. No. 46303

Seq. ID jC-gmle01810085d12a1

Method BLASTX NCBI GI q2851417 BLAST score 323 E value 5.0e-30 Match length 99 66 % identity

TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION NCBI Description

FACTOR 3)

Seq. No. 46304

Seq. ID jC-qmle01810085f07a1

Method BLASTX NCBI GI q3929395 BLAST score 403 E value 3.0e-39 Match length 121 % identity 65

VACUOLAR ATP SYNTHASE 98 KD SUBUNIT (VACUOLAR ATPASE 98 KD NCBI Description

SUBUNIT) >gi 1237128 (U36396) vacuolar ATPase 98 kDa

subunit [Neurospora crassa]

% identity

NCBI Description

51



```
Seq. No.
Seq. ID
                   jC-gmle01810085g03a1
                   BLASTX
Method
                   g4006856
NCBI GI
BLAST score
                   151
                   9.0e-10
E value
Match length
                   40
% identity
                   72
                   (Z99707) receptor kinase-like protein [Arabidopsis
NCBI Description
                   46306
Seq. No.
                   jC-gmle01810086d01a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g100203
BLAST score
                   269
                   1.0e-23
E value
                   119
Match length
                   50
% identity
                   cysteine proteinase (EC 3.4.22.-) precursor - tomato
NCBI Description
                   >gi_19195_emb_CAA78403_ (Z14028) pre-pro-cysteine
                   proteinase [Lycopersicon esculentum]
Seq. No.
                   46307
                   jC-gmle01810086d01d1
Seq. ID
Method
                   BLASTX
                   q118157
NCBI GI
BLAST score
                   182
                   2.0e-13
E value
Match length
                   89
                   44
% identity
                   CRUZIPAIN PRECURSOR (MAJOR CYSTEINE PROTEINASE) (CRUZAINE)
NCBI Description
                   >gi 320915_pir__A60667 cysteine proteinase cruzain (EC
                   3.4.22.-) - Trypanosoma cruzi >gi_162048 (M84342) cruzain
                   [Trypanosoma cruzi]
                   46308
Seq. No.
                   jC-gmle01810086d06a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3582352
BLAST score
                   234
                   1.0e-19
E value
                   129
Match length
                   43
% identity
                  (AB003518) heat shock protein [Coriolus versicolor]
NCBI Description
                   46309
Seq. No.
Seq. ID
                   jC-qmle01810086d07d1
Method
                   BLASTX
NCBI GI
                   g136644
BLAST score
                   178
                   6.0e-13
E value
Match length
                   71
```

UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN

23K ubiquitin carrier protein E2 - wheat >gi_170782

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 100765 pir A34506



(M28059) ubiquitin carrier protein [Triticum vulgare]

```
46310
Seq. No.
                  jC-gmle01810086f04a1
Seq. ID
                  BLASTN
Method
                  g2661020
NCBI GI
                  376
BLAST score
                  0.0e + 00
E value
                  376
Match length
                  100
% identity
NCBI Description Glycine max catalase (cat4) mRNA, complete cds
                  46311
Seq. No.
                  jC-gmle01810086f11a1
Seq. ID
                  BLASTX
Method
                   g419894
NCBI GI
                   308
BLAST score
                   3.0e-28
E value
                   92
Match length
                   64
% identity
                  glycine hydroxymethyltransferase (EC 2.1.2.1) precursor,
NCBI Description
                   mitochondrial - yeast (Saccharomyces cerevisiae)
                   >gi_296561_emb_CAA49927_ (X70529) ORF YBR1732
                   [Saccharomyces cerevisiae] >gi_536692_emb_CAA85226
                   (Z36131) ORF YBR263w [Saccharomyces cerevisiae]
                   46312
Seq. No.
                   jC-gmle01810086g12a1
Seq. ID
                   BLASTX
Method
                   g535454
NCBI GI
                   235
BLAST score
                   1.0e-19
E value
                   55
Match length
                   78
% identity
                  (U13940) cysteine proteinase [Alnus glutinosa]
NCBI Description
                   46313
Seq. No.
                   iC-qmle01810087a03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4097880
                   642
BLAST score
E value
                   3.0e-67
                   155
Match length
% identity
                   (U70866) polyprotein [Bean pod mottle virus]
NCBI Description
                   46314
Seq. No.
                   jC-gmle01810087b05a1
Seq. ID
Method
                   BLASTX
                   q3928096
NCBI GI
BLAST score
                   217
                   2.0e-17
E value
                   62
Match length
 % identity
                   (AC005770) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

46315

Seq. No.



```
Seq. ID
                  jC-gmle01810087b05d1
Method
                  BLASTN
                  q3928074
NCBI GI
                  33
BLAST score
                  7.0e-09
E value
                  53
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T7F6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  46316
Seq. No.
Seq. ID
                  jC-gmle01810087c02a1
Method
                  BLASTX
                  a1362086
NCBI GI
BLAST score
                  312
                  1.0e-28
E value
                  131
Match length
                  49
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_2129919_pir__S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
                  46317
Seq. No.
                  jC-gmle01810087c02d1
Seq. ID
Method
                  BLASTX
                  q3334258
NCBI GI
                  270
BLAST score
                  1.0e-23
E value
                   97
Match length
                   57
% identity
                  5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE
NCBI Description
                  METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12
                   INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE
                   SYNTHASE) >gi 2129456 pir S65083
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Chlamydomonas
                   reinhardtii >gi_1017759 (U36197) cobalamin-independent
                  methionine synthase [Chlamydomonas reinhardtii]
                   >gi 1587968 prf 2207381A Met synthase [Chlamydomonas
                   reinhardtii]
                   46318
Seq. No.
                   jC-gmle01810087c12a1
Seq. ID
```

Method BLASTX NCBI GI g3282239 BLAST score 411 2.0e-40 E value 129 Match length % identity 59

(U88966) rapamycin associated protein FRAP2 [Homo sapiens] NCBI Description

46319 Seq. No.

jC-gmle01810087f01a1 Seq. ID



```
BLASTN
Method
                  g4097879
NCBI GI
BLAST score
                  200
                  1.0e-108
E value
                  444
Match length
                  86
% identity
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  46320
Seq. No.
                  jC-gmle01810087f06a1
Seq. ID
                  BLASTX
Method
                  g4039155
NCBI GI
BLAST score
                  296
                  9.0e-27
E value
                  141
Match length
                  40
% identity
                  (AF104258) putative copper-inducible 35.6 kDa protein
NCBI Description
                  [Festuca rubra]
                  46321
Seq. No.
                  jC-gmle01810087f09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2384903
BLAST score
                  211
                  1.0e-16
E value
                  153
Match length
                  37
% identity
                  (AF022981) similar to the carnitine/choline
NCBI Description
                  acetyltransferase family [Caenorhabditis elegans]
                   46322
Seq. No.
                   jC-gmle01810088a01a1
Seq. ID
Method
                   BLASTX
                   q3334320
NCBI GI
BLAST score
                   356
                   5.0e-40
E value
                   128
Match length
% identity
                   65
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                   ribosome-associated protein p40 [Glycine max]
                   46323
Seq. No.
                   jC-gmle01810088a01d1
Seq. ID
Method
                   BLASTX
                   q730683
NCBI GI
                   151
BLAST score
                   7.0e-10
E value
Match length
                   42
% identity
                   64
                   40S RIBOSOMAL PROTEIN SA (P40) (34/67 KD LAMININ BINDING
NCBI Description
                   PROTEIN) >gi 476088 (U02370) 34/67 kD laminin binding
```

protein [Urechis caupo]

Seq. No.

jC-gmle01810088c04a1 Seq. ID

Method BLASTN

7455



```
q510545
NCBI GI
BLAST score
                   42
                   3.0e-14
E value
                  107
Match length
                   91
% identity
NCBI Description P.sativum mRNA for starch branching enzyme I
                   46325
Seq. No.
                   jC-gmle01810088e10d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2651310
BLAST score
                   164
E value
                   3.0e-11
Match length
                   103
                   29
% identity
                   (AC002336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   46326
                   jC-gmle01810088f05a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3096949
BLAST score
                   298
                   3.0e-27
E value
Match length
                   89
                   58
% identity
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
                   46327
Seq. No.
                   jC-gmle01810088f05d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3096949
                   183
BLAST score
E value
                   1.0e-13
Match length
                   85
% identity
                   41
                   (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi 3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
                   46328
Seq. No.
                   jC-gmle01810088g02d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2246442
BLAST score
                   300
E value
                   2.0e-27
Match length
                   99
                   61
% identity
                  (U63298) farnesyltransferase alpha subunit [Pisum sativum]
NCBI Description
```

Seq. No. 46329

Seq. ID jC-gmle01810089d06a1

Method BLASTN
NCBI GI g4097879
BLAST score 111



```
8.0e-56
E value
Match length
                  187
% identity
                  90
                  Bean pod mottle virus complete segment RNA1 polyprotein
NCBI Description
                  gene, complete cds
                  46330
Seq. No.
                  jC-gmle01810089e01a1
Seq. ID
Method
                  BLASTN
                  g1107480
NCBI GI
BLAST score
                  130
                  6.0e-67
E value
Match length
                  326
% identity
                  46
NCBI Description Acanthamoeba polyubiquitin gene
                  46331
Seq. No.
                  jC-gmle01810089e01d1
Seq. ID
Method
                  BLASTN
                  g156481
NCBI GI
BLAST score
                  144
                  4.0e-75
E value
                  397
Match length
% identity
NCBI Description C.elegans polyubiquitin (UbiA) gene, complete cds
Seq. No.
                  46332
                  jC-gmle01810089e07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g631978
BLAST score
                  450
                  7.0e-45
E value
Match length
                  130
% identity
                  cytochrome P-450 oxidase - Mentha piperita
NCBI Description
                  >gi_493475_emb_CAA83941_ (Z33875) cytochrome P-450 oxidase
                   [Mentha x piperita]
                   46333
Seq. No.
Seq. ID
                   jC-gmle01810089f11d1
                  BLASTX
Method
NCBI GI
                   g3152594
BLAST score
                   153
                   3.0e-10
E value
Match length
                   84
% identity
                  (AC002986) Contains repeats similar to RECA protein
NCBI Description
                   gb L26100 from Acinetobacter calcoaceticus. [Arabidopsis
                   thaliana]
Seq. No.
                   46334
Seq. ID
                   jC-qmle01810089f12d1
```

Method BLASTX
NCBI GI g3269291
BLAST score 437
E value 3.0e-43
Match length 149



```
% identity
                  (AL030978) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  46335
Seq. No.
                  jC-qmle01810089g01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4522009
BLAST score
                  278
                  1.0e-24
E value
                  114
Match length
                  52
% identity
                  (AC007069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  46336
Seq. No.
                  jC-gmle01810090b04a1
Seq. ID
                  BLASTN
Method
                  g1055367
NCBI GI
                  315
BLAST score
                  1.0e-177
E value
                  394
Match length
                  95
% identity
                  Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  46337
Seq. No.
                   jC-gmle01810090f04a1
Seq. ID
                  BLASTN
Method
                  g999189
NCBI GI
BLAST score
                  345
                  0.0e+00
E value
                   446
Match length
                  100
% identity
                  dihydrofolate reductase-thymidylate synthase=bifunctional
NCBI Description
                  enzyme [Glycine max, seedling, mRNA, 1794 nt]
                   46338
Seq. No.
                   jC-gmle01810090g08a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2924257
                   163
BLAST score
                   2.0e-86
E value
Match length
                   275
                   90
% identity
NCBI Description Tobacco chloroplast genome DNA
                   46339
Seq. No.
                   jC-gmle01810090h08a1
Seq. ID
Method
                   BLASTX
                   q4049399
NCBI GI
BLAST score
                   148
                   3.0e-09
E value
                   100
Match length
% identity
```

Seq. No. 46340

NCBI Description

(Y09581) FRO2 [Arabidopsis thaliana]

NCBI GI

BLAST score

g56539

103



```
jC-gmle01810091d07d1
Seq. ID
Method
                  BLASTX
                  g2982431
NCBI GI
                  175
BLAST score
                  1.0e-12
E value
                  140
Match length
% identity
                  (AL022224) leucine rich repeat-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  46341
Seq. No.
                  jC-gmle01810091f02a1
Seq. ID
                  BLASTX
Method
                  g4115936
NCBI GI
                  193
BLAST score
                  1.0e-14
E value
                  38
Match length
                  92
% identity
                  (AF118223) No definition line found [Arabidopsis thaliana]
NCBI Description
                  46342
Seq. No.
                  jC-gmle01810091f04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3420054
                  313
BLAST score
E value
                  1.0e-28
                  152
Match length
                   47
% identity
                  (AC004680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46343
Seq. No.
                   jC-gmle01810091f11a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1498495
                   178
BLAST score
E value
                   2.0e-95
Match length
                   346
                   88
% identity
                  Penicillium citrinum heat shock protein 70 mRNA, partial
NCBI Description
                   46344
Seq. No.
                   jC-gmle01810091f11d1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2992153
BLAST score
                   40
E value
                   3.0e-13
Match length
                   69
% identity
                   Schizosaccharomyces pombe mRNA for heat shock protein,
NCBI Description
                   complete cds
                   46345
Seq. No.
                   jC-gmle01810091g02d1
Seq. ID
Method
                   BLASTN
```



E value 8.0e-51 Match length 275 % identity 99

NCBI Description R.norvegicus gene encoding prolactin, exon 5

>gi_206360_gb_J00764_RATPRLHR5 Rat (hooded) prolactin gene

: exon v and flanks

Seq. No. 46346

Seq. ID jC-gmle01810091h04d1

Method BLASTX
NCBI GI g99730
BLAST score 379
E value 2.0e-36
Match length 118
% identity 59

NCBI Description hypothetical protein 3 - Arabidopsis thaliana

retrotransposon Tal-2 (strain Kashmir) (fragment) >gi_1345512_emb_CAA37920_ (X53975) orf 3 [Arabidopsis

thaliana]

Seq. No.

46347

Seq. ID jC-gmle01810092d02a1

Method BLASTN
NCBI GI g3452136
BLAST score 235
E value 1.0e-129
Match length 255
% identity 99

NCBI Description Glycine max mRNA for glucose-6-phosphate-dehydrogenase,

partial

Seq. No. 46348

Seq. ID jC-gmle01810092d02d1

Method BLASTN
NCBI GI g3452136
BLAST score 236
E value 1.0e-130
Match length 252
% identity 99

NCBI Description Glycine max mRNA for glucose-6-phosphate-dehydrogenase,

partial

Seq. No. 46349

Seq. ID jC-gmle01810092d08a1

Method BLASTX
NCBI GI g2576255
BLAST score 383
E value 4.0e-37
Match length 94
% identity 82

NCBI Description (AJ001729) TH65 protein [Arabidopsis thaliana]

Seq. No. 46350

Seq. ID jC-gmle01810092e07a1

Method BLASTX NCBI GI g531754 BLAST score 146



```
3.0e-09
E value
Match length
                  78
% identity
                  38
                   (X81068) probable mitochondrial protein [Saccharomyces
NCBI Description
                  cerevisiae]
                   46351
Seq. No.
                   jC-gmle01810092e10d1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3661613
BLAST score
                   175
                  1.0e-93
E value
Match length
                   407
% identity
                   86
                  Aspergillus terreus aconitase (Aco) mRNA, nuclear gene
NCBI Description
                   encoding mitochondrial protein, complete cds
                   46352
Seq. No.
                   jC-gmle01810092f07d1
Seq. ID
Method
                   BLASTX
                   g1707010
NCBI GI
BLAST score
                   154
E value
                   4.0e-10
Match length
                   36
% identity
                   78
                   (U78721) mitochondrial carrier protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   46353
Seq. No.
                   jC-gmle01810092f08d1
Seq. ID
                   BLASTX
Method
                   q2781357
NCBI GI
                   192
BLAST score
E value
                   1.0e-14
                   55
Match length
% identity
                   60
                  (AC003113) F2401.13 [Arabidopsis thaliana]
NCBI Description
                   46354
Seq. No.
                   jC-gmle01810092f09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3482978
BLAST score
                   303
E value
                   8.0e-28
Match length
                   105
                   64
% identity
                  (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46355
Seq. ID
                   jC-qmle01810092g04a1
Method
                   BLASTN
                   q4530125
NCBI GI
BLAST score
```

BLAST score 58
E value 6.0e-24
Match langth 228

Match length 228 % identity 82

NCBI Description Phaseolus vulgaris receptor-like protein kinase homolog



RK20-1 mRNA, complete cds

```
46356
Seq. No.
                  jC-gmle01810092g06d1
Seq. ID
                  BLASTX
Method
                  g541967
NCBI GI
                  206
BLAST score
                  2.0e-16
E value
                  73
Match length
                  59
% identity
                  glycine cleavage system protein T precursor - garden pea
NCBI Description
                  >gi 407475 emb CAA52800 (X74793) T-protein of the glycine
                  decarboxylase complex [Pisum sativum]
                   46357
Seq. No.
                   jC-gmle01810092g09a1
Seq. ID
                  BLASTX
Method
                   q3513736
NCBI GI
BLAST score
                   178
                   5.0e-13
E value
                   42
Match length
                   79
% identity
                   (AF080118) No definition line found [Arabidopsis thaliana]
NCBI Description
                   >gi_4539367_emb_CAB40061.1_ (AL049525) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   46358
                   jC-gmle01810093b12d1
Seq. ID
                   BLASTN
Method
                   g18741
NCBI GI
                   102
BLAST score
                   3.0e-50
E value
                   271
Match length
                   85
% identity
                   Glycine max gene encoding ribulose-1,5-bisphosphate
NCBI Description
                   carboxylase small subunit
                   46359
Seq. No.
                   jC-qmle01810093d10a1
Seq. ID
Method
                   BLASTX
                   q2827649
NCBI GI
                   124
BLAST score
                   1.0e-08
E value
                   97
Match length
% identity
                  (AL021637) putative protein [Arabidopsis thaliana]
NCBI Description
                   46360
Seq. No.
                   jC-qmle01810093e02a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2979688
BLAST score
                   315
E value
                   3.0e-29
Match length
                   94
                   68
% identity
                   (AF035619) pyridoxine biosynthesis protein [Cercospora
NCBI Description
```

nicotianae]



```
Seq. No.
                  46361
Seq. ID
                  jC-gmle01810093f03d1
Method
                  BLASTX
NCBI GI
                  g129320
                  198
BLAST score
                  2.0e-15
E value
Match length
                  39
                  87
% identity
NCBI Description P21 PROTEIN >gi 99943 pir A33176 P21 protein - soybean
Seq. No.
                  46362
Seq. ID
                  jC-gmle01810093f06d1
Method
                  BLASTX
                  g4415923
NCBI GI
BLAST score
                  158
E value
                  1.0e-10
Match length
                  65
% identity
                  52
                  (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  46363
Seq. ID
                  jC-gmle01810094a09a1
Method
                  BLASTX
                  g2739369
NCBI GI
BLAST score
                  561
E value
                  6.0e-58
Match length
                  131
% identity
                  80
                  (AC002505) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  46364
Seq. ID
                  jC-gmle01810094b09d1
                  BLASTX
Method
                  g2499417
NCBI GI
BLAST score
                  214
E value
                  3.0e-17
                  50
Match length
                  78
% identity
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
NCBI Description
                  >gi_1085826_pir__S49248 H-protein - Flaveria anomala
                  >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
                  anomala]
                  46365
Seq. No.
Seq. ID
                  jC-gmle01810094c12a1
Method
                  BLASTX
NCBI GI
                  q4530126
BLAST score
                  392
                  5.0e-38
E value
Match length
                  133
                  62
% identity
```

Seq. No. 46366

NCBI Description

[Phaseolus vulgaris]

(AF078082) receptor-like protein kinase homolog RK20-1

Seq. ID

Method



```
jC-gmle01810094d10a1
Seq. ID
                  BLASTX
Method
                  q3249084
NCBI GI
BLAST score
                  216
                  2.0e-17
E value
Match length
                  127
% identity
                  20
                  (AC004473) Similar to red-1 (related to thioredoxin) gene
NCBI Description
                  gb X92750 from Mus musculus. ESTs gb_AA712687 and
                  gb_Z37223 come from this gene [Arabidopsis thaliana]
Seq. No.
                  46367
                  jC-gmle01810094e04d1
Seq. ID
Method
                  BLASTX
                  q2980784
NCBI GI
BLAST score
                  404
E value
                  2.0e-39
Match length
                   95
                  18
% identity
                  (AL022198) puative protein [Arabidopsis thaliana]
NCBI Description
                  46368
Seq. No.
                  jC-gmle01810094e05d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3738302
BLAST score
                  216
E value
                  2.0e-17
Match length
                   49
% identity
                   76
                   (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                  >qi 4249398 (AC006072) putative tubby protein [Arabidopsis
                   thaliana]
                   46369
Seq. No.
Seq. ID
                   jC-gmle01810094e07d1
                  BLASTX
Method
                  g3309243
NCBI GI
BLAST score
                   160
                   7.0e-11
E value
                   33
Match length
                   91
% identity
                   (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
                   limon]
                   46370
Seq. No.
Seq. ID
                   jC-qmle01810094e12a1
Method
                   BLASTX
                   g1871184
NCBI GI
BLAST score
                   146
                   1.0e-09
E value
                   70
Match length
                   37
% identity
                  (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46371
Seq. No.
```

7464

jC-gmle01810094f06d1

BLASTX



NCBI GI g232040 BLAST score 160 E value 5.0e-11 Match length 62 % identity 53

NCBI Description ELONGATION FACTOR 3 (EF-3) >gi_477560_pir__A49204

translation elongation factor EF-3 - Pneumocystis carinii >gi 169412 (M87665) elongation factor 3 [Pneumocystis

carinii]

Seq. No. 46372

Seq. ID jC-gmle01810094f11a1

Method BLASTX
NCBI GI g627561
BLAST score 327
E value 1.0e-30
Match length 79
% identity 73

NCBI Description pepti

peptidylprolyl isomerase (EC 5.2.1.8) FKBP1L, form 1 - human >gi_546582 bbs_147143 (S69815) peptidyl-prolyl cis-trans isomerase, PPIase=12 kda FK506 binding protein homolog [human, fetal brain, Peptide, 108 aa] [Homo sapiens] >gi_965468 (L37086) calcineurin [Homo sapiens] >gi_1122217_dbj_BAA07232_ (D38037) hFKBP12-like protein [Homo sapiens] >gi_1585685_prf_2201446A FK506-binding

protein [Homo sapiens]

Seq. No. 46373

Seq. ID jC-gmle01810094g04a1

Method BLASTX
NCBI GI g586477
BLAST score 193
E value 8.0e-15
Match length 54
% identity 67

NCBI Description

HYPOTHETICAL 44.2 KD GTP-BINDING PROTEIN IN SCO2-MRF1
INTERGENIC REGION >gi_626828_pir__S45881 probable purine
nucleotide-binding protein YBR025c - yeast (Saccharomyces
cerevisiae) >gi_498754_emb_CAA53682_ (X76078) YBR0309
[Saccharomyces cerevisiae] >gi_536234_emb_CAA84967_
(Z35894) ORF YBR025c [Saccharomyces cerevisiae]
>gi_1587583_prf__2206497F ORF YBR0309 [Saccharomyces

cerevisiae]

Seq. No. 46374

Seq. ID jC-gmle01810094g04d1

Method BLASTX
NCBI GI 92388943
BLAST score 296
E value 8.0e-27
Match length 79
% identity 68

NCBI Description (Z98978) SPAC27E2.03c, putative gtp-binding protein,

len:392a a, similar eg. to YBR025C, YBN5 YEAST, P38219, hypothetica 1 44.2 kd protein, (394aa), fasta scores, opt:1664, E():0, (63.7% identity in 391 aa overlap), also

sim



46375

Seq. No.

Seq. No.

46380

Seq. ID jC-gmle01810094g12a1 BLASTX Method NCBI GI g2832628 BLAST score 214 3.0e-17 E value Match length 66 % identity (AL021711) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 46376 jC-gmro02800022g05d1 Seq. ID Method BLASTX NCBI GI q2213626 BLAST score 151 E value 7.0e-10 Match length 82 % identity 38 (AC000103) F21J9.18 [Arabidopsis thaliana] NCBI Description Seq. No. 46377 Seq. ID jC-gmro02800023b11a1 Method BLASTX g3096927 NCBI GI BLAST score 166 E value 1.0e-11 Match length 120 % identity (AL023094) putative protein [Arabidopsis thaliana] NCBI Description 46378 Seq. No. jC-gmro02800024d08a1 Seq. ID BLASTX Method NCBI GI g126405 229 BLAST score 4.0e-19 E value Match length 87 % identity 57 SEED LIPOXYGENASE-3 >gi 81918 pir S01142 lipoxygenase (EC NCBI Description 1.13.11.12) - garden pea >gi_20800_emb_CAA30666_ (X07807) lipocygenase (AA 1 - 861) [Pīsum sativum] >gi_469156_emb_CAA55319_ (X78581) lipoxygenase [Pisum sativum] 46379 Seq. No. jC-gmro02800024d09d1 Seq. ID Method BLASTX NCBI GI g3522956 BLAST score 267 E value 2.0e-23 59 Match length 73 % identity (AC004411) putative pectinacetylesterase precursor NCBI Description [Arabidopsis thaliana]

7466



```
jC-gmro02800025g05a1
Seq. ID
                     BLASTX
Method
                     q132886
NCBI GI
BLAST score
                     339
                     6.0e-32
E value
                     98
Match length
% identity
                     66
                     60S RIBOSOMAL PROTEIN L32 >gi_71335_pir__R5HU32 ribosomal protein L32 - human >gi_71336_pir__R5MS32 ribosomal protein
NCBI Description
                     L32 - mouse >gi_71337_pir_ R5RT32_ribosomal protein L32 - rat >gi_36132_emb_CAA27048_(X03342) rpL32 (aa 1-135) [Homo sapiens] >gi_57117_emb_CAA29777_(X06483) ribosomal protein
                     L32 [Rattus norvegicus] >gi 200781 (K02060) ribosomal
                     protein L32-3A [Mus musculus] >gi 226004 prf 1405339A
                     ribosomal protein L32 [Rattus norvegicus]
                     >gi 4506635 ref NP 000985.1 pRPL32_ ribosomal protein L32
Seq. No.
                     46381
Seq. ID
                     jC-gmro02800026e05a1
Method
                     BLASTX
NCBI GI
                     q4544402
                     389
BLAST score
E value
                     1.0e-37
Match length
                     124
% identity
                     57
                     (AC007047) putative leucine rich repeat protein
NCBI Description
                     [Arabidopsis thaliana]
Seq. No.
                     46382
                     jC-gmro02800026e07d1
Seq. ID
Method
                     BLASTX
NCBI GI
                     g3063457
BLAST score
                     380
                     1.0e-36
E value
Match length
                     122
% identity
                     61
                    (AC003981) F22013.19 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                     46383
                     jC-gmro02800027c08d1
Seq. ID
                     BLASTX
Method
                     g4388726
NCBI GI
BLAST score
                     167
                     1.0e-11
E value
Match length
                     41
                     73
% identity
                     (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                     [Arabidopsis thaliana]
                     46384
Seq. No.
                     jC-gmro02800027c11a1
Seq. ID
                     BLASTX
Method
NCBI GI
                     g4544464
BLAST score
                     390
                     7.0e-38
E value
```

133

56

Match length % identity



```
(AC006580) putative chloroplast nucleoid DNA binding
NCBI Description
                  protein [Arabidopsis thaliana]
                  46385
Seq. No.
                  jC-gmro02800028b04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4519936
                  138
BLAST score
                  4.0e-14
E value
Match length
                  94
                  38
% identity
                  (AB019186) RPR1 [Oryza sativa]
NCBI Description
Seq. No.
                  46386
                  jC-gmro02800028e09a1
Seq. ID
                  BLASTX
Method
                  q2244855
NCBI GI
BLAST score
                  205
                  5.0e-16
E value
                  158
Match length
% identity
                  45
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  46387
Seq. No.
                  jC-gmro02800029c05a1
Seq. ID
Method
                  BLASTX
                  q730565
NCBI GI
BLAST score
                  456
                  1.0e-45
E value
Match length
                  105
                  77
% identity
                  60S RIBOSOMAL PROTEIN L3 >qi 423069 pir S34195 ribosomal
NCBI Description
                  protein L3 - human >gi 313659 emb CAA51839 (X73460)
                   ribosomal protein L3 [Homo sapiens]
                   >gi_3850177_emb_CAA18450_ (AL022326) dJ333H23.1.1 (60S
                   Ribosomal Protein L3) [Homo sapiens]
                   >gi 4506649_ref_NP_000958.1_pRPL3_ ribosomal protein L3
                   46388
Seq. No.
Seq. ID
                   jC-qmro02800029e02d1
                   BLASTN
Method
NCBI GI
                   g1163180
BLAST score
                   44
                   7.0e-16
E value
Match length
                   112
                   85
% identity
NCBI Description Glycine max arginine decarboxylase mRNA, complete cds
Seq. No.
                   46389
                   jC-gmro02800030d02d1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1370173
BLAST score
                   135
                   8.0e-70
E value
Match length
                   340
% identity
                   88
```

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAB1Y



```
46390
Seq. No.
                  jC-qmro02800030e04a1
Seq. ID
Method
                  BLASTN
                  g169980
NCBI GI
BLAST score
                  278
                  1.0e-155
E value
Match length
                  326
                  97
% identity
NCBI Description
                  Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                  46391
                  jC-gmro02800031a11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490310
BLAST score
                  308
                  2.0e-28
E value
Match length
                  86
                  70
% identity
                  (AL035678) somatic embryogenesis receptor-like kinase-like
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  46392
Seq. ID
                  jC-gmro02800031b10a1
                  BLASTX
Method
                  q3334320
NCBI GI
                  515
BLAST score
                  2.0e-52
E value
Match length
                  136
% identity
                  71
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                   46393
Seq. ID
                  jC-qmro02800031h07d1
Method
                  BLASTN
NCBI GI
                  g1684850
BLAST score
                  38
E value
                   4.0e-12
Match length
                  108
% identity
                  89
NCBI Description Phaseolus vulgaris DnaJ-like protein mRNA, partial cds
Seq. No.
                   46394
                   jC-gmro02800031h12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4490317
                  347
BLAST score
                  1.0e-32
E value
Match length
                  88
% identity
                  76
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 46395

Seq. ID jC-gmro02800032b01d1

Method BLASTN NCBI GI g4204760



```
BLAST score
                  1.0e-22
E value
Match length
                  116
                  85
% identity
NCBI Description Glycine max peroxidase precursor (sEPa2) mRNA, partial cds
Seq. No.
                  jC-gmro02800032b03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2293067
BLAST score
                  49
E value
                  2.0e-18
Match length
                  170
% identity
                  88
NCBI Description S.rostrata mRNA for early nodulin
                   46397
Seq. No.
Seq. ID
                   jC-gmro02800032e05a1
                  BLASTX
Method
                   q2832612
NCBI GI
                   172
BLAST score
                   4.0e-12
E value
Match length
                   147
% identity
                   30
                  (AL021711) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   46398
Seq. No.
Seq. ID
                   jC-gmro02800032f12a1
Method
                   BLASTX
NCBI GI
                   q3661603
BLAST score
                   162
E value
                   3.0e-11
Match length
                   42
                   81
% identity
                  (AF092841) ribonucleoside-diphosphate reductase large
NCBI Description
                   subunit [Arabidopsis thaliana]
Seq. No.
                   46399
                   jC-gmro02800032g12a1
Seq. ID
Method
                   BLASTN
                   g452768
NCBI GI
BLAST score
                   193
E value
                   1.0e-104
                   257
Match length
% identity
                   94
NCBI Description P.acutifolius alcohol dehydrogenase-1F mRNA, complete CDS
Seq. No.
                   46400
                   jC-gmro02800033c07d1
Seq. ID
                   BLASTX
Method
                   g1769901
NCBI GI
```

Method BLASTX
NCBI GI g1769901
BLAST score 296
E value 9.0e-27
Match length 74
% identity 74

NCBI Description (X95737) proline transporter 1 [Arabidopsis thaliana]



>gi_2088642 (AF002109) proline transporter 1 [Arabidopsis
thaliana]

Seq. No. 46401

Seq. ID jC-gmro02800033e10d1

Method BLASTN
NCBI GI g2894303
BLAST score 38
E value 4.0e-12

Match length 86 % identity 68

NCBI Description Nicotiana tabacum TUQG2 gene, complete CDS

Seq. No. 46402

Seq. ID jC-gmro02800033f09a1

Method BLASTX
NCBI GI g2879849
BLAST score 163
E value 2.0e-11
Match length 85
% identity 41

NCBI Description (AJ225894) kinesin [Syncephalastrum racemosum]

Seq. No. 46403

Seq. ID jC-gmro02800033f11a1

Method BLASTX
NCBI GI g3776567
BLAST score 116
E value 2.0e-12
Match length 82
% identity 49

NCBI Description (AC005388) Strong similarity to F21B7.33 gi_2809264 from A.

thaliana BAC gb_AC002560. EST gb_N65119 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 46404

Seq. ID jC-gmro02800033h06a1

Method BLASTX
NCBI GI g3935138
BLAST score 594
E value 1.0e-61
Match length 159
% identity 70

NCBI Description (AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No. 46405

Seq. ID jC-gmro02800033h07a1

Method BLASTX
NCBI GI g2160144
BLAST score 332
E value 7.0e-31
Match length 156
% identity 41

NCBI Description (AC000375) Strong similarity to Arabidopsis oligopeptide

transporter (gb_X77503). [Arabidopsis thaliana]

Seq. No. 46406



```
jC-gmro02800034b10a1
Seq. ID
Method
                  BLASTN
                  q1045041
NCBI GI
                  83
BLAST score
                   5.0e-39
E value
Match length
                  191
                  86
% identity
NCBI Description A.thaliana mRNA for KNAT3 homeobox protein
Seq. No.
                   46407
                   jC-gmro02800034d05a1
Seq. ID
Method
                   BLASTN
                   g347452
NCBI GI
BLAST score
                   78
                   1.0e-35
E value
Match length
                   277
                   15
% identity
                  Soybean hydroxyproline-rich glycoprotein (sbHRGP3) mRNA,
NCBI Description
                  partial cds
                   46408
Seq. No.
                   jC-gmro02800034e07a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539435
BLAST score
                   662
                   1.0e-69
E value
                   142
Match length
                   85
% identity
                  (AL049523) putative protein [Arabidopsis thaliana]
NCBI Description
                   46409
Seq. No.
                   jC-gmro02800034h09a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q169326
BLAST score
                   352
E value
                   0.0e + 00
Match length
                   480
                   94
% identity
                  Bean (P.vulgaris) NADP-dependent malic enzyme mRNA,
NCBI Description
                   complete cds
                   46410
Seq. No.
                   jC-gmro02800034h10a1
Seq. ID
Method
                   BLASTX
                   g4510376
NCBI GI
BLAST score
                   286
                   7.0e-26
E value
Match length
                   102
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46411
Seq. No.
                   jC-gmro02800034h12a1
Seq. ID
                   BLASTX
Method
                   g4217999
NCBI GI
```

190

3.0e-14

BLAST score

E value



```
Match length
                  46
% identity
                  (AC006135) putative ubiquitin--protein ligase
NCBI Description
                  (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
                  46412
Seq. No.
                  jC-gmro02800035a01a1
Seq. ID
                  BLASTX
Method
                  g1396054
NCBI GI
                  233
BLAST score
                  1.0e-19
E value
                  92
Match length
                  54
% identity
                  (D86180) phosphoribosylanthranilate transferase [Pisum
NCBI Description
                  sativum]
                  46413
Seq. No.
                  jC-gmro02800035f07d1
Seq. ID
                  BLASTX
Method
                  g3420052
NCBI GI
BLAST score
                  366
                   6.0e-35
E value
                  84
Match length
                  79
% identity
                   (AC004680) putative ubiqinone reductase [Arabidopsis
NCBI Description
                   thaliana]
                   46414
Seq. No.
                   jC-gmro02800036d03d1
Seq. ID
                   BLASTN
Method
                   g4190975
NCBI GI
                   99
BLAST score
                   2.0e-48
E value
                   222
Match length
% identity
                  Vigna radiata mRNA for cytokinin-specific binding protein,
NCBI Description
                   complete cds
                   46415
Seq. No.
                   jC-gmro02800037a11d1
Seq. ID
                   BLASTX
Method
                   q4006870
NCBI GI
BLAST score
                   291
                   4.0e-26
E value
                   97
Match length
% identity
                   62
                  (Z99707) patatin-like protein [Arabidopsis thaliana]
NCBI Description
                   46416
Seq. No.
                   jC-gmro02800038c11a1
Seq. ID
Method
                   BLASTN
                   q1217993
NCBI GI
                   181
BLAST score
                   3.0e-97
E value
                   329
Match length
% identity
                   89
NCBI Description Glycine max dynamin-like protein SDL12A mRNA, complete cds
```



```
Seq. No.
                  46417
                  jC-qmro02800038g05a1
Seq. ID
Method
                  BLASTN
                  q1326160
NCBI GI
                  59
BLAST score
E value
                  2.0e-24
                  226
Match length
% identity
                  Phaseolus vulgaris dehydrin mRNA, complete cds
NCBI Description
Seq. No.
                  46418
Seq. ID
                  jC-gmro02800038g12a1
                  BLASTX
Method
                  q1449179
NCBI GI
BLAST score
                   357
                   5.0e-34
E value
                  131
Match length
% identity
                   71
                   (D86506) N-ethylmaleimide sensitive fusion protein
NCBI Description
                   [Nicotiana tabacum]
                   46419
Seq. No.
                   jC-gmro02800038h02a1
Seq. ID
                   BLASTX
Method
                   g3176687
NCBI GI
                   593
BLAST score
E value
                   2.0e-61
Match length
                   166
                   63
% identity
                   (ACO03671) Strong similarity to trehalose-6-phosphate
NCBI Description
                   synthase homolog from A. thaliana chromosome 4 contig
                   gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and
                   gb_R64855 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   46420
                   jC-gmro02800038h07a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4335773
BLAST score
                   218
                   1.0e-17
E value
Match length
                   82
% identity
                   62
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46421
Seq. No.
                   jC-gmro02800038h11d1
Seq. ID
Method
                   BLASTX
                   q3335372
NCBI GI
                   296
BLAST score
                   9.0e-27
E value
                   84
Match length
% identity
                   68
                   (AC003028) putative SRG1 protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 46422

Seq. ID jC-gmro02800039g04d1

E value

Match length

5.0e-67

234



```
Method
                  BLASTN
NCBI GI
                  q703234
BLAST score
                  40
                  3.0e-13
E value
Match length
                  84
                  88
% identity
NCBI Description Pisum sativum (clone HW272) gene fragment
Seq. No.
                  46423
Seq. ID
                  jC-gmro02800039g06a1
Method
                  BLASTX
NCBI GI
                  q1619300
BLAST score
                  388
E value
                  2.0e-37
Match length
                  96
                  73
% identity
NCBI Description
                  (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                  46424
Seq. ID
                  jC-gmro02800039g12a1
Method
                  BLASTX
NCBI GI
                  g136140
BLAST score
                  209
E value
                  2.0e-16
Match length
                  132
                  39
% identity
                  PUTATIVE AC9 TRANSPOSASE >gi 72973 pir TQZMCA probable
NCBI Description
                  transposase - maize transposon Ac9
Seq. No.
                  46425
Seq. ID
                  jC-gmro02800039h02a1
Method
                  BLASTX
NCBI GI
                  g1703292
BLAST score
                  264
                  5.0e-23
E value
Match length
                  122
% identity
                  65
                  HIGH AFFINITY AMMONIUM TRANSPORTER >qi 551219 emb CAA53473
NCBI Description
                   (X75879) amt1 [Arabidopsis thaliana]
                  46426
Seq. No.
Seq. ID
                  jC-gmro02800040b05d1
Method
                  BLASTX
NCBI GI
                  g3461849
BLAST score
                  361
                  2.0e-34
E value
                  143
Match length
                  49
% identity
                  (AC005315) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  46427
Seq. No.
Seq. ID
                  jC-gmro02800040f04a1
Method
                  BLASTN
NCBI GI
                  g4115338
BLAST score
                  130
```



% identity 21

NCBI Description Pisum sativum (Alaska) ubuquitin (PUB4) gene, complete cds

Seq. No. 46428

Seq. ID jC-gmro02800040g01a1

Method BLASTX
NCBI GI g3142300
BLAST score 505
E value 2.0e-51
Match length 131
% identity 69

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 46429

Seq. ID jC-gmro02800041a09a1

Method BLASTN
NCBI GI g439616
BLAST score 149
E value 2.0e-78
Match length 193
% identity 98

NCBI Description Soybean G protein alpha subunit mRNA, complete cds

Seq. No. 46430

Seq. ID jC-gmro02800041c09a1

Method BLASTX
NCBI GI g4263527
BLAST score 167
E value 1.0e-11
Match length 80
% identity 45

NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 46431

Seq. ID jC-gmro02800041d09a1

Method BLASTX
NCBI GI g3881836
BLAST score 587
E value 9.0e-61
Match length 147
% identity 72

NCBI Description (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240);

cDNA EST EMBL:T00686 comes from this gene; cDNA EST EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728 comes from this gene; cDNA EST EMBL:C10626 comes from this

ge

Seq. No. 46432

Seq. ID jC-gmro02800041h09a1

Method BLASTX
NCBI GI g3377517
BLAST score 607
E value 3.0e-63
Match length 148

Seq. ID



```
% identity
                  (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
NCBI Description
                  46433
Seq. No.
                  jC-gmro02800041h11a1
Seq. ID
                  BLASTX
Method
                  g2213620
NCBI GI
                  145
BLAST score
                  5.0e-09
E value
                  125
Match length
                  35
% identity
                  (AC000103) F21J9.13 [Arabidopsis thaliana]
NCBI Description
                  46434
Seq. No.
                  jC-gmro02800042b09d1
Seq. ID
                  BLASTN
Method
                  g1163180
NCBI GI
                  80
BLAST score
                  3.0e-37
E value
                  252
Match length
                  91
% identity
                  Glycine max arginine decarboxylase mRNA, complete cds
NCBI Description
                   46435
Seq. No.
                   jC-gmro02800042c02a1
Seq. ID
                   BLASTX
Method
                   g4455360
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
                   122
Match length
                   5
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   46436
Seq. No.
                   jC-gmro02800043f10a1
Seq. ID
                   BLASTX
Method
                   q3367568
NCBI GI
                   164
BLAST score
                   6.0e-12
E value
                   67
Match length
% identity
                   51
                   (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   46437
Seq. No.
                   jC-gmro02800043g12a1
Seq. ID
                   BLASTN
Method
                   q986968
NCBI GI
BLAST score
                   96
                   1.0e-46
E value
Match length
                   296
                   83
% identity
                   Glycine max TGACG-motif binding protein (STGA1) mRNA,
NCBI Description
                   complete cds
                   46438
Seq. No.
```

jC-gmro02800043h10a1



```
Method
                  BLASTX
NCBI GI
                  q4454039
BLAST score
                  467
E value
                  8.0e-47
Match length
                  144
                  62
% identity
                  (AL035394) putative Na+/H+-exchanging protein [Arabidopsis
NCBI Description
Seq. No.
                  46439
                  jC-gmro02800043h12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2244965
BLAST score
                  591
                  3.0e-61
E value
Match length
                  166
% identity
                  70
                  (Z97340) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  46440
Seq. No.
                  jC-gmro02800044c03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1326160
BLAST score
                  57
                  3.0e-23
E value
Match length
                  190
                  95
% identity
                  Phaseolus vulgaris dehydrin mRNA, complete cds
NCBI Description
                  46441
Seq. No.
                  jC-gmro02800044f02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2905771
BLAST score
                  140
E value
                   9.0e-73
Match length
                  156
% identity
                   97
                  Glycine max glyceraldehyde-3 phosphate dehydrogenase
NCBI Description
                   (GAPDH) mRNA, partial cds
                   46442
Seq. No.
                  jC-gmro02910001c04d1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1654140
BLAST score
                   390
E value
                   9.0e-38
Match length
                  110
                   67
% identity
                  (U37840) lipoxygenase [Lycopersicon esculentum]
NCBI Description
```

Seq. No. 46443

Seq. ID jC-gmro02910001g06d1

Method BLASTX
NCBI GI g1173624
BLAST score 206
E value 2.0e-16
Match length 72

Seq. No.

46449



```
% identity
                   (U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid
NCBI Description
                  SM9108']
Seq. No.
                  46444
Seq. ID
                  jC-gmro02910002a03a1
Method
                  BLASTX
NCBI GI
                  g3482920
BLAST score
                  135
E value
                  1.0e-09
Match length
                  82
% identity
                  49
                  (AC003970) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  46445
Seq. No.
                  jC-qmro02910002a10d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529683
BLAST score
                  149
                  1.0e-09
E value
                  39
Match length
                   69
% identity
NCBI Description
                  (AC002535) unknown protein [Arabidopsis thaliana]
Seq. No.
                   46446
                   jC-qmro02910002f03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129563
BLAST score
                   593
E value
                   2.0e-61
Match length
                   111
                   92
% identity
                  cM4 protein - Arabidopsis thaliana >gi 928928_emb_CAA62030_
NCBI Description
                   (X90382) cM4 [Arabidopsis thaliana]
                   46447
Seq. No.
                   jC-gmro02910002f11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3831457
BLAST score
                   429
                   2.0e-42
E value
Match length
                   141
% identity
                   (AC005700) putative ion channel protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   46448
                   jC-gmro02910002f12a1
Seq. ID
Method
                   BLASTX
                   q4455179
NCBI GI
BLAST score
                   153
                   7.0e-10
E value
                   64
Match length
                   45
% identity
                  (AL035521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

7479

Method

NCBI GI

BLASTX q3600051



```
jC-gmro02910002g01d1
Seq. ID
                  BLASTX
Method
                  g4191775
NCBI GI
                  147
BLAST score
                  3.0e-09
E value
                  31
Match length
                  84
% identity
                   (AC005917) putative acyl-CoA cholesterol acyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                  46450
Seq. No.
                  jC-gmro02910002g04a1
Seq. ID
                  BLASTN
Method
                  g2264316
NCBI GI
BLAST score
                  59
                  2.0e-24
E value
                  148
Match length
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRO11, complete sequence [Arabidopsis thaliana]
                   46451
Seq. No.
                   jC-gmro02910002g12a1
Seq. ID
                   BLASTX
Method
                   g3193309
NCBI GI
                   164
BLAST score
                   2.0e-11
E value
Match length
                   136
% identity
                   27
                  (AF069300) No definition line found [Arabidopsis thaliana]
NCBI Description
                   46452
Seq. No.
                   jC-gmro02910003a05a1
Seq. ID
                   BLASTX
Method
                   q4432860
NCBI GI
                   147
BLAST score
                   3.0e-09
E value
                   48
Match length
% identity
                   60
                   (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
                   46453
Seq. No.
                   jC-gmro02910003h07a1
Seq. ID
                   BLASTX
Method
                   g1076685
NCBI GI
BLAST score
                   151
                   2.0e-10
E value
                   41
Match length
                   33
% identity
                   SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_
NCBI Description
                   (D30038) SPF1 protein [Ipomoea batatas]
                   46454
Seq. No.
                   jC-gmro02910004b07d1
Seq. ID
```



```
BLAST score
E value
                  1.0e-12
Match length
                   86
                   56
% identity
                   (AF080120) contains similarity to the single-strand binding
NCBI Description
                  proteins family (Pfam: SSB.hmm, score: 24.02) [Arabidopsis
                  thaliana]
                   46455
Seq. No.
                   jC-gmro02910004c09a1
Seq. ID
                   BLASTX
Method
                   g1620371
NCBI GI
BLAST score
                   442
E value
                   9.0e-44
                   114
Match length
                   75
% identity
                  (Y08782) peroxidase ATP23a [Arabidopsis thaliana]
NCBI Description
                   46456
Seq. No.
                   jC-gmro02910004e08d1
Seq. ID
                   BLASTX
Method
                   g2648032
NCBI GI
                   374
BLAST score
                   6.0e-36
E value
Match length
                   128
                   58
% identity
                  (AJ001374) alpha-glucosidase [Solanum tuberosum]
NCBI Description
                   46457
Seq. No.
                   jC-gmro02910004e12a1
Seq. ID
                   BLASTX
Method
                   g3924596
NCBI GI
BLAST score
                   254
                   1.0e-21
E value
Match length
                   124
                   47
% identity
                   (AF069442) putative phospho-ser/thr phosphatase
NCBI Description
                   [Arabidopsis thaliana]
                   46458
Seq. No.
                   jC-gmro02910004f05a1
Seq. ID
                   BLASTX
Method
                   g2342690
NCBI GI
                   512
BLAST score
E value
                   5.0e-52
                   162
Match length
 % identity
                   (AC000106) Similar to Homo copine I (gb_U83246).
NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                   46459
                   jC-qmro02910004g02d1
 Seq. ID
Method
                   BLASTX
```

g3927836

680 1.0e-71

147

NCBI GI BLAST score

E value Match length



```
% identity
                  (AC005727) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  46460
                  jC-gmro02910005b09a1
Seq. ID
Method
                  BLASTN
                  g18764
NCBI GI
BLAST score
                  282
                  1.0e-157
E value
Match length
                  366
                  94
% identity
                 G.max tefS1 gene for elongation factor EF-1a
NCBI Description
Seq. No.
                  46461
                  jC-gmro02910005d06d1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3108209
BLAST score
                  187
E value
                  5.0e-14
Match length
                  34
                  97
% identity
                  (AF028809) eukaryotic cap-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  46462
Seq. ID
                  jC-qmro02910005d11a1
Method
                  BLASTX
NCBI GI
                  g419760
BLAST score
                  383
                  3.0e-37
E value
Match length
                  105
% identity
                  34
                  P-glycoprotein atpgp1 - Arabidopsis thaliana
NCBI Description
                  >gi_3849833_emb CAA43646 (X61370) P-glycoprotein
                  [Arabidopsis thaliana]
                  46463
Seq. No.
Seq. ID
                  jC-gmro02910005g01a1
Method
                  BLASTX
NCBI GI
                  q1620371
BLAST score
                  150
E value
                  7.0e-10
Match length
                  37
% identity
                  78
                  (Y08782) peroxidase ATP23a [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  46464
                  jC-gmro02910005g03a1
Seq. ID
Method
                  BLASTN
                  g4138646
NCBI GI
BLAST score
                  59
```

E value 2.0e-24 Match length 143 % identity 93

NCBI Description Trifolium repens mRNA for peroxidase

Seq. No. 46465

Seq. ID

Method



```
iC-gmro02910006a01a1
Seq. ID
                  BLASTX
Method
                  q3850588
NCBI GI
                  416
BLAST score
                  9.0e-41
E value
                  111
Match length
                  36
% identity
                  (AC005278) Contains similarity to gb AB011110 KIAA0538
NCBI Description
                  protein from Homo sapiens brain and to phospholipid-binding
                  domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come
                  from this gene. [Arabidopsis thaliana]
                  46466
Seq. No.
                  jC-gmro02910006b02d1
Seq. ID
                  BLASTX
Method
                  g322752
NCBI GI
                  209
BLAST score
                  1.0e-16
E value
                  74
Match length
                  62
% identity
                  auxin-independent growth promoter - Nicotiana tabacum
NCBI Description
                  >gi 559921 emb CAA56570 (X80301) axi 1 [Nicotiana tabacum]
                   46467
Seq. No.
                   jC-gmro02910006c02d1
Seq. ID
                   BLASTX
Method
                   g2290528
NCBI GI
                   331
BLAST score
                   7.0e-31
E value
                   68
Match length
                   96
% identity
                  (U94746) ATAN11 [Arabidopsis thaliana]
NCBI Description
                   46468
Seq. No.
                   jC-gmro02910006c05a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2462744
                   323
BLAST score
                   7.0e-30
E value
Match length
                   153
% identity
                  (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46469
Seq. No.
                   jC-gmro02910006c09a1
Seq. ID
                   BLASTX
Method
                   q3954807
NCBI GI
                   327
BLAST score
E value
                   1.0e-30
                   101
Match length
 % identity
                   (AJ011862) flavonoid 3',5'-hydroxylase [Catharanthus
NCBI Description
                   roseus]
                   46470
Seq. No.
```

jC-gmro02910006d01d1

BLASTX

NCBI Description



```
q2462834
NCBI GI
BLAST score
                  158
E value
                  7.0e-11
                  73
Match length
                  48
% identity
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  46471
Seq. No.
                  jC-gmro02910006g02d1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3860255
BLAST score
                  247
E value
                  5.0e-21
                  80
Match length
                  68
% identity
                  (AC005824) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46472
Seq. No.
                   jC-gmro02910006g08a1
Seq. ID
                  BLASTX
Method
                   q2288998
NCBI GI
                   387
BLAST score
E value
                   2.0e-37
Match length
                   114
                   67
% identity
                   (AC002335) peroxidase isolog [Arabidopsis thaliana]
NCBI Description
                   46473
Seq. No.
                   jC-gmro02910006h12d1
Seq. ID
                   BLASTN
Method
                   g22069
NCBI GI
                   45
BLAST score
                   2.0e-16
E value
Match length
                   73
                   90
% identity
                  V.radiata mRNA for ACC synthase
NCBI Description
                   46474
Seq. No.
                   jC-gmro02910007b08a1
Seq. ID
                   BLASTN
Method
                   g20894
NCBI GI
                   98
BLAST score
                   1.0e-47
E value
Match length
                   126
% identity
                   94
NCBI Description Pea U4 snRNA (clone pPSUN4.1)
                   46475
Seq. No.
                   jC-gmro02910007c01d1
Seq. ID
Method
                   BLASTX
                   q3128218
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
                   37
Match length
                   78
 % identity
                  (AC004077) putative end13 protein [Arabidopsis thaliana]
```



```
46476
Seq. No.
                  jC-gmro02910007d09a1
Seq. ID
                  BLASTX
Method
                  q4512685
NCBI GI
                  590
BLAST score
                  4.0e-61
E value
                  162
Match length
                  70
% identity
                  (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)
                  hypothetical protein [Arabidopsis Thaliana]
                   46477
Seq. No.
                   jC-gmro02910007f02d1
Seq. ID
                  BLASTN
Method
                  g218325
NCBI GI
                   94
BLAST score
                   2.0e-45
E value
                   174
Match length
                   89
% identity
NCBI Description Vigna radiata mRNA for invertase, complete cds
                   46478
Seq. No.
                   jC-gmro02910008a12d1
Seq. ID
                   BLASTN
Method
                   q2739005
NCBI GI
                   54
BLAST score
                   1.0e-21
E value
                   90
Match length
                   90
% identity
                  Glycine max cytochrome P450 monooxygenase CYP93C1p
NCBI Description
                   (CYP93C1) mRNA, complete cds
                   46479
Seq. No.
                   jC-gmro02910008b02a1
Seq. ID
                   BLASTX
Method
                   q4314388
NCBI GI
                   236
BLAST score
                   1.0e-19
E value
                   58
Match length
                   74
% identity
                   (AC006232) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46480
 Seq. No.
                   jC-gmro02910008b04d1
 Seq. ID
                   BLASTX
Method
                   g731935
 NCBI GI
                   220
 BLAST score
 E value
                   8.0e-18
                   84
Match length
 % identity
                   50
                   HYPOTHETICAL 66.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC
 NCBI Description
                   REGION >gi_1077820_pir__S50802 hypothetical protein YJL069c
                   - yeast (Saccharomyces cerevisiae) >gi_498997_emb_CAA84053_
                    (Z34288) HRE594 [Saccharomyces cerevisiae]
                   >gi_895894_emb_CAA61308_ (X88851) hypothetical protein
```

[Saccharomyces cerevisiae] >gi_1008221_emb_CAA89360_



(Z49344) ORF YJL069c [Saccharomyces cerevisiae]

```
Seq. No.
                  46481
                  jC-gmro02910008c02a1
Seq. ID
Method
                  BLASTX
                  g4490317
NCBI GI
BLAST score
                  184
                  1.0e-13
E value
                  79
Match length
                  47
% identity
NCBI Description
                  (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  46482
Seq. ID
                  jC-qmro02910008d10d1
Method
                  BLASTN
NCBI GI
                  q2738997
BLAST score
                  265
E value
                  1.0e-147
Match length
                  383
% identity
                  93
                  Glycine max cytochrome P450 monooxygenase CYP98A2p
NCBI Description
                   (CYP98A2) mRNA, complete cds
Seq. No.
                  46483
Seq. ID
                  jC-gmro02910008d12a1
Method
                  BLASTX
NCBI GI
                  g3757516
BLAST score
                  143
                  8.0e-09
E value
                  134
Match length
                  31
% identity
NCBI Description
                  (AC005167) putative TMV resistance protein [Arabidopsis
                  thaliana]
                  46484
Seq. No.
Seq. ID
                  jC-qmro02910008g01a1
                  BLASTX
Method
NCBI GI
                  q4512685
BLAST score
                  171
E value
                  4.0e-12
Match length
                  43
% identity
                  72
                  (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4559325 gb AAD22987.1 AC007087 6 (AC007087)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  46485
Seq. ID
                  jC-gmro02910008g09a1
Method
                  BLASTX
                  g2129918
NCBI GI
BLAST score
                  302
E value
                  2.0e-27
Match length
                  94
% identity
                  65
                  BPF-1 protein - parsley >gi_396197_emb_CAA48413_ (X68337)
NCBI Description
                  BPF-1 [Petroselinum crispum] >gi 441310 emb_CAA44518_
```

(X62653) BPF-1 [Petroselinum crispum]



```
46486
Seq. No.
                  jC-gmro02910009a07a1
Seq. ID
                  BLASTX
Method
                  q1769556
NCBI GI
BLAST score
                  190
                  1.0e-14
E value
Match length
                   66
% identity
                   (U81158) Forsythia x intermedia
NCBI Description
                   (+)-pinoresinol/(+)-lariciresinol reductase (PLR) protein,
                   complete sequence [Forsythia x intermedia]
                   46487
Seq. No.
                   jC-gmro02910009b01a1
Seq. ID
                   BLASTX
Method
                   g3068704
NCBI GI
                   568
BLAST score
                   1.0e-58
E value
                   164
Match length
                   66
% identity
                   (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   46488
Seq. No.
                   jC-gmro02910009b07a1
Seq. ID
                   BLASTX
Method
                   g3548802
NCBI GI
                   635
BLAST score
                   2.0e-66
E value
Match length
                   156
                   73
% identity
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4335769 gb AAD17446 (AC006284) putative axil protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
                   46489
Seq. No.
                   jC-gmro02910009c07a1
Seq. ID
                   BLASTX
Method
                   q3482929
NCBI GI
                   568
BLAST score
                   8.0e-59
E value
                   120
Match length
 % identity
                   (AC003970) Putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   46490
 Seq. No.
                   jC-gmro02910009c08a1
 Seq. ID
 Method
                   BLASTX
                   q2342690
NCBI GI
 BLAST score
                   133
 E value
                   9.0e-10
                   72
 Match length
                   37
 % identity
                    (AC000106) Similar to Homo copine I (gb_U83246).
 NCBI Description
```

[Arabidopsis thaliana]



```
46491
Seq. No.
                  jC-gmro02910009c10d1
Seq. ID
                  BLASTX
Method
                  g3947735
NCBI GI
                  331
BLAST score
                  9.0e-31
E value
                  154
Match length
                  43
% identity
NCBI Description (AJ009720) NL27 [Solanum tuberosum]
                   46492
Seq. No.
                   jC-gmro02910009g02a1
Seq. ID
                  BLASTX
Method
                   g2088651
NCBI GI
BLAST score
                   213
E value
                   4.0e-17
                   104
Match length
% identity
                   42
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   46493
Seq. No.
                   jC-gmro02910010a09a1
Seq. ID
                   BLASTX
Method
                   g3157927
NCBI GI
BLAST score
                   167
                   2.0e-18
E value
                   108
Match length
                   55
% identity
                   (AC002131) Contains similarity to GDP-dissociation
NCBI Description
                   inhibitor gb_L07918 from Mus musculus. [Arabidopsis
                   thaliana]
                   46494
Seq. No.
                   jC-gmro02910010b02d1
Seq. ID
                   BLASTN
Method
                   g3789722
NCBI GI
                   129
BLAST score
                   3.0e-66
E value
                   400
Match length
                   89
 % identity
NCBI Description Glycine max peroxidase (PC7) mRNA, complete cds
                   46495
 Seq. No.
                   jC-gmro02910010b12a1
 Seq. ID
                   BLASTX
 Method
                   g2245136
 NCBI GI
                   239
 BLAST score
                   3.0e-20
 E value
                   104
 Match length
                   54
 % identity
                   (Z97344) trehalose-6-phosphate synthase homolog
 NCBI Description
                    [Arabidopsis thaliana]
```

Seq. No. 46496

Seq. ID jC-gmro02910010d04a1

Method BLASTX



```
NCBI GI
                  q117535
BLAST score
                  315
E value
                  6.0e-29
Match length
                  163
% identity
                  45
                  CRYSTAL PROTEIN PRECURSOR >gi 102223 pir A34576 crystal
NCBI Description
                  protein precursor - slime mold (Dictyostelium discoideum)
                  >gi 7234 emb CAA36702 (X52464) crystal protein
                  [Dictyostelium discoideum]
                  46497
Seq. No.
                  jC-gmro02910010e03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2191136
                  203
BLAST score
                  8.0e-16
E value
                  133
Match length
                  38
% identity
                  (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                  coded for by A. thaliana cDNA T46230; coded for by A.
                  thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                  [Arabidopsis thaliana]
Seq. No.
                  46498
Seq. ID
                  jC-qmro02910011a08d1
Method
                  BLASTN
NCBI GI
                  g535762
BLAST score
                  63
                  8.0e-27
E value
                  163
Match length
% identity
NCBI Description
                 Stylosanthes humilis peroxidase mRNA
                  46499
Seq. No.
Seq. ID
                  jC-gmro02910011a09a1
Method
                  BLASTX
NCBI GI
                  g2982452
BLAST score
                  342
E value
                  3.0e-32
Match length
                  121
% identity
                  (AL022223) receptor protein kinase-like protein
NCBI Description
                  [Arabidopsis thaliana]
```

Seq. No. 46500

Seq. ID jC-gmro02910011h03d1

Method BLASTX
NCBI GI g4415916
BLAST score 271
E value 6.0e-24
Match length 79
% identity 56

NCBI Description (AC006282) putative pectin methylesterase [Arabidopsis

thaliana]

Seq. No. 46501

Seq. ID jC-gmro02910012c03a1



Method BLASTN NCBI GI g2642237 304 BLAST score 1.0e-170 E value Match length 356 % identity 96 Glycine max endoplasmic reticulum HSC70-cognate binding NCBI Description protein precursor (BIP) mRNA, complete cds Seq. No. 46502 Seq. ID jC-gmro02910012c06d1 Method BLASTX NCBI GI g2914695 BLAST score 320 E value 1.0e-29 Match length 106 58 % identity (AC003974) putative ubiquitin specific protease NCBI Description [Arabidopsis thaliana] 46503 Seq. No. jC-gmro02910012d04a1 Seq. ID Method BLASTX g3924597 NCBI GI BLAST score 194 7.0e-15 E value Match length 93 % identity 44 NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana] Seq. No. 46504 jC-gmro02910012d04d1 Seq. ID Method BLASTX NCBI GI q3924597 BLAST score 162 5.0e-11 E value Match length 90 48 % identity NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana] Seq. No. 46505 jC-gmro02910012h12a1 Seq. ID Method BLASTX NCBI GI q3982577 BLAST score 192 E value 1.0e-14 Match length 58 60 % identity (AF023141) histidinol dehydrogenase [Thlaspi goesingense] NCBI Description 46506 Seq. No. jC-gmro02910013a10a1 Seq. ID

Method BLASTN NCBI GI g2924257 BLAST score 212 1.0e-115 E value Match length 356

Seq. ID

Method



```
% identity
NCBI Description Tobacco chloroplast genome DNA
                  46507
Seq. No.
                  jC-gmro02910013b07a1
Seq. ID
                  BLASTX
Method
                  g3445210
NCBI GI
                  412
BLAST score
                  2.0e-40
E value
                  140
Match length
                  50
% identity
                   (AC004786) putative flavonol 3-o-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                  46508
Seq. No.
                   jC-gmro02910013c02a1
Seq. ID
                  BLASTX
Method
                  g2459419
NCBI GI
                   238
BLAST score
                  7.0e-20
E value
                   158
Match length
                   39
% identity
                  (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46509
Seq. No.
                   jC-gmro02910013c06d1
Seq. ID
                   BLASTX
Method
                   g3128191
NCBI GI
                   176
BLAST score
                   1.0e-12
E value
                   60
Match length
                   57
% identity
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
                   46510
Seq. No.
                   jC-gmro02910013c07d1
Seq. ID
                   BLASTX
Method
                   q629670
NCBI GI
BLAST score
                   252
                   1.0e-21
E value
                   69
Match length
                   70
% identity
NCBI Description hypothetical protein - tomato
                   46511
Seq. No.
                   jC-gmro02910013d01a1
Seq. ID
                   BLASTX
Method
                   q3510251
NCBI GI
BLAST score
                   440
                   9.0e-44
E value
Match length
                   129
                   67
% identity
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.
                   46512
```

jC-gmro02910013d05a1

BLASTX

E value

9.0e-49



```
g4567302
NCBI GI
                  176
BLAST score
                  1.0e-12
E value
                  138
Match length
                  41
% identity
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                  46513
Seq. No.
                  jC-gmro02910013d08d1
Seq. ID
                  BLASTN
Method
                  g1223925
NCBI GI
                  47
BLAST score
                  2.0e-17
E value
                  115
Match length
% identity
                  85
NCBI Description Vigna radiata carboxypeptidase II mRNA, partial cds
                   46514
Seq. No.
                   jC-gmro02910013d11a1
Seq. ID
                   BLASTX
Method
                   g3970973
NCBI GI
                   539
BLAST score
                   3.0e-55
E value
                   167
Match length
                   45
% identity
                   (AC004812) similar to human HsGCN1 U77700 (PID:g2282576);
NCBI Description
                   similar to yeast translation activator GCN1 (PID:g462168)
                   [Homo sapiens]
                   46515
Seq. No.
                   jC-gmro02910013e05a1
Seq. ID
                   BLASTX
Method
                   g1906830
NCBI GI
                   364
BLAST score
                   1.0e-34
E value
                   82
Match length
                   91
% identity
                  (Y11829) heat shock protein [Arabidopsis thaliana]
NCBI Description
                   46516
 Seq. No.
                   jC-qmro02910013g09a1
 Seq. ID
                   BLASTX
Method
                   q2492782
NCBI GI
BLAST score
                   170
                   6.0e-12
E value
Match length
                   45
                   76
 % identity
                   ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)
 NCBI Description
                   (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992)
                   alpha-galactosidase [Coffea arabica]
                   46517
 Seq. No.
                   jC-gmro02910013h05a1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g4467156
 BLAST score
                   484
```

NCBI Description



```
Match length
% identity
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  46518
Seq. No.
                   jC-gmro02910013h07a1
Seq. ID
                   BLASTX
Method
                  g2760830
NCBI GI
                   368
BLAST score
                   3.0e-35
E value
                   91
Match length
                   73
% identity
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   46519
Seq. No.
                   jC-gmro02910014c11a1
Seq. ID
                   BLASTX
Method
                   g3088646
NCBI GI
                   166
BLAST score
                   2.0e-11
E value
                   63
Match length
                   44
% identity
                   (AF056493) pectin methylesterase [Pisum sativum]
NCBI Description
                   >gi_3426335 (AF081457) pectin methylesterase [Pisum
                   sativum]
                   46520
Seq. No.
                   jC-gmro02910014d06a1
Seq. ID
                   BLASTN
Method
                   g1335861
NCBI GI
                   300
BLAST score
                   1.0e-168
E value
                   356
Match length
% identity
                   Glycine max clathrin heavy chain mRNA, complete cds
NCBI Description
                   46521
Seq. No.
                   jC-gmro02910014d07a1
Seq. ID
Method
                   BLASTX
                   q4539351
NCBI GI
                   416
BLAST score
                   8.0e-41
E value
                   129
Match length
 % identity
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   46522
 Seq. No.
                   jC-qmro02910014d11a1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q3892057
                   434
 BLAST score
                   7.0e-43
 E value
                   144
 Match length
                    60
 % identity
```

(AC002330) hypothetical protein [Arabidopsis thaliana]



```
46523
Seq. No.
                  jC-gmro02910014e07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2213612
BLAST score
                  182
                  2.0e-13
E value
                  60
Match length
                   57
% identity
                   (AC000103) F21J9.6 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46524
                   jC-gmro02910015d01a1
Seq. ID
                   BLASTX
Method
                   g1173027
NCBI GI
BLAST score
                   196
E value
                   2.0e-15
Match length
                   58
                   72
% identity
                   60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal
NCBI Description
                   protein L31 [Nicotiana glutinosa]
                   46525
Seq. No.
                   jC-gmro02910015d06d1
Seq. ID
                   BLASTX
Method
                   g3763921
NCBI GI
                   235
BLAST score
                   1.0e-19
E value
                   52
Match length
                   79
% identity
                   (AC004450) putative pirin protein [Arabidopsis thaliana]
NCBI Description
                   46526
Seq. No.
                   jC-gmro02910015e10d1
Seq. ID
                   BLASTX
Method
                   g3643608
NCBI GI
                   260
BLAST score
                   1.0e-22
E value
                   66
Match length
                   77
% identity
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46527
                   jC-gmro02910015g05d1
Seq. ID
                   BLASTN
Method
                   g2444419
NCBI GI
                   35
BLAST score
                   3.0e-10
E value
Match length
                   71
                   87
 % identity
                   Glycine max ribosome-associated protein p40 mRNA, complete
 NCBI Description
                   cds
 Seq. No.
                   46528
                   jC-gmro02910016b04a1
 Seq. ID
                   BLASTX
 Method
                   g2408068
 NCBI GI
```

188

BLAST score

NCBI Description



```
5.0e-14
E value
                  114
Match length
                  32
% identity
                  (Z99165) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  46529
Seq. No.
                  jC-gmro02910016d08a1
Seq. ID
                  BLASTX
Method
                  g710465
NCBI GI
                  178
BLAST score
                   4.0e-13
E value
                   80
Match length
% identity
                  OEP86=outer envelope protein [Peas, Peptide Chloroplast,
NCBI Description
                   878 aa]
                   46530
Seq. No.
                   jC-gmro02910016d11a1
Seq. ID
                   BLASTX
Method
                   q3287679
NCBI GI
BLAST score
                   556
                   3.0e-57
E value
                   147
Match length
                   73
% identity
                   (AC003979) T22J18.6 [Arabidopsis thaliana]
NCBI Description
                   46531
Seq. No.
                   jC-gmro02910016e07a1
Seq. ID
                   BLASTX
Method
                   q3157941
NCBI GI
                   333
BLAST score
                   5.0e-31
E value
                   163
Match length
                   42
% identity
                   (AC002131) Contains similarity to hypothetical protein
NCBI Description
                   gb_U95973 from A. thaliana. [Arabidopsis thaliana]
                   46532
Seq. No.
                   jC-gmro02910016e11a1
 Seq. ID
                   BLASTX
Method
                   g4510385
NCBI GI
                   638
BLAST score
                   9.0e-67
E value
                   172
Match length
                   69
 % identity
                   (AC007017) unknown protein [Arabidopsis thaliana]
 NCBI Description
                    46533
 Seq. No.
                    jC-gmro02910016f01a1
 Seq. ID
                   BLASTX
 Method
                    g4467118
 NCBI GI
                   179
 BLAST score
                    5.0e-13
 E value
                    53
 Match length
                    64
 % identity
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
```

E value

1.0e-08



46534

```
Seq. No.
                  jC-gmro02910016f03a1
Seq. ID
                  BLASTX
Method
                  g4539423
NCBI GI
                   397
BLAST score
                  2.0e-38
E value
                  105
Match length
                   73
% identity
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Arabidopsis thaliana]
                   46535
Seq. No.
                   jC-gmro02910016f08d1
Seq. ID
                   BLASTN
Method
                   q498788
NCBI GI
BLAST score
                   33
                   7.0e-09
E value
                   113
Match length
                   82
% identity
                  S.tuberosum (Desiree) cycl II mRNA. for cytochrome cl
NCBI Description
                   46536
Seq. No.
                   jC-gmro02910016g05a1
Seq. ID
                   BLASTX
Method
                   g4127662
NCBI GI
                   404
BLAST score
                   2.0e-39
E value
                   143
Match length
% identity
                   54
                  (Y11176) fructosidase [Cichorium intybus]
NCBI Description
                   46537
Seq. No.
                   jC-gmro02910017f10d1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1321819
BLAST score
                   285
                   1.0e-159
E value
Match length
                   309
                   98
% identity
                   G.max mRNA for glycinamide ribonucleotide synthetase
NCBI Description
Seq. No.
                   46538
                   jC-gmro02910017g01a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2832685
                   156
BLAST score
                   7.0e-11
E value
Match length
                   44
% identity
                   (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
                   46539
Seq. No.
                   jC-gmro02910017g02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2780194
BLAST score
                   142
```



```
Match length
                  44
% identity
                  (AJ003197) adenine nucleotide translocator [Lupinus albus]
NCBI Description
Seq. No.
                  46540
                  jC-qmro02910019a07a1
Seg. ID
                  BLASTX
Method
                  q1495259
NCBI GI
                  305
BLAST score
                  7.0e-28
E value
                  80
Match length
                  75
% identity
                  (X97826) orf04 [Arabidopsis thaliana]
NCBI Description
                   46541
Seq. No.
                   jC-gmro02910019d09a1
Seq. ID
                   BLASTN
Method
                   q2244901
NCBI GI
                   40
BLAST score
                   4.0e-13
E value
Match length
                   92
                   86
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   46542
Seq. No.
                   jC-gmro02910019e01d1
Seq. ID
                   BLASTX
Method
                   g3790593
NCBI GI
                   145
BLAST score
                   4.0e-09
E value
Match length
                   40
                   55
% identity
                   (AF079185) RING-H2 finger protein RHY1a [Arabidopsis
NCBI Description
                   thaliana]
                   46543
Seq. No.
                   jC-gmro02910019e09a1
Seq. ID
                   BLASTX
Method
                   g3036816
NCBI GI
                   389
BLAST score
                   7.0e-38
E value
                   106
Match length
                   70
 % identity
                   (AL022373) myosin-like protein [Arabidopsis thaliana]
 NCBI Description
                   46544
 Seq. No.
                   jC-gmro02910019g08d1
 Seq. ID
                   BLASTX
 Method
                   q2911797
 NCBI GI
 BLAST score
                   140
                   1.0e-08
 E value
                   41
 Match length
                    66
 % identity
                    (AF008183) 4-coumarate:CoA ligase 2 [Populus balsamifera
 NCBI Description
```

subsp. trichocarpa X Populus deltoides]

Method

NCBI GI

BLASTN q3047074



```
46545
Seq. No.
                  jC-gmro02910020b10d1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2369713
BLAST score
                  87
                  3.0e-41
E value
                  155
Match length
                  89
% identity
NCBI Description Beta vulgaris cDNA for elongation factor
                  46546
Seq. No.
                  jC-gmro02910020d02d1
Seq. ID
                  BLASTX
Method
                  g4580390
NCBI GI
BLAST score
                  298
                   6.0e-27
E value
                  89
Match length
                   67
% identity
                   (AC007171) putative disease resistance response protein
NCBI Description
                   [Arabidopsis thaliana]
                   46547
Seq. No.
                   jC-gmro02910020f04a1
Seq. ID
                   BLASTX
Method
                   g2947059
NCBI GI
BLAST score
                   241
                   6.0e-21
E value
                   60
Match length
                   75
% identity
                   (AC002521) similar to myb transforming protein [Arabidopsis
NCBI Description
                   thaliana]
                   46548
Seq. No.
                   jC-gmro02910020g04d1
Seq. ID
                   BLASTX
Method
                   g3047065
NCBI GI
                   159
BLAST score
                   9.0e-11
E value
                   34
Match length
                   79
% identity
                   (AF058825) contains similarity to human OS-9 precurosor
NCBI Description
                   (GB:U41635) [Arabidopsis thaliana]
                   46549
Seq. No.
                   jC-gmro02910020h10d1
Seq. ID
                   BLASTX
Method
                   g2618689
NCBI GI
                   210
BLAST score
                   7.0e-17
E value
                   47
Match length
                   87
% identity
                   (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46550
Seq. No.
                   jC-qmro02910021a01d1
 Seq. ID
```



33

BLAST score

```
4.0e-09
E value
                  33
Match length
                  100
% identity
NCBI Description Arabidopsis thaliana BAC F21E10
                  46551
Seq. No.
                  jC-gmro02910021a09d1
Seq. ID
                  BLASTN
Method
                  g1934971
NCBI GI
                  54
BLAST score
                  4.0e-22
E value
                  98
Match length
                  89
% identity
NCBI Description P.sativum mRNA for dihydropterin
                  pyrophosphokinase/dihydropteroate synthase
                   46552
Seq. No.
                   jC-qmro02910021e10d1
Seq. ID
                  BLASTN
Method
                   g1698669
NCBI GI
                   479
BLAST score
                   0.0e+00
E value
                   487
Match length
                   100
% identity
                  Zea mays S-like RNase (kin1) mRNA, complete cds
NCBI Description
Seq. No.
                   46553
                   jC-gmro02910021f02d1
Seq. ID
                   BLASTN
Method
                   g4544405
NCBI GI
                   161
BLAST score
                   2.0e-85
E value
                   307
Match length
                   44
% identity
                   Arabidopsis thaliana chromosome II BAC F2818 genomic
NCBI Description
                   sequence, complete sequence
                   46554
Seq. No.
                   jC-gmro02910021f03d1
Seq. ID
                   BLASTN
Method
                   g2618601
NCBI GI
                   216
BLAST score
                   1.0e-118
E value
Match length
                   305
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MHJ24, complete sequence [Arabidopsis thaliana]
                   46555
Seq. No.
                   jC-gmro02910021g06d1
Seq. ID
                   BLASTN
Method
                   q16473
NCBI GI
                   487
BLAST score
                   0.0e+00
E value
Match length
                   507
 % identity
                   99
```



```
NCBI Description Arabidopsis thaliana 25S-18S ribosomal DNA spacer
                  46556
Seq. No.
                  jC-gmro02910021g08d1
Seq. ID
                  BLASTN
Method
                  g2828186
NCBI GI
                  317
BLAST score
                  1.0e-178
E value
                  394
Match length
                  79
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18I23, complete sequence [Arabidopsis thaliana]
                  46557
Seq. No.
                  jC-gmro02910022a03a1
Seq. ID
                  BLASTX
Method
                  g1703446
NCBI GI
                  252
BLAST score
                  8.0e-22
E value
                  90
Match length
% identity
                  62
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                  >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana
                  >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
                  thaliana]
Seq. No.
                  46558
                  jC-gmro02910022a05d1
Seq. ID
                  BLASTX
Method
                  g3822036
NCBI GI
                  289
BLAST score
                  5.0e-26
E value
                  118
Match length
                   54
% identity
                  (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
NCBI Description
                   46559
Seq. No.
                   jC-gmro02910022a08d1
Seq. ID
                   BLASTN
Method
                   g22272
NCBI GI
BLAST score
                   336
                   0.0e + 00
E value
                   340
Match length
                   100
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
                   46560
Seq. No.
                   jC-gmro02910022a10d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1173027
```

NCBI GI g1173027 BLAST score 294 E value 1.0e-26 Match length 82 % identity 70

NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal

protein L31 [Nicotiana glutinosa]



```
Seq. No.
                   jC-gmro02910022a11d1
Seq. ID
                   BLASTN
Method
                   g3236234
NCBI GI
                   35
BLAST score
                   3.0e-10
E value
                   75
Match length
                   87
% identity
                   Arabidopsis thaliana chromosome II BAC F13M22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   46562
Seq. No.
                   jC-gmro02910022b02d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2190992
BLAST score
                   386
                   3.0e-37
E value
                   137
Match length
                   54
% identity
                   (AF004358) glutathione S-transferase TSI-1 [Aegilops
NCBI Description
                   tauschii]
                   46563
Seq. No.
                   jC-gmro02910022b03d1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1848280
BLAST score
                   184
E value
                   3.0e-99
Match length
                   245
                   91
 % identity
                   Sorghum bicolor membrane intrinsic protein (Mip1) mRNA,
NCBI Description
                   partial cds
                    46564
 Seq. No.
                    jC-gmro02910022b04d1
 Seq. ID
 Method
                   BLASTN
                   g4105560
 NCBI GI
                    35
 BLAST score
                    4.0e-10
 E value
 Match length
                    63
                    89
 % identity
                   Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA,
 NCBI Description
                    complete cds
                    46565
 Seq. No.
                    jC-gmro02910022b10d1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g4490317
 BLAST score
                    152
 E value
                    7.0e-10
```

Match length 72 % identity 44

(AL035678) putative protein [Arabidopsis thaliana] NCBI Description

46566 Seq. No.

Seq. ID jC-gmro02910022b11d1

Method BLASTN



NCBI GI g3789951 BLAST score 149 E value 4.0e-78 Match length 205 % identity 93

NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 46567

Seq. ID jC-gmro02910022c03d1

Method BLASTX
NCBI GI g4539660
BLAST score 193
E value 1.0e-14
Match length 76
% identity 54

NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 46568

Seq. ID jC-gmro02910022c04d1

Method BLASTN

NCBI GI g2981206

BLAST score 379

E value 0.0e+00

Match length 391

% identity 99

NCBI Description Zea mays photosystem I complex PsaH subunit precursor

(psaH) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Seq. No. 46569

Seq. ID jC-gmro02910022c08d1

Method BLASTN
NCBI GI g666053
BLAST score 279
E value 1.0e-156
Match length 395
% identity 93

NCBI Description H.vulgare mRNA for photosysteme I antenna protein

Seq. No. 46570

Seq. ID jC-gmro02910022c10d1

Method BLASTN
NCBI GI g3777601
BLAST score 254
E value 1.0e-141
Match length 430
% identity 90

NCBI Description Oryza sativa clone LS195 50S ribosomal protein L10 (rpl10)

mRNA, nuclear gene encoding chloroplast protein, complete

cds

Seq. No. 46571

Seq. ID jC-gmro02910022c12d1

Method BLASTN NCBI GI g312289



```
BLAST score
                  7.0e-49
E value
Match length
                  116
                  97
% identity
NCBI Description O.sativa short highly repeated, interspersed DNA
                  46572
Seq. No.
                  jC-gmro02910022d01d1
Seq. ID
                  BLASTX
Method
                   g2494264
NCBI GI
                   360
BLAST score
                   3.0e - 34
E value
                   159
Match length
                   46
% identity
                   HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105
NCBI Description
                   >gi_1651837_dbj_BAA16764_ (D90900) elongation factor EF-G
                   [Synechocystis sp.]
                   46573
Seq. No.
                   jC-gmro02910022d02d1
Seq. ID
                   BLASTX
Method
                   g3953471
NCBI GI
BLAST score
                   442
                   7.0e-44
E value
                   111
Match length
                   67
% identity
                  (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                   46574
Seq. No.
                   jC-gmro02910022d06d1
Seq. ID
                   BLASTN
Method
                   q296203
NCBI GI
                   93
BLAST score
                   7.0e-45
E value
                   173
Match length
                   92
% identity
NCBI Description P. miliaceum mRNA for alanine aminotransferase
                   46575
 Seq. No.
                   jC-gmro02910022d09d1
 Seq. ID
                   BLASTN
Method
                   g173246
 NCBI GI
 BLAST score
                   46
                   1.0e-16
 E value
                   74
 Match length
                   91
 % identity
 NCBI Description Yarrowia lipolytica autonomously replicating sequence 68
                    and centromere
                    46576
 Seq. No.
                    jC-gmro02910022d10d1
 Seq. ID
                    BLASTN
 Method
                    g19090
 NCBI GI
                    187
 BLAST score
                    1.0e-101
 E value
```

7503

293

93

Match length

% identity



NCBI Description H.vulgare PsaG mRNA

Seq. No. Seq. ID 46577

jC-gmro02910022d12a1

BLASTX Method NCBI GI g2224911 BLAST score 191 E value 5.0e-15 Match length 73 % identity 53

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

46578 Seq. No.

jC-gmro02910022e03d1 Seq. ID

Method BLASTX NCBI GI g3095111 BLAST score 157 2.0e-10 E value Match length 108 % identity 39

(AF051894) 15 kDa selenoprotein [Homo sapiens] NCBI Description

46579 Seq. No.

Seq. ID jC-gmro02910022e08d1

Method BLASTX NCBI GI g1542941 BLAST score 611 1.0e-63 E value Match length 151

% identity 74

NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

46580 Seq. No.

jC-gmro02910022e10d1 Seq. ID

Method BLASTX NCBI GI q585421 300 BLAST score 2.0e-27 E value Match length 102 % identity 57

LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir__JQ2391 NCBI Description

lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana >gi 431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No. 46581

Seq. ID jC-gmro02910022e11d1

Method BLASTX NCBI GI g4263712 BLAST score 450 E value 1.0e-44 Match length 116 % identity

(AC006223) putative ribosomal protein S12 [Arabidopsis NCBI Description

thaliana]

Seq. No. 46582



```
jC-gmro02910022e12d1
Seq. ID
                  BLASTN
Method
                  q295500
NCBI GI
BLAST score
                  46
                  1.0e-16
E value
Match length
                  82
% identity
                  89
                  Triticum aestivum heat shock protein 16.9C (hsp16.9C) mRNA,
NCBI Description
                  3' end
                  46583
Seq. No.
                  jC-gmro02910022f01d1
Seq. ID
                  BLASTN
Method
                  g3290003
NCBI GI
BLAST score
                  460
E value
                  0.0e + 00
Match length
                  504
% identity
                  97
                  Zea mays pathogenesis related protein-1 (PR-1) mRNA,
NCBI Description
                  complete cds
                  46584
Seq. No.
                  jC-gmro02910022f02d1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2182266
BLAST score
                  61
E value
                  1.0e-25
                  125
Match length
                  87
% identity
NCBI Description Hordeum vulgare lipoxygenase (LoxB) mRNA, complete cds
                  46585
Seq. No.
                  jC-gmro02910022f06d1
Seq. ID
Method
                  BLASTX
                  q3914667
NCBI GI
BLAST score
                  372
E value
                  9.0e-36
Match length
                  84
% identity
                  85
                  50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 2459427 (AC002332) putative chloroplast 50S ribosomal
                  protein L28 [Arabidopsis thaliana]
                   46586
Seq. No.
                   jC-gmro02910022f12d1
Seq. ID
                   BLASTN
Method
                   g22451
NCBI GI
                   206
BLAST score
                   1.0e-112
E value
                   238
Match length
                   96
% identity
                  Z.mays pyruvate, orthophosphate dikinase (PPDK1) gene, 3'
NCBI Description
```

end

Seq. No. 46587

Seq. ID jC-gmro02910022g03d1

Method BLASTN



```
q2895780
NCBI GI
BLAST score
                  178
E value
                  1.0e-95
                  273
Match length
                  92
% identity
                  Zea mays nitrate-induced NOI protein mRNA, complete cds
NCBI Description
Seq. No.
                  jC-gmro02910022g06d1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4559292
                  368
BLAST score
                  2.0e-35
E value
                  106
Match length
                  66
% identity
                  (AF124148) trehalase 1 GMTRE1 [Glycine max]
NCBI Description
                  46589
Seq. No.
                  jC-gmro02910022g07d1
Seq. ID
                  BLASTN
Method
                  q2274987
NCBI GI
                  190
BLAST score
E value
                  1.0e-102
                  326
Match length
                  90
% identity
NCBI Description Hordeum vulgare mRNA for expressed sequence tag
                   46590
Seq. No.
                   jC-gmro02910022g09d1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4417286
                  149
BLAST score
E value
                   2.0e-09
                   62
Match length
% identity
NCBI Description (AC007019) putative shikimate kinase [Arabidopsis thaliana]
                   46591
Seq. No.
                   jC-gmro02910022g11d1
Seq. ID
                   BLASTN
Method
                   q3290005
NCBI GI
BLAST score
                   466
E value
                   0.0e + 00
Match length
                   528
                   97
% identity
NCBI Description Zea mays pathogenesis related protein-5 (PR-5) mRNA,
                   complete cds
Seq. No.
                   46592
                   jC-gmro02910022h01d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3386617
BLAST score
                   403
E value
                   2.0e-39
Match length
                   96
```

7506

NCBI Description (AC004665) putative cell division protein (ftsY)

80

% identity



[Arabidopsis thaliana]

```
46593
Seq. No.
                  jC-gmro02910022h06d1
Seq. ID
                  BLASTN
Method
                  q902526
NCBI GI
                  477
BLAST score
                  0.0e + 00
E value
Match length
                  485
                  100
% identity
                  Zea mays clone MubG7 ubiquitin fusion protein gene,
NCBI Description
                  complete cds
                   46594
Seq. No.
Seq. ID
                   jC-gmro02910022h11d1
Method
                  BLASTX
NCBI GI
                   q2104536
BLAST score
                  544
                   1.0e-55
E value
                   115
Match length
% identity
                   (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   46595
Seq. No.
                   jC-gmro02910022h12d1
Seq. ID
Method
                   BLASTX
                   g2623310
NCBI GI
BLAST score
                   200
E value
                   2.0e-15
                   144
Match length
                   43
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 3402721 (AC004261) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   46596
                   jC-gmro02910023a03a1
Seq. ID
                   BLASTX
Method
                   g3540180
NCBI GI
BLAST score
                   186
                   9.0e-14
E value
Match length
                   50
% identity
                   68
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   46597
Seq. No.
                   jC-gmro02910023a06d1
Seq. ID
                   BLASTX
Method
                   g2833460
NCBI GI
BLAST score
                   361
                   2.0e-34
E value
                   152
Match length
% identity
                   48
NCBI Description RIBOFLAVIN-SPECIFIC DEAMINASE >gi 1001153 dbj BAA10295
                   (D64001) riboflavin biosynthesis protein [Synechocystis
```

sp.]



105

53

Match length % identity

NCBI Description

```
46598
Seq. No.
Seq. ID
                  jC-gmro02910023a11d1
Method
                  BLASTX
NCBI GI
                  q3688177
BLAST score
                  251
                  2.0e-21
E value
                  75
Match length
% identity
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                  46599
Seq. No.
                  jC-gmro02910023e03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q100226
BLAST score
                  146
                  4.0e-09
E value
Match length
                  72
% identity
                  hypothetical protein - tomato >gi_19275_emb_CAA78112_
NCBI Description
                  (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi_445619_prf__1909366A Leu zipper protein
                  [Lycopersicon esculentum]
                  46600
Seq. No.
Seq. ID
                  jC-gmro02910023e12a1
Method
                  BLASTX
                  q2497964
NCBI GI
BLAST score
                  214
E value
                  4.0e-17
Match length
                  49
                  86
% identity
                  MOLYBDOPTERIN BIOSYNTHESIS CNX3 PROTEIN (MOLYBDENUM
NCBI Description
                  COFACTOR BIOSYNTHESIS ENZYME CNX3) >gi_662873_emb_CAA88106_
                   (Z48046) Cnx3 [Arabidopsis thaliana]
Seq. No.
                   46601
                   jC-gmro02910023f05a1
Seq. ID
                  BLASTX
Method
                   g2911077
NCBI GI
BLAST score
                   142
                   6.0e-09
E value
Match length
                   61
                   49
% identity
                   (AL021960) gibberellin 20-oxidase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   46602
Seq. No.
                   jC-gmro02910023g02d1
Seq. ID
                   BLASTX
Method
                   g3540180
NCBI GI
BLAST score
                   308
E value
                   5.0e-28
```

(AC004122) Unknown protein [Arabidopsis thaliana]



Seq. No. 46603

Seq. ID jC-gmro02910023h02d1

Method BLASTX
NCBI GI g1730796
BLAST score 363
E value 1.0e-34
Match length 135
% identity 56

NCBI Description HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION >gi 2132760 pir S60964 probable membrane protein

YNL163c - yeast (Saccharomyces cerevisiae)

>gi_1050790 emb_CAA63276_ (X92517) N1718 [Saccharomyces
cerevisiae] >gi_1302132_emb_CAA96050_ (Z71439) ORF YNL163c

[Saccharomyces cerevisiae]

Seq. No. 46604

Seq. ID jC-gmro02910024a10d1

Method BLASTX
NCBI GI 94249409
BLAST score 324
E value 3.0e-30
Match length 93
% identity 65

NCBI Description (AC006072) putative sugar transporter [Arabidopsis

thaliana]

Seq. No. 46605

Seq. ID jC-gmro02910024e06a1

Method BLASTX
NCBI GI g2911067
BLAST score 409
E value 6.0e-40
Match length 123
% identity 69

NCBI Description (AL021960) UV-damaged DNA-binding protein-like

[Arabidopsis thaliana]

Seq. No. 46606

Seq. ID jC-gmro02910024h06a1

Method BLASTX
NCBI GI g132935
BLAST score 176
E value 1.0e-12
Match length 58
% identity 57

NCBI Description 60S RIBOSOMAL PROTEIN L37A (YL37) (RP47)

>gi_101568_pir__S18431 ribosomal protein L35a.e.c16 - yeast
(Saccharomyces cerevisiae) >gi_4392_emb_CAA41035_ (X57969)

ribosomal protein L37a [Saccharomyces cerevisiae] >gi_1244773 (U43703) Lpi4p [Saccharomyces cerevisiae]

>gi_1370305_emb_CAA97847_ (Z73499) ORF YPL143w

[Saccharomyces cerevisiae]

Seq. No. 46607

Seq. ID jC-gmro02910024h07a1

Method BLASTX NCBI GI g2078350



53

thaliana]

% identity

NCBI Description

```
BLAST score
                  2.0e-49
E value
                  108
Match length
% identity
                  86
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
                  46608
Seq. No.
                  jC-gmro02910025c06a1
Seq. ID
                  BLASTX
Method
                  g3077640
NCBI GI
                  233
BLAST score
                  2.0e-19
E value
                  57
Match length
                  75
% identity
                  (AJ223151) O-methyltransferase [Prunus dulcis]
NCBI Description
                  46609
Seq. No.
                  jC-gmro02910025e01d1
Seq. ID
                  BLASTX
Method
                  g3135253
NCBI GI
BLAST score
                  167
                  9.0e-12
E value
Match length
                  97
                  37
% identity
                  (AC003058) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  46610
                  jC-gmro02910025g05a1
Seq. ID
                  BLASTX
Method
                  g2746335
NCBI GI
BLAST score
                  173
                  2.0e-12
E value
                  64
Match length
                  41
% identity
                  (AF037205) RING zinc finger protein [Mus musculus]
NCBI Description
                  46611
Seq. No.
                   jC-gmro02910025g10d1
Seq. ID
                  BLASTN
Method
                  g4098966
NCBI GI
                   39
BLAST score
                  1.0e-12
E value
                  103
Match length
                  84
% identity
                  Glycine max putative reistance gene analog genomic sequence
NCBI Description
                   46612
Seq. No.
                   jC-gmro02910025h11a1
Seq. ID
Method
                   BLASTX
                   g3135253
NCBI GI
BLAST score
                   328
                   1.0e-30
E value
Match length
                   120
```

7510

(AC003058) putative receptor protein kinase [Arabidopsis



```
46613
Seq. No.
Seq. ID
                  jC-gmro02910025h11d1
Method
                  BLASTX
NCBI GI
                  g3176723
BLAST score
                  157
                   6.0e-11
E value
Match length
                   63
% identity
                  (AC002392) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   46614
Seq. No.
                   jC-gmro02910026a06d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1935019
BLAST score
                   302
E value
                   2.0e-27
Match length
                   95
% identity
                  (Z93774) sucrose transport protein [Vicia faba]
NCBI Description
                   46615
Seq. No.
Seq. ID
                   jC-gmro02910026e07a1
                   BLASTN
Method
NCBI GI
                   q1196896
BLAST score
                   82
E value
                   1.0e-38
                   182
Match length
% identity
NCBI Description Glycine max acidic ribosomal protein PO mRNA, complete cds
                   46616
Seq. No.
                   jC-gmro02910026e09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3776573
BLAST score
                   194
E value
                   6.0e-15
Match length
                   54
% identity
                   (AC005388) Similar to nodulins and lipase homolog F14J9.5
NCBI Description
                   gi_3482914 from Arabidopsis thaliana BAC gb AC003970.
                   Alternate first exon from 72258 to 72509. [Arabidopsis
                   thaliana]
Seq. No.
                   46617
                   jC-gmro02910026f01a1
Seq. ID
                   BLASTX
Method
                   g1931651
NCBI GI
BLAST score
                   222
                   4.0e-18
E value
                   54
Match length
                   78
% identity
                  (U95973) membrane-associated salt-inducible protein isolog
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 46618

Seq. ID jC-gmro02910026g03d1



```
BLASTX
Method
                  g2827143
NCBI GI
BLAST score
                  344
E value
                  5.0e-40
Match length
                  153
% identity
                  63
                  (AF027174) cellulose synthase catalytic subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  46619
                  jC-gmro02910026g05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539335
BLAST score
                  190
E value
                  3.0e-14
Match length
                  53
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                  46620
Seq. No.
                  jC-qmro02910026h07a1
Seq. ID
```

Method BLASTX g2104529 NCBI GI BLAST score 194 7.0e-15 E value 67 Match length % identity

(AF001308) putative hexose transporter [Arabidopsis NCBI Description

thaliana]

46621 Seq. No. Seq. ID jC-qmro02910027c05a1 Method BLASTX

NCBI GI q3341681 BLAST score 195 E value 7.0e-15 Match length 105 % identity 50

(AC003672) small GTP-binding protein [Arabidopsis thaliana] NCBI Description

>gi_741994_prf__2008312A GTP-binding protein [Arabidopsis

thaliana]

Seq. No. 46622

jC-qmro02910027e01d1 Seq. ID

Method BLASTN g2055229 NCBI GI BLAST score 98 8.0e-48 E value 277 Match length 92 % identity

Soybean mRNA for SRC2, complete cds NCBI Description

Seq. No. 46623

jC-gmro02910027e02d1 Seq. ID

BLASTX Method g2642154 NCBI GI BLAST score 216



E value 2.0e-17 Match length 78 % identity 46

NCBI Description (AC003000) unknown protein [Arabidopsis thaliana] >gi 3790595 (AF079186) RING-H2 finger protein RHC2a

[Arabidopsis thaliana]

Seq. No. 46624

Seq. ID jC-gmro02910029f12d1

Method BLASTX
NCBI GI g2920706
BLAST score 298
E value 5.0e-27
Match length 127
% identity 46

NCBI Description (Y13568) beta-xylosidase [Emericella nidulans]

Seq. No. 46625

Seq. ID jC-gmro02910030f01d1

Method BLASTX
NCBI GI g3805956
BLAST score 252
E value 1.0e-21
Match length 44
% identity 93

NCBI Description (Y13769) laccase [Populus balsamifera subsp. trichocarpa]

Seq. No. 46626

Seq. ID jC-gmro02910030g08a1

Method BLASTX
NCBI GI g3377824
BLAST score 131
E value 9.0e-10
Match length 118
% identity 32

NCBI Description (AF075598) contains similarity to reverse transcriptases

[Arabidopsis thaliana]

Seq. No. 46627

Seq. ID jC-gmro02910031a02a1

Method BLASTX
NCBI GI g1350680
BLAST score 280
E value 4.0e-25
Match length 86
% identity 63

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 46628

Seq. ID jC-gmro02910031a05d1

Method BLASTX
NCBI GI g2464905
BLAST score 299
E value 4.0e-27
Match length 65
% identity 85

NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]



```
46629
Seq. No.
Seq. ID
                  jC-qmro02910031f03a1
                  BLASTX
Method
NCBI GI
                  q541943
BLAST score
                  152
                   3.0e-14
E value
                   58
Match length
                   52
% identity
                  metallothionein - soybean >gi_228682_prf__1808316A
NCBI Description
                  metallothionein-like protein [Glycine max]
                   46630
Seq. No.
Seq. ID
                   jC-gmro02910032b04a1
                   BLASTX
Method
NCBI GI
                   g3892722
BLAST score
                   141
E value
                   9.0e-09
                   45
Match length
                   62
% identity
                  (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                   46631
Seq. No.
                   jC-gmro02910032c01d1
Seq. ID
                   BLASTX
Method
                   q2828296
NCBI GI
BLAST score
                   889
                   4.0e-96
E value
                   184
Match length
% identity
                   56
                  (AL021687) RNase L inhibitor [Arabidopsis thaliana]
NCBI Description
                   46632
Seq. No.
                   jC-gmro02910032d01d1
Seq. ID
                   BLASTN
Method
                   g405634
NCBI GI
BLAST score
                   382
                   0.0e+00
E value
                   414
Match length
                   98
% identity
NCBI Description Z.mays zmcpt mRNA triose phosphate/phosphate translocator
Seq. No.
                   46633
                   jC-gmro02910032d07a1
Seq. ID
                   BLASTX
Method
                   g4107099
NCBI GI
                   306
BLAST score
                   7.0e-28
E value
                   103
Match length
                   53
% identity
NCBI Description
                  (AB015141) AHP1 [Arabidopsis thaliana]
                   >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                   thaliana]
```

Seq. ID jC-gmro02910032e01a1 Method BLASTX

Seq. No.

46634



g1173104 NCBI GI BLAST score 255 6.0e-22 E value 53 Match length % identity 77 RIBONUCLEASE 2 PRECURSOR >gi 289210 (M98336) ribonuclease NCBI Description [Arabidopsis thaliana] $>gi_2\overline{6}42160$ (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana] 46635 Seq. No. Seq. ID jC-gmro02910032g02d1 BLASTX Method g2880048 NCBI GI BLAST score 145 3.0e-09 E value Match length 34 % identity 74 (AC002340) unknown protein [Arabidopsis thaliana] NCBI Description 46636 Seq. No. Seq. ID jC-gmro02910032g10a1 Method BLASTX NCBI GI g4335772 BLAST score 295 1.0e-26 E value 138 Match length % identity (AC006284) unknown protein [Arabidopsis thaliana] NCBI Description 46637 Seq. No. jC-gmro02910034b05d1 Seq. ID Method BLASTX g1755186 NCBI GI 276 BLAST score 2.0e-24 E value Match length 81 % identity 67 (U75204) germin-like protein [Arabidopsis thaliana] NCBI Description 46638 Seq. No. jC-gmro02910034b07d1 Seq. ID BLASTN Method q2791947 NCBI GI BLAST score 81 1.0e-37 E value Match length 193 85 % identity NCBI Description Lupinus luteus mRNA for ribosomal protein L13a 46639 Seq. No. jC-gmro02910034d01d1 Seq. ID

Method BLASTX g3395432 NCBI GI 305 BLAST score 6.0e-28 E value Match length 73 % identity 78

NCBI Description

thaliana





```
(AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  46640
Seq. No.
Seq. ID
                  jC-qmro02910035a06d1
Method
                  BLASTX
NCBI GI
                  q4097555
BLAST score
                  151
                  1.0e-09
E value
Match length
                  43
                  60
% identity
                  (U64910) ATFP7 [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                  jC-gmro02910035d10d1
Method
                  BLASTX
NCBI GI
                  q3242785
BLAST score
                  285
E value
                  1.0e-25
Match length
                  124
                  52
% identity
                  (AF055355) respiratory burst oxidase protein C [Arabidopsis
NCBI Description
                  thaliana]
                   46642
Seq. No.
                   jC-gmro02910035h06d1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1488255
BLAST score
                   423
                   6.0e-42
E value
Match length
                   93
% identity
NCBI Description
                   (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
                   >gi_2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase
                   (FAH1) [Arabidopsis thaliana] >gi 3925365 (AF068574)
                   ferulate-5-hydroxylase [Arabidopsis thaliana]
Seq. No.
                   46643
                   jC-gmro02910035h12a1
Seq. ID
Method
                   BLASTX
                   q3831444
NCBI GI
BLAST score
                   739
                   1.0e-78
E value
Match length
                   165
% identity
                   82
                  (AC005819) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   46644
Seq. No.
                   jC-gmro02910036d05d1
Seq. ID
                   BLASTX
Method
                   g4038030
NCBI GI
BLAST score
                   158
                   8.0e-11
E value
Match length
                   59
% identity
                   44
```

(AC005936) putative protein kinase, 5' partial [Arabidopsis

Ú,



```
Seq. No.
                  jC-qmro02910036d07a1
Seq. ID
                  BLASTX
Method
                  g4218991
NCBI GI
BLAST score
                  423
E value
                  1.0e-41
                  138
Match length
% identity
                  (AF098632) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   jC-gmro02910036e05a1
Seq. ID
                   BLASTX
Method
                   q3176874
NCBI GI
                   336
BLAST score
                   1.0e-31
E value
Match length
                   114
                   61
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
                   46647
Seq. No.
                   jC-qmro02910037c01d1
Seq. ID
                   BLASTX
Method
                   g3688598
NCBI GI
                   270
BLAST score
E value
                   9.0e-24
                   63
Match length
                   79
% identity
                  (AB009029) Cycloartenol Synthase [Panax ginseng]
NCBI Description
                   46648
Seq. No.
                   jC-gmro02910037c12a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4572674
BLAST score
                   445
E value
                   3.0e-44
Match length
                   128
% identity
                  (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46649
Seq. No.
                   jC-gmro02910037d08a1
Seq. ID
                   BLASTN
Method
                   q3493646
NCBI GI
BLAST score
                   36
                   9.0e-11
E value
Match length
                   56
                   91
% identity
                   Pimpinella brachycarpa transcription activator (MADS1)
NCBI Description
                   mRNA, complete cds
 Seq. No.
                   46650
                   jC-gmro02910037d11a1
Seq. ID
```

130

BLASTX

366

g4204303

Method

NCBI GI BLAST score



5.0e-35 E value Match length 74 % identity (AC003027) 1cl prt seq No definition line found NCBI Description [Arabidopsis thaliana] 46651 Seq. No. Seq. ID jC-qmro02910037f08d1 BLASTX Method g2618701 NCBI GI BLAST score 174 2.0e-12 E value 60 Match length % identity (AC002510) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 46652 Seq. ID jC-gmro02910038b10a1 BLASTX Method g3881079 NCBI GI 183 BLAST score E value 1.0e-13 Match length 63 49 % identity (AL032657) cDNA EST yk207f6.5 comes from this gene; cDNA NCBI Description EST yk201f11.5 comes from this gene; cDNA EST yk207f6.3 comes from this gene [Caenorhabditis elegans] 46653 Seq. No. Seq. ID jC-gmro02910038h05a1 BLASTX Method q2493318 NCBI GI BLAST score 140 1.0e-08 E value 73 Match length % identity 42 BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ NCBI Description (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum] 46654 Seq. No. Seq. ID jC-qmro02910039a09d1 Method BLASTN NCBI GI q310575 BLAST score 127 3.0e-65 E value Match length 170 96 % identity NCBI Description Glycine max nodulin-26 mRNA, complete cds 46655 Seq. No.

jC-gmro02910039b08a1 Seq. ID

Method BLASTN q1184986 NCBI GI BLAST score 34 2.0e-09 E value 70 Match length



```
% identity
                  Nicotiana tabacum GTP-binding protein NTGB1 mRNA, partial
NCBI Description
                  46656
Seq. No.
Seq. ID
                  jC-gmro02910039c02d1
                  BLASTN
Method
                  q303900
NCBI GI-
                  151
BLAST score
                  2.0e-79
E value
                  251
Match length
                  77
% identity
NCBI Description Soybean gene for ubiquitin, complete cds
                  46657
Seq. No.
                   jC-gmro02910039d03d1
Seq. ID
                  BLASTN
Method
                  g3452136
NCBI GI
BLAST score
                   220
                   1.0e-120
E value
                   252
Match length
                   98
% identity
NCBI Description Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
                  partial
                   46658
Seq. No.
                   jC-gmro02910039d07d1
Seq. ID
                   BLASTX
Method
                   g2232254
NCBI GI
                   336
BLAST score
                   2.0e-31
E value
                   77
Match length
% identity
NCBI Description (AF005237) old-yellow-enzyme homolog [Catharanthus roseus]
Seq. No.
                   jC-gmro02910039d08a1
Seq. ID
                   BLASTX
Method
                   q3935168
NCBI GI
BLAST score
                   162
                   3.0e-11
E value
Match length
                   66
% identity
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]
                   46660
Seq. No.
                   jC-qmro02910039e12d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2660676
BLAST score
                   164
                   2.0e-11
E value
Match length
                   52
% identity
                   (AC002342) Dreg-2 like protein [Arabidopsis thaliana]
NCBI Description
```

46661

jC-gmro02910039g04a1

Seq. No.

Seq. ID



```
BLASTX
Method
                  g4455232
NCBI GI
                  453
BLAST score
                  2.0e-45
E value
                  106
Match length
                  74
% identity
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                  46662
Seq. No.
                  jC-gmro02910039h02d1
Seq. ID
                  BLASTX
Method
                  q4572676
NCBI GI
                  162
BLAST score
                  5.0e-11
E value
                  80
Match length
                   40
% identity
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
                   46663
Seq. No.
                   jC-gmro02910040b10a1
Seq. ID
                  BLASTX
Method
                   g3128199
NCBI GI
                  155
BLAST score
                   2.0e-10
E value
                   55
Match length
                   56
% identity
NCBI Description (AC004521) putative proteinase [Arabidopsis thaliana]
Seq. No.
                   46664
                   jC-gmro02910040e05a1
Seq. ID
                   BLASTX
Method
                   g4522009
NCBI GI
                   163
BLAST score
                   4.0e-16
E value
                   99
Match length
                   51
% identity
NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]
                   46665
Seq. No.
Seq. ID
                   jC-gmro02910040e08a1
                   BLASTX
Method
NCBI GI
                   q2781347
BLAST score
                   447
E value
                   2.0e-44
                   135
Match length
% identity
NCBI Description (AC003113) F2401.3 [Arabidopsis thaliana]
Seq. No.
                   46666
Seq. ID
                   jC-gmro02910040f07a1
Method
                   BLASTN
NCBI GI
                   g1431628
BLAST score
                   98
E value
                   1.0e-47
Match length
                   306
```

83

NCBI Description V.radiata mRNA for pectinacetylesterase

% identity



ţ.

```
46667
Seq. No.
                  jC-gmro02910040f07d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1431629
                  206
BLAST score
                  3.0e-16
E value
Match length
                  52
% identity
                  (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                  46668
Seq. No.
                  jC-gmro02910041005a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539383
BLAST score
                  144
E value
                  6.0e-09
Match length
                  50
% identity
                  (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  46669
                  jC-gmrc02910041061a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201554
BLAST score
                  532
E value
                  2.0e-54
Match length
                  135
% identity
                  74
                  (AJ006501) beta-D-glucosidase [Tropaeolum majus]
NCBI Description
                  46670
Seq. No.
                  jC-gmro02910041075a1
Seq. ID
                  BLASTX
Method
                  g3142303
NCBI GI
BLAST score
                  186
                  6.0e-14
E value
Match length
                  105
% identity
                  41
NCBI Description
                  (AC002411) Strong similarity to MRP-like ABC transporter
                  gb U92650 from A. thaliana and canalicular multi-drug
                  resistance protein gb_L49379 from Rattus norvegicus.
                  [Arabidopsis thaliana]
                  46671
Seq. No.
```

jC-gmro02910041076a1 Seq. ID

BLASTN Method g18644 NCBI GI BLAST score 358 E value 0.0e+00Match length 362 100 % identity

NCBI Description Soybean mRNA for HMG-1 like protein

46672 Seq. No.

jC-gmro02910043a12d1 Seq. ID



```
Method
NCBI GI
                  g2352812
BLAST score
                   180
                   3.0e-13
E value
Match length
                  75
% identity
                   53
                  (AF008597) desacetoxyvindoline-4-hydroxylase [Catharanthus
NCBI Description
                   46673
Seq. No.
Seq. ID
                   jC-qmro02910046b09a1
                  BLASTN
Method
                   g169127
NCBI GI
BLAST score
                   59
                   2.0e-24
E value
Match length
                   199
% identity
                   87
                  Pisum sativum (clone pCLp) nuclear encoded precursor to
NCBI Description
                   chloroplast protein mRNA, complete cds
                   46674
Seq. No.
Seq. ID
                   jC-qmro02910046b09d1
                   BLASTX
Method
                   g461753
NCBI GI
                   234
BLAST score
                   1.0e-19
E value
Match length
                   63
                   75
% identity
                  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                   PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB
                   proteinase regulatory chain homolog precursor, chloroplast
                   - garden pea >gi_169128 (L09547) nuclear encoded precursor
                   to chloroplast protein [Pisum sativum]
                   46675
Seq. No.
Seq. ID
                   jC-gmro02910046b10a1
Method
                   BLASTN
NCBI GI
                   g347454
BLAST score
                   76
E value
                   4.0e-35
Match length
                   136
% identity
                   90
                   Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'
NCBI Description
                   46676
Seq. No.
                   jC-qmro02910046c04d1
Seq. ID
Method
                   BLASTX
                   g3395440
NCBI GI
```

BLAST score 178 7.0e-13 E value 70 Match length % identity

(AC004683) hypothetical protein [Arabidopsis thaliana] NCBI Description

46677 Seq. No.

jC-gmro02910046d03d1 Seq. ID



```
BLASTN
Method
                  g439616
NCBI GI
BLAST score
                  249
É value
                  1.0e-138
Match length
                  453
% identity
                  97
NCBI Description Soybean G protein alpha subunit mRNA, complete cds
                  46678
Seq. No.
Seq. ID
                  jC-gmro02910046d05d1
Method
                  BLASTX
NCBI GI
                  g2982455
BLAST score
                  181
                  3.0e-13
E value
                   40
Match length
% identity
                  (AL022223) putative uracil phosphoribosyl transferase
NCBI Description
                   [Arabidopsis thaliana]
                   46679
Seq. No.
Seq. ID
                   jC-qmro02910046e05d1
Method
                  BLASTX
NCBI GI
                   q3395441
BLAST score
                   177
                   8.0e-13
E value
Match length
                   41
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46680
                   jC-gmro02910046g01a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4206765
BLAST score
                   213
E value
                   5.0e-17
Match length
                   86
% identity
                  (AF104329) putative type 1 membrane protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   46681
Seq. ID
                   jC-qmro02910046h11d1
Method
                   BLASTX
NCBI GI
                   g3395440
BLAST score
                   167
E value
                   1.0e-11
Match length
                   93
% identity
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
                   46682
Seq. No.
                   jC-gmro02910047a04d1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2626742
BLAST score
                   111
```

1.0e-55

259

E value Match length



% identity 85

NCBI Description Glycine max mRNA for phosphoenolpyruvate carboxylase,

complete cds, clone: GmPEPC7

Seq. No. 46683

Seq. ID jC-gmro02910047a05a1

Method BLASTX
NCBI GI g3176711
BLAST score 241
E value 3.0e-20
Match length 79
% identity 65

NCBI Description (AC002392) bZIP-like protein [Arabidopsis thaliana]

Seq. No. 46684

Seq. ID jC-gmro02910047g01a1

Method BLASTN
NCBI GI g527624
BLAST score 45
E value 4.0e-16
Match length 137
% identity 83

NCBI Description Arabidopsis thaliana clone HAT14 homeobox protein mRNA,

partial cds

Seq. No. 46685

Seq. ID jC-gmro02910047g09a1

Method BLASTN
NCBI GI g166411
BLAST score 224
E value 1.0e-123
Match length 416
% identity 88

NCBI Description Medicago sativa NADH-glutamate synthase mRNA, comlete cds

Seq. No. 46686

Seq. ID jC-gmro02910048c03a1

Method BLASTN
NCBI GI 9497233
BLAST score 258
E value 1.0e-143
Match length 274
% identity 99

NCBI Description Glycine max 3-methylcrotonyl-CoA carboxylase precursor

gene, biotin- carboxylase domain, partial cds

Seq. No. 46687

Seq. ID jC-gmro02910048d02d1

Method BLASTN
NCBI GI g1336081
BLAST score 113
E value 8.0e-57
Match length 230
% identity 87

NCBI Description Glycine max var. Century ascorbate peroxidase 2 (APx2)

mRNA, complete cds



```
Seq. No.
                  jC-gmro02910048d04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351073
BLAST score
                  41
E value
                  9.0e-14
                  61
Match length
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MYJ24, complete sequence [Arabidopsis thaliana]
                  46689
Seq. No.
                  jC-gmro02910048h06d1
Seq. ID
Method
                  BLASTX
                  q1742883
NCBI GI
BLAST score
                  152
E value
                  7.0e-10
Match length
                  79
% identity
                  (D90820) 2-dehydro-3-deoxygluconokinase (EC 2.7.1.45)
NCBI Description
                   (2-keto-3- Deoxygluconokinase) (3-deoxy-2-oxo-d-gluconate
                  kinase) (Kdg kinase). [Escherichia coli]
                  >qi 1742891 dbj BAA15570_ (D90821)
                  2-dehydro-3-deoxygluconokinase (EC 2.7.1.45) (2-keto-3-
                   Deoxygluconokinase) (3-deoxy-2-oxo-d-gluconate kinase) (Kdg
                   kinase). [Escherichia coli] >gi_1788071 (AE000272) putative
                  kinase [Escherichia coli]
                   46690
Seq. No.
                   jC-qmro02910049a03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4559334
BLAST score
                   332
                   4.0e-31
E value
Match length
                   85
% identity
                  (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46691
                   jC-gmro02910049c04a1
Seq. ID
Method
                   BLASTN
                   g3005575
NCBI GI
BLAST score
                   85
                   1.0e-40
E value
                   113
Match length
% identity
                   94
                  Glycine max putative high affinity nitrate transporter
NCBI Description
                   (NRT2) mRNA, complete cds
                   46692
Seq. No.
                   jC-gmro02910049e05a1
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g2129953
BLAST score 297
E value 4.0e-27
Match length 72
% identity 76



NCBI Description laccase (EC 1.10.3.2) - common tobacco >gi_1685087 (U43542) diphenol oxidase [Nicotiana tabacum]

Seq. No. 46693

Seq. ID jC-gmro02910049f02a1

Method BLASTX
NCBI GI g3914801
BLAST score 274
E value 2.0e-24
Match length 108
% identity 46

% identity 46
NCBI Description DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA

POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT) >gi 2739048 (AF025424) RNA polymerase I 127 kDa

subunit [Rattus norvegicus]

Seq. No. 46694

Seq. ID jC-gmro02910049f04a1

Method BLASTX
NCBI GI g3834303
BLAST score 356
E value 6.0e-34
Match length 118
% identity 62

NCBI Description (AC005679) F9K20.3 [Arabidopsis thaliana]

Seq. No. 46695

Seq. ID jC-gmro02910049f05a1

Method BLASTN
NCBI GI g310577
BLAST score 209
E value 1.0e-114
Match length 309
% identity 92

NCBI Description Glycine max nodulin-26 mRNA, complete cds

Seq. No. 46696

Seq. ID jC-gmro02910050h12d1

Method BLASTN
NCBI GI g3005575
BLAST score 123
E value 7.0e-63
Match length 155
% identity 95

NCBI Description Glycine max putative high affinity nitrate transporter

(NRT2) mRNA, complete cds

Seq. No. 46697

Seq. ID jC-gmro02910051a09a1

Method BLASTN
NCBI GI g3982595
BLAST score 287
E value 1.0e-160
Match length 389
% identity 93

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds



```
Seq. No.
                  jC-qmro02910051a10d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3021280
BLAST score
                  234
E value
                  1.0e-19
                  102
Match length
                  43
% identity
                   (AL022347) serine /threonine kinase - like protein -
NCBI Description
                   [Arabidopsis thaliana]
                  46699
Seq. No.
Seq. ID
                  jC-gmro02910051a12a1
Method
                  BLASTX
NCBI GI
                  g2129613
BLAST score
                  470
E value
                   3.0e-47
Match length
                  136
% identity
                   62
                  homeotic protein BEL1 - Arabidopsis thaliana >gi 1122533
NCBI Description
                   (U39944) BELL1 [Arabidopsis thaliana]
                   46700
Seq. No.
Seq. ID
                  jC-gmro02910051c03a1
Method
                  BLASTN
NCBI GI
                  q18764
BLAST score
                   308
                   1.0e-173
E value
Match length
                   412
% identity
                   94
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                   46701
Seq. No.
                   jC-gmro02910051d04a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3335377
BLAST score
                   207
                   3.0e-16
E value
Match length
                  74
                   57
% identity
                   (AC003028) putative cytoskeletal protein [Arabidopsis
NCBI Description
                   thaliana] >gi_3395442 (AC004683) putative cytoskeletal
                  protein [Arabidopsis thaliana]
                   46702
Seq. No.
                   jC-gmro02910051d04d1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3395421
```

BLAST score 33 E value 7.0e-09 Match length 37 % identity 97

Arabidopsis thaliana chromosome II BAC T19C21 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 46703

Seq. ID jC-gmro02910051h07a1



```
Method
                   BLASTX
NCBI GI
                   g3738297
BLAST score
                   237
E value
                   7.0e-20
Match length
                   76
% identity
                   25
```

(AC005309) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

46704

Seq. ID jC-gmro02910052a04a1

Method BLASTN NCBI GI g609224 BLAST score 105 E value 5.0e-52 Match length 229 % identity

P.sativum mRNA for SAMS-2 >qi 609558 qb L36681 PEADENSYNB NCBI Description

Pisum sativum S-adenosylmethionine synthase mRNA, complete

Seq. No.

46705

jC-gmro02910052a09a1 Seq. ID

Method BLASTN NCBI GI g609224 BLAST score 182 E value 7.0e-98 Match length 318 % identity 89

NCBI Description P.sativum mRNA for SAMS-2 >gi 609558 gb L36681 PEADENSYNB

Pisum sativum S-adenosylmethionine synthase mRNA, complete

cds

Seq. No.

46706

jC-gmro02910052b02a1 Seq. ID

Method BLASTX NCBI GI g3183368 BLAST score 172 3.0e-12 E value Match length 108 % identity 45

HYPOTHETICAL 64.0 KD PROTEIN C20G4.05C IN CHROMOSOME I NCBI Description

>gi 2330761 emb CAB11255 (Z98600) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 46707

Seq. ID jC-gmro02910052g08a1

Method BLASTX g3395428 NCBI GI BLAST score 166 E value 2.0e-11 Match length 52 % identity 63

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 46708

jC-gmro02910054a06d1 Seq. ID

Method BLASTX



```
g1931652
NCBI GI
                  204
BLAST score
                  3.0e-16
E value
Match length
                  57
% identity
                  67
                  (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  46709
Seq. ID
                  jC-gmro02910054d03d1
Method
                  BLASTN
                  g2245682
NCBI GI
BLAST score
                  69
E value
                  2.0e-30
Match length
                  112
% identity
                  95
NCBI Description Glycine max peroxidase precursor (GMIPER1) mRNA, complete
```

Seq. No. 46710 jC-qmro02910054f12a1 Seq. ID Method BLASTN g493019 NCBI GI BLAST score 136

E value 2.0e-70 Match length 140 % identity 99

NCBI Description Glycine max delta-aminolevulinic acid dehydratase (Alad)

mRNA, complete cds

Seq. No. 46711

jC-gmro02910054g11d1 Seq. ID

Method BLASTN NCBI GI g780266 BLAST score 71 E value 1.0e-31

Match length 213 % identity 86

NCBI Description M.sativa mRNA for B-like cyclin

Seq. No.

46712

Seq. ID jC-gmro02910054h03d1

Method BLASTX g4107480 NCBI GI BLAST score 172 E value 3.0e-12 Match length 54 36 % identity

NCBI Description (AL035085) putative mitochondrial carrier protein

[Schizosaccharomyces pombe]

Seq. No. 46713

Seq. ID jC-gmro02910055g01a1

Method BLASTX NCBI GI q2462911 BLAST score 495 E value 5.0e-50



```
Match length
% identity
                  57
                  (Z83832) UDP-glucose:sterol glucosyltransferase [Avena
NCBI Description
Seq. No.
                  46714
Seq. ID
                  jC-gmro02910056c08a1
                  BLASTX
Method
                  q4539350
NCBI GI
                  457
BLAST score
E value
                  9.0e-46
                  99
Match length
% identity
                  (AL035539) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                  46715
Seq. No.
Seq. ID
                  jC-qmro02910056d09a1
Method
                  BLASTX
                  q2809232
NCBI GI
                  218
BLAST score
                  4.0e-18
E value
Match length
                  79
% identity
                  56
                  (AC002560) F21B7.1 [Arabidopsis thaliana]
NCBI Description
                  46716
Seq. No.
Seq. ID
                  jC-qmro02910056g05a1
                  BLASTX
Method
                  g1817584
NCBI GI
BLAST score
                  179
                  4.0e-13
E value
Match length
                  83
% identity
NCBI Description
                  (Y08991) adaptor protein [Homo sapiens]
                  46717
Seq. No.
                  jC-gmro02910056g09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076318
BLAST score
                  306
E value
                  1.0e-28
Match length
                  78
% identity
                  dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)
NCBI Description
                  precursor - Arabidopsis thaliana (fragment)
                  >qi 559395 emb CAA86300 (Z46230) dihydrolipoamide
                  acetyltransferase (E2) subunit of PDC [Arabidopsis
                  thaliana]
                  46718
Seq. No.
                  jC-gmro02910057a02a1
Seq. ID
                  BLASTX
Method
                  g4567235
NCBI GI
BLAST score
                  179
```

7530

4.0e-13

68

60

E value Match length

% identity



NCBI Description (AC007119) putative phosphatidylinositol/phophatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No. 46719

Seq. ID jC-gmro02910057b08a1

Method BLASTN
NCBI GI g310579
BLAST score 225
E value 1.0e-123
Match length 237
% identity 99

NCBI Description Glycine max protein kinase 2 (SPK-2) mRNA, complete cds

Seq. No. 46720

Seq. ID jC-gmro02910057d07a1

Method BLASTX
NCBI GI g3176686
BLAST score 495
E value 2.0e-50
Match length 104
% identity 84

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 46721

Seq. ID jC-gmro02910057e09a1

Method BLASTX
NCBI GI g2465529
BLAST score 617
E value 2.0e-64
Match length 133
% identity 87

NCBI Description (AF000355) phosphate transporter [Medicago truncatula]

Seq. No. 46722

Seq. ID jC-gmro02910057h03a1

Method BLASTN
NCBI GI g1752733
BLAST score 217
E value 1.0e-119
Match length 225
% identity 99

NCBI Description Glycine max mRNA for beta-glucan-elicitor receptor,

complete cds

Seq. No. 46723

Seq. ID jC-gmro02910057h09a1

Method BLASTX
NCBI GI g4567283
BLAST score 324
E value 4.0e-30
Match length 91
% identity 73

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 46724

Seq. ID

Method NCBI GI



```
jC-gmro02910060a05d1
Seq. ID
                  BLASTX
Method
                  g1396054
NCBI GI
BLAST score
                  216
                  2.0e-17
E value
Match length
                  57
% identity
                  67
                  (D86180) phosphoribosylanthranilate transferase [Pisum
NCBI Description
                  sativum]
                  46725
Seq. No.
                   jC-gmro02910060b04d1
Seq. ID
                  BLASTX
Method
                  g2493321
NCBI GI
BLAST score
                  262
                   5.0e-23
E value
Match length
                   57
                   81
% identity
                  L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO)
NCBI Description
                   >gi_2129952_pir__S66353 L-ascorbate oxidase (EC 1.10.3.3)
                  precursor - common tobacco >gi_599594 dbj_BAA07734
                   (D43624) ascorbate oxidase precursor [Nicotiana tabacum]
                   46726
Seq. No.
                   jC-gmro02910060q12a1
Seq. ID
                   BLASTN
Method
                   g18764
NCBI GI
BLAST score
                   351
                   0.0e+00
E value
Match length
                   363
% identity
                   99
                  G.max tefS1 gene for elongation factor EF-la
NCBI Description
                   46727
Seq. No.
Seq. ID
                   jC-gmro02910060h03d1
Method
                   BLASTN
NCBI GI
                   q4210834
BLAST score
                   36
E value
                   9.0e-11
Match length
                   52
% identity
                  Pisum sativum mRNA for ketol-acid reductoisomerase
NCBI Description
Seq. No.
                   46728
                   jC-gmro02910061b02d1
Seq. ID
                   BLASTN
Method
                   q167072
NCBI GI
BLAST score
                   116
                   2.0e-58
E value
Match length
                   215
% identity
                   89
NCBI Description
                  Barley ubiquitin (mub1) gene, complete cds
                   46729
Seq. No.
```

7532

jC-gmro02910061b04d1

BLASTX

g1834353

أأك ليري والأكار ومبيدات



```
BLAST score
                  5.0e-34
E value
Match length
                  141
                  47
% identity
                  (Y10986) hypothetical protein 194 [Arabidopsis thaliana]
NCBI Description
                  46730
Seq. No.
Seq. ID
                  jC-qmro02910061b12a1
Method
                  BLASTN
NCBI GI
                  q18764
BLAST score
                  432
                  0.0e+00
E value
                  440
Match length
                  100
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
Seq. No.
                  46731
Seq. ID
                  jC-gmro02910062a06a1
                  BLASTX
Method
                  g2924793
NCBI GI
BLAST score
                  138
E value
                  1.0e-19
Match length
                  89
                  53
% identity
NCBI Description (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
Seq. No.
                  46732
Seq. ID
                  jC-gmro02910062a06d1
Method
                  BLASTX
NCBI GI
                  q1174498
BLAST score
                  204
E value
                  4.0e-16
Match length
                  63
% identity
                  67
                  SYNAPTOBREVIN-RELATED PROTEIN >gi_600710 (M90418) formerly
NCBI Description
                  called HAT24; synaptobrevin-related protein [Arabidopsis
                  thaliana]
                  46733
Seq. No.
                  jC-gmro02910062a10d1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3318610
BLAST score
                  81
                  7.0e-38
E value
Match length
                  183
% identity
                  84
                  Glycine max mRNA for mitochondrial phosphate transporter,
NCBI Description
```

complete cds

46734 Seq. No.

jC-gmro02910062b09a1 Seq. ID

Method BLASTX NCBI GI g3256068 BLAST score 244 E value 1.0e-20 Match length 76 % identity 66



(Y14068) Heat Shock Factor 3 [Arabidopsis thaliana] NCBI Description

Seq. No. 46735

Seq. ID jC-qmro02910062b12d1

Method BLASTX NCBI GI q2088651 BLAST score 213 5.0e-17 E value Match length 66 59 % identity

(AF002109) hypersensitivity-related gene 201 isolog NCBI Description

[Arabidopsis thaliana]

46736 Seq. No.

Seq. ID jC-gmro02910062e02d1

Method BLASTX g2270994 NCBI GI BLAST score 228 9.0e-19 E value 94 Match length % identity

(AF004809) Ca+2-binding EF hand protein [Glycine max] NCBI Description

Seq. No.

jC-gmro02910062h01d1 Seq. ID

BLASTN Method NCBI GI q18727 BLAST score 200 1.0e-108 E value Match length 320 93 % identity

Soybean mRNA for reductase involved in deoxychalcone NCBI Description

synthesis (NAD(P)H dependent 6'-deoxychalcone synthase)

Seq. No. 46738

jC-gmro02910062h11d1 Seq. ID

Method BLASTX g3850630 NCBI GI BLAST score 257 3.0e-22 E value Match length 72

% identity 58

(AJ012581) cytochrome P450 [Cicer arietinum] NCBI Description

46739 Seq. No.

jC-gmro02910063b02a1 Seq. ID

BLASTX Method NCBI GI g2191136 BLAST score 239 6.0e-20 E value Match length 140 % identity 37

(AF007269) Similar to UTP-Glucose Glucosyltransferase; NCBI Description

coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]



```
Seq. No.
                  jC-gmro02910063d05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1915974
BLAST score
                   414
E value
                  8.0e-41
Match length
                  105
% identity
                  77
                  (U62329) fructokinase [Lycopersicon esculentum] >gi 2102693
NCBI Description
                   (U64818) fructokinase [Lycopersicon esculentum]
Seq. No.
                   46741
                  jC-gmro02910063e01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4140691
BLAST score
                  204
                   2.0e-25
E value
Match length
                  110
% identity
                  (AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]
NCBI Description
Seq. No.
                   46742
                   jC-gmro02910063g02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g441205
BLAST score
                   66
                   3.0e-29
E value
Match length
                   90
% identity
                   93
                  Soybean lox1gm4 gene encoding lipxygenase L-4
NCBI Description
                   46743
Seq. No.
                   jC-gmro02910063g03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2801701
BLAST score
                   210
                   5.0e-17
E value
Match length
                   77
% identity
                   51
NCBI Description
                   (AF042379) spindle pole body protein spc97 homolog GCP2
                   [Homo sapiens]
                   46744
Seq. No.
                   jC-qmro02910064b06d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3786009
BLAST score
                   176
                   1.0e-12
E value
Match length
                   51
% identity
                   78
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46745
Seq. No.
Seq. ID
                   jC-gmro02910064c10a1
```

Method BLASTX NCBI GI g2864625 BLAST score 242



2.0e-20 E value Match length 58 % identity 84

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No.

46746

Seq. ID

jC-gmro02910064e03a1

Method BLASTX NCBI GI q3176725 BLAST score 163 E value 3.0e-11 Match length 59

% identity

(AC002392) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

46747

Seq. ID

jC-gmro02910064e06a1

Method BLASTX NCBI GI g2498629 BLAST score 255 E value 4.0e-22 Match length 112 % identity 7

NCBI Description

TRANSCRIPTIONAL REPRESSOR NF-X1 >gi 2135825 pir I38869

NFX1 - human >gi 563217 (U15306) NFX1 [Homo sapiens] >gi 4505387 ref NP 002495.1 pNFX1 nuclear transcription

factor, X-box binding

Seq. No.

46748

Seq. ID jC-gmro02910064f02a1

Method BLASTX NCBI GI g231536 BLAST score 239 4.0e-20 E value Match length 74 % identity 64

NCBI Description CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)

(LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi 99683 pir S22399 leucyl aminopeptidase

(EC 3.4.11.1) - Arabidopsis thaliana

>gi 16394 emb CAA45040 (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative

leucine aminopeptidase [Arabidopsis thaliana]

Seq. No. 46749

jC-gmro02910064g05d1 Seq. ID

Method BLASTX g2288981 NCBI GI BLAST score 247 3.0e-21 E value Match length 66 % identity 39

NCBI Description (AC002335) calcium binding protein isolog [Arabidopsis

thaliana] >gi 3763938 (AC004450) putative calcium binding

protein [Arabidopsis thaliana]

Seq. No.

46750

BLAST score

E value

165

3.0e-11



```
jC-gmro02910065a11d1
      Seq. ID
                         BLASTN
      Method
                         q169988
      NCBI GI
      BLAST score
                         104
      E value
                         1.0e-51
      Match length
                         140
      % identity
                         94
                        Glycine max NADP-specific isocitrate dehydrogenase (idh1)
      NCBI Description
                         mRNA, 3' end
                         46751
      Seq. No.
                         jC-gmro02910065c07d1
      Seq. ID
      Method
                         BLASTX
                         g1097875
      NCBI GI
      BLAST score
                         224
      E value
                         2.0e-18
      Match length
                         70
NCBI Description peroxidase:ISOTYPE=RPA [Oryza sativa]
                         46752
      Seq. No.
                         jC-gmro02910065d01d1
      Seq. ID
      Method
                         BLASTN
      NCBI GI
                         g2245682
      BLAST score
                         34
      E value
                         1.0e-09
      Match length
                         82
      % identity
                         85
      NCBI Description
                         Glycine max peroxidase precursor (GMIPER1) mRNA, complete
      Seq. No.
                         46753
                         jC-gmro02910065d09d1
      Seq. ID
                         BLASTN
      Method
      NCBI GI
                         g3334662
      BLAST score
                         310
      E value
                         1.0e-174
      Match length
                         366
      % identity
                         95
      NCBI Description G.max mRNA for putative cytochrome P450, clone CP4
                         46754
      Seq. No.
                         jC-gmro02910065f05d1
      Seq. ID
                         BLASTN
      Method
                         q4204758
      NCBI GI
      BLAST score
                         444
                         0.0e+00
      E value
      Match length
                         479
      % identity
                         98
      NCBI Description Glycine max peroxidase precursor (sEPa1) mRNA, partial cds
      Seq. No.
                         46755
                         jC-gmro02910065f12a1
      Seq. ID
      Method
                         BLASTX
      NCBI GI
                         g4539423
```



```
Match length
                  53
% identity
                  (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                  [Arabidopsis thaliana]
                  46756
Seq. No.
                  jC-gmro02910065h06d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1402910
BLAST score
                  298
E value
                  3.0e-27
Match length
                  91
% identity
                  (X98316) peroxidase [Arabidopsis thaliana]
NCBI Description
                  >gi 1429223 emb_CAA67550_ (X99096) peroxidase [Arabidopsis
                  thaliana]
Seq. No.
                  46757
Seq. ID
                  jC-qmro02910066c07a1
Method
                  BLASTX
NCBI GI
                  q4510363
BLAST score
                  438
E value
                  2.0e-43
Match length
                  120
% identity
                  (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  46758
Seq. ID
                  jC-qmro02910066d08a1
Method
                  BLASTX
NCBI GI
                  g2760839
BLAST score
                  281
E value
                  3.0e-25
Match length
                  104
% identity
                  53
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                  46759
Seq. No.
                  jC-gmro02910066e10d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3834352
BLAST score
                  229
                  6.0e-19
E value
Match length
                  110
% identity
                  45
                  (AB010992) 3b-hydroxylase [Lycopersicon esculentum]
NCBI Description
                  46760
Seq. No.
```

jC-gmro02910066f09d1 Seq. ID

BLASTX Method NCBI GI g1644427 140 BLAST score 1.0e-08 E value Match length 33 79 % identity

NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]



```
46761
Seq. No.
                  jC-gmro02910066g02a1
Seq. ID
Method
                  BLASTX
                  q4567245
NCBI GI
                   434
BLAST score
                   4.0e-43
E value
                  120
Match length
% identity
                  25
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46762
Seq. No.
                   jC-gmro02910066h12d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2996172
BLAST score
                   403
                   2.0e-39
E value
Match length
                   88
                   82
% identity
                   (AF051760) putative 60S ribosomal protein L15 [Picea
NCBI Description
                  mariana]
                   46763
Seq. No.
                                                                    jC-gmro02910067b04a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2062169
BLAST score
                   576
                   1.0e-59
E value
Match length
                   149
% identity
                   68
                   (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis
NCBI Description
                   thaliana]
                   46764
Seq. No.
                   jC-gmro02910067b11d1
Seq. ID
                   BLASTX
Method
                   g1173624
NCBI GI
                   420
BLAST score
                   3.0e-41
E value
Match length
                   120
% identity
                   67
                   (U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid
NCBI Description
                   SM9108']
                   46765
Seq. No.
                   jC-gmro02910067d08a1
Seq. ID
Method
                   BLASTX
                   g3776567
NCBI GI
                   144
BLAST score
E value
                   7.0e-09
                   54
Match length
% identity
                   52
                   (AC005388) Strong similarity to F21B7.33 gi_2809264 from A.
NCBI Description
                   thaliana BAC gb AC002560. EST gb_N65119 comes from this
```

Seq. No. 46766

gene. [Arabidopsis thaliana]



```
jC-gmro02910067e06a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4572671
BLAST score
                  256
                  3.0e-22
E value
                  72
Match length
% identity
                  68
                   (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                  46767
Seq. No.
                  jC-gmro02910067f02a1
Seq. ID
                  BLASTX
Method
                  q1330401
NCBI GI
BLAST score
                  193
E value
                  1.0e-14
Match length
                  96
% identity
                  44
                  (U58762) T27F7.1 gene product [Caenorhabditis elegans]
NCBI Description
Seq. No.
                  46768
                  jC-qmro02910067f05a1
Seq. ID
Method
                  BLASTX
                  g2465923
NCBI GI
BLAST score
                  174
E value
                  2.0e-12
Match length
                  163
% identity
                  12
                  (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   46769
Seq. No.
                   jC-gmro02910067f08d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g488571
BLAST score
                  216
                  1.0e-17
E value
Match length
                   59
% identity
                   71
                  (U09462) histone H3.2 [Medicago sativa]
NCBI Description
Seq. No.
                   46770
                   jC-qmro02910067f10a1
Seq. ID
                   BLASTN
Method
                   g3080430
NCBI GI
BLAST score
                   43
E value
                   6.0e-15
Match length
                   79
                   89
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
NCBI Description
                   (ESSAII project)
Seq. No.
                   46771
                   jC-gmro02910067g04a1
Seq. ID
```

Method BLASTX
NCBI GI g3367788
BLAST score 333

```
5.0e-31
E value
                  105
Match length
% identity
                  57
                  (AL031154) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  46772
Seq. No.
                  jC-gmro02910068a09a1
Seq. ID
                  BLASTX
Method
                  q2388566
NCBI GI
BLAST score
                  382
                  9.0e-37
E value
Match length
                  152
                   51
% identity
                   (AC000098) Similar to Arabidopsis Fe(II) transport protein
NCBI Description
                   (gb_U27590). [Arabidopsis thaliana]
                   46773
Seq. No.
```

 Seq. ID
 jC-gmro02910068c01d1

 Method
 BLASTX

 NCBI GI
 g3757522

 BLAST score
 189

 E value
 3.0e-14

Match length 55 % identity 64

NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No. 46774

Seq. ID jC-gmro02910068c03a1

Method BLASTN
NCBI GI g2760166
BLAST score 34
E value 1.0e-09
Match length 54
% identity 51

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBK20, complete sequence [Arabidopsis thaliana]

Seq. No. 46775

Seq. ID jC-gmro02910068e08a1

Method BLASTX
NCBI GI g4220477
BLAST score 228
E value 7.0e-19
Match length 125
% identity 45

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 46776

Seq. ID jC-gmro02910069a03a1

Method BLASTX
NCBI GI g1177022
BLAST score 277
E value 2.0e-24
Match length 98
% identity 56

NCBI Description HYPOTHETICAL PROTEIN KIAA0052



```
46777
Seq. No.
                   jC-gmro02910069a06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3292833
BLAST score
                   259
                   2.0e-22
E value
Match length
                   105
% identity
                   48
                   (AL031018) putative membrane protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46778
                   jC-gmro02910069e02a1
Seq. ID
Method
                   BLASTX
                   g4415924
NCBI GI
BLAST score
                   339
E value
                   9.0e-32
Match length
                   138
% identity
                   (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   46779
Seq. No.
                   jC-gmro02910069e09d1
Seq. ID
Method
                   BLASTX
                   g2191174
NCBI GI
BLAST score
                   191
E value
                   2.0e-14
Match length
                   50
% identity
                   72
                   (AF007270) similar to the peptidase family S16 [Arabidopsis
NCBI Description
                   thaliana]
                   46780
Seq. No.
                   jC-gmro02910069f10d1
Seq. ID
                   BLASTN
Method
                   g1575730
NCBI GI
BLAST score
                   36
                   3.0e-11
E value
Match length
                   141
% identity
                   81
                   Glycine max 14-3-3 related protein SGF14D mRNA, complete
NCBI Description
                   46781
Seq. No.
                   jC-gmro02910069h08a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3913927
BLAST score
                   453
                   6.0e-62
E value
                   149
Match length
                   82
% identity
NCBI Description
                   ACID BETA-FRUCTOFURANOSIDASE PRECURSOR (ACID
                   SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) (AI)
                   (VACUOLAR INVERTASE) >gi_1084382_pir__S55521 beta-fructofuranosidase (EC 3.2.1.26) - fava bean
```

>gi_861159_emb_CAA89992_ (Z49831) vacuolar invertase; beta-fructofuranosidase [Vicia faba]



Seq. No. 46782

Seq. ID jC-gmro02910070b01a1

Method BLASTX
NCBI GI g1172584
BLAST score 373
E value 3.0e-36
Match length 87
% identity 75

NCBI Description POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE)

>gi_1076478_pir__S52984 catechol oxidase (EC 1.10.3.1)
precursor - apple tree >gi_507280 (L29450) polyphenol

oxidase [Malus domestica]

Seq. No. 46783

Seq. ID jC-gmro02910070f08a1

Method BLASTX
NCBI GI g2642448
BLAST score 427
E value 2.0e-42
Match length 108
% identity 23

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 46784

Seq. ID jC-gmro02910071a08a1

Method BLASTX
NCBI GI g4539457
BLAST score 287
E value 1.0e-25
Match length 63
% identity 81

NCBI Description (AL049500) heat shock transcription factor-like protein

[Arabidopsis thaliana]

Seq. No. 46785

Seq. ID jC-gmro02910071g04a1

Method BLASTX
NCBI GI g2370232
BLAST score 250
E value 3.0e-21
Match length 52
% identity 87

NCBI Description (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]

Seq. No. 46786

Seq. ID jC-gmro02910071g08a1

Method BLASTX
NCBI GI g1922964
BLAST score 260
E value 7.0e-23
Match length 96
% identity 56

NCBI Description (AC000106) Similar to Schizosaccharomyces CCAAT-binding

factor (gb U88525). EST gb T04310 comes from this gene.



[Arabidopsis thaliana]

```
46787
Seq. No.
                  jC-gmro02910072d01a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3292831
BLAST score
                  213
                  5.0e-17
E value
Match length
                  145
% identity
                  34
                  (AL031018) putative serine/threonine kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  46788
Seq. ID
                  jC-gmro02910072f01a1
Method
                  BLASTX
                  q2760839
NCBI GI
BLAST score
                  236
E value
                  8.0e-20
Match length
                  66
% identity
                  62
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  46789
                  jC-gmro02910072f09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4191616
BLAST score
                  179
                  6.0e-13
E value
Match length
                  50
% identity
                  66
                  (AF120334) GTP-binding protein NGB [Homo sapiens]
NCBI Description
                  46790
Seq. No.
                  jC-gmro02910072h09a1
Seq. ID
Method
                  BLASTX
                  g2618703
NCBI GI
BLAST score
                  302
                  2.0e-27
E value
Match length
                  66
% identity
                  82
NCBI Description
                   (AC002510) putative heat shock transcription factor
                   [Arabidopsis thaliana]
Seq. No.
                  46791
                  jC-gmro02910072h11d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2252630
BLAST score
                  173
                  3.0e-12
E value
Match length
                  42
% identity
                  79
NCBI Description
                  (U95973) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 46792

Seq. ID jC-gmro02910073h08d1

Method BLASTX

Match length

140



```
g4063742
NCBI GI
                  150
BLAST score
                  1.0e-09
E value
Match length
                  55
% identity
                  53
                  (AC005851) putative phaseolin G-box binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  46793
Seq. No.
                  jC-gmro02910073h09d1
Seq. ID
                  BLASTX
Method
                  q4468978
NCBI GI
BLAST score
                  326
                  3.0e-30
E value
Match length
                  109
% identity
                  56
                  (AL035605) peroxidase-like protein [Arabidopsis thaliana]
NCBI Description
                   46794
Seq. No.
                   jC-gmro02910074a12d1
Seq. ID
Method
                   BLASTN
                   g19533
NCBI GI
                   158
BLAST score
                   1.0e-83
E value
                   294
Match length
% identity
                   88
NCBI Description M.crystallinum ppc1 gene 5' region
Seq. No.
                   46795
                   jC-gmro02910074b08a1
Seq. ID
                   BLASTX
Method
                   q4490718
NCBI GI
                   178
BLAST score
                   5.0e-13
E value
Match length
                   47
                   72
% identity
                  (AL035709) bZIP transcription factor-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   46796
Seq. No.
                   jC-gmro02910074c08a1
Seq. ID
                   BLASTN
Method
                   g3318610
NCBI GI
                   353
BLAST score
                   0.0e+00
E value
Match length
                   516
% identity
                   93
NCBI Description Glycine max mRNA for mitochondrial phosphate transporter,
                   complete cds
                   46797
Seq. No.
                   jC-qmro02910074d06d1
Seq. ID
                   BLASTN
Method
                   q3193221
NCBI GI
BLAST score
                   71
E value
                   6.0e-32
```



% identity Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene NCBI Description encoding mitochondrial protein, partial cds Seq. No. 46798 jC-qmro02910074e04d1 Seq. ID Method BLASTX NCBI GI q1311536 BLAST score 281 E value 1.0e-25 Match length 60

(L77969) aquaporin [Spinacia oleracea] NCBI Description

46799 Seq. No.

% identity

Seq. ID jC-gmro02910074e07a1

83

Method BLASTN NCBI GI q1399449 BLAST score 176 E value 3.0e-94 Match length 481 % identity 90

NCBI Description Lupinus albus beta-tubulin 2 (TubB2) gene, complete cds

46800 Seq. No.

jC-gmro02910074f08a1 Seq. ID

Method BLASTN g2288886 NCBI GI BLAST score 132 5.0e-68 E value 429 Match length % identity 62

Arabidopsis thaliana mRNA for mevalonate diphosphate NCBI Description

decarboxylase

46801 Seq. No.

jC-gmro02910074g03a1 Seq. ID

BLASTX Method NCBI GI g2673915 BLAST score 351 3.0e-33 E value Match length 103 62 % identity

(AC002561) putative cytochrome P-450 [Arabidopsis thaliana] NCBI Description

46802 Seq. No.

jC-gmro02910074g03d1 Seq. ID

BLASTX Method NCBI GI g2673915 BLAST score 197 E value 2.0e-15 Match length 72 47 % identity

(AC002561) putative cytochrome P-450 [Arabidopsis thaliana] NCBI Description

46803 Seq. No.

jC-gmro02910075a06a1 Seq. ID



Method BLASTN
NCBI GI g4140370
BLAST score 47
E value 2.0e-17
Match length 95
% identity 87

NCBI Description Morus alba 3-hydroxy-3-methylglutaryl-coenzyme A reductase

(HMGR) gene, complete cds

Seq. No. 46804

Seq. ID jC-gmro02910075c02d1

Method BLASTX
NCBI GI 94220461
BLAST score 179
E value 5.0e-13
Match length 77
% identity 56

NCBI Description (AC006216) ESTs gb_T75642 and gb_AA650997 come from this

gene. [Arabidopsis thaliana]

Seq. No. 46805

Seq. ID jC-gmro02910075c12a1

Method BLASTN
NCBI GI g4098318
BLAST score 227
E value 1.0e-124
Match length 491
% identity 87

NCBI Description Triticum aestivum beta-tubulin 1 (tubb1) mRNA, complete cds

Seq. No. 46806

Seq. ID jC-gmro02910075d04a1

Method BLASTN
NCBI GI g609224
BLAST score 187
E value 1.0e-101
Match length 327
% identity 89

NCBI Description P.sativum mRNA for SAMS-2 >gi_609558_gb_L36681_PEADENSYNB

Pisum sativum S-adenosylmethionine synthase mRNA, complete

cds

Seq. No. 46807

Seq. ID jC-gmro02910075d05d1

Method BLASTN
NCBI GI g669002
BLAST score 141
E value 2.0e-73
Match length 267
% identity 96

NCBI Description Glycine max calnexin mRNA, complete cds

Seq. No. 46808

Seq. ID jC-gmro02910075e01d1

Method BLASTX
NCBI GI g4218010
BLAST score 197



```
2.0e-15
E value
Match length
                   82
                   50
% identity
                   (AC006135) putative sugar transporter [Arabidopsis
NCBI Description
                   thaliana] >gi_4309720_gb_AAD15490_ (AC006439) putative
                   sugar transporter [Arabidopsis thaliana]
                   46809
Seq. No.
                   jC-gmro02910075f07d1
Seq. ID
                   BLASTX
Method
                   g1488267
NCBI GI
                   277
BLAST score
                   2.0e-24
E value
Match length
                   88
                   77
% identity
                   (U57412) low affinity calcium antiporter CAX2 [Arabidopsis
NCBI Description
                   thaliana]
                   46810
Seq. No.
                   jC-gmst02400001b10d1
Seq. ID
                   BLASTN
Method
                   g257814
NCBI GI
                   35
BLAST score
                   3.0e-10
E value
Match length
                   160
% identity
                   86
NCBI Description phenylalanine ammonia-lyase [soybeans, mRNA, 1427 nt]
                   46811
Seq. No.
                   jC-gmst02400001d07a1
Seq. ID
                   BLASTN
Method
                   g2435504
NCBI GI
                   39
BLAST score
                   1.0e-12
E value
                   75
Match length
                   88
% identity
                   Chlamydomonas reinhardtii acetolactate synthase mRNA,
NCBI Description
                   complete cds
                   46812
Seq. No.
                   jC-gmst02400001d09d1
Seq. ID
                   BLASTN
Method
                   g2656024
NCBI GI
BLAST score
                   43
E value
                   8.0e-15
                   83
Match length
                   88
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K15E6
                   46813
Seq. No.
Seq. ID
                   jC-qmst02400002d01d1
```

BLASTX Method NCBI GI q2842490 BLAST score 182 2.0e-13 E value 54 Match length



```
% identity
                    (AL021749) heat-shock protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    46814
                    jC-gmst02400003c08d1
 Seq. ID
                    BLASTX
 Method
                    q4204859
 NCBI GI
 BLAST score
                    152
                    2.0e-10
 E value
 Match length
                    48
                    69
  % identity
                    (U55859) heat shock protein 80 [Triticum aestivum]
 NCBI Description
                    46815
  Seq. No.
  Seq. ID
                    jC-gmst02400003e07d1
 Method
                    BLASTX
                    q3805960
 NCBI GI
                    244
 BLAST score
                    1.0e-20
 E value
 Match length
                    48
  % identity
                    83
                    (Y13771) laccase [Populus balsamifera subsp. trichocarpa]
 NCBI Description
Seq. No.
                    46816
                    jC-gmst02400003g10d1
  Seq. ID
 Method
                    BLASTX
                    g2826844
 NCBI GI
  BLAST score
                    208
  E value
                    2.0e-16
  Match length
                    51
                    76
  % identity
                    (AJ002237) loxc homologue [Lycopersicon esculentum]
  NCBI Description
                    46817
  Seq. No.
                    jC-gmst02400004f11a1
  Seq. ID
                    BLASTX
  Method
                    g2213629
  NCBI GI
  BLAST score
                    164
  E value
                    3.0e-11
                    144
  Match length
  % identity
                    27
                    (AC000103) F21J9.21 [Arabidopsis thaliana]
  NCBI Description
                    46818
  Seq. No.
                    jC-qmst02400005c12a1
  Seq. ID
                    {\tt BLASTX}
  Method
  NCBI GI
                    g3851636
                    262
  BLAST score
                    7.0e-23
  E value
  Match length
                    91
  % identity
                    58
                     (AF098519) unknown [Avicennia marina] >gi 4128206
  NCBI Description
                     (AF056316) 40S ribosome protein S7 [Avicennia marina]
```

Seq. No. 46819

Seq. ID jC-gmst02400006b11d1

Method BLASTX

E value

Match length

1.0e-19

67



```
g4406782
NCBI GI
                  309
BLAST score
                  3.0e-28
E value
Match length
                  70
                  79
% identity
                  (AC006532) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  46820
Seq. No.
                  jC-gmst02400007b12a1
Seq. ID
                  BLASTN
Method
                  g20412
NCBI GI
                  88
BLAST score
                  6.0e-42
E value
                  220
Match length
% identity
                  85
NCBI Description P.amygdalus mRNA for alpha-tubulin
                  46821
Seq. No.
                  jC-gmst02400007d05d1
Seq. ID
                  BLASTX
Method
                  g2104536
NCBI GI
BLAST score
                  188
                  3.0e-14
E value
Match length
                  48
% identity
                  69
                  (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  46822
                  jC-gmst02400007h01a1
Seq. ID
                  BLASTX
Method
                  g2982452
NCBI GI
BLAST score
                  182
                  2.0e-13
E value
                  133
Match length
% identity
                   35
                  (AL022223) receptor protein kinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   46823
Seq. No.
                   jC-gmst02400007h08d1
Seq. ID
Method
                   BLASTX
                   q3924603
NCBI GI
BLAST score
                   252
E value
                   1.0e-21
Match length
                   75
% identity
                  (AF069442) putative WD-repeat protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   46824
                   iC-qmst02400008a03a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2352812
BLAST score
                   236
```



```
% identity
                  (AF008597) desacetoxyvindoline-4-hydroxylase [Catharanthus
NCBI Description
                  roseus]
                  46825
Seq. No.
                  jC-gmst02400008b01a1
Seq. ID
                  BLASTN
Method
                  q18764
NCBI GI
BLAST score
                  235
                  1.0e-129
E value
                  315
Match length
                  94
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
Seq. No.
                  46826
                  jC-gmst02400008b04a1
Seq. ID
                  BLASTX
Method
                  q4558678
NCBI GI
BLAST score
                  180
                   5.0e-13
E value
Match length
                  71
% identity
                   45
                  (AC006586) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46827
Seq. No.
                   jC-gmst02400008c02a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3063691
BLAST score
                   289
                  7.0e-26
E value
Match length
                  167
% identity
                   38
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   46828
Seq. No.
                   jC-gmst02400008e01d1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1399306
BLAST score
                   41
                   8.0e-14
E value
Match length
                   155
                   88
% identity
                  Glycine max phosphoinositide-specific phospholipase C P25
NCBI Description
                  mRNA, complete cds
Seq. No.
                   46829
                   jC-gmst02400008g01a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q257814
                   330
BLAST score
E value
                   0.0e + 00
```

Match length 436 % identity

phenylalanine ammonia-lyase [soybeans, mRNA, 1427 nt] NCBI Description

Seq. No. 46830

jC-gmst02400008h04a1 Seq. ID



```
BLASTN
Method
                  g3832527
NCBI GI
                  138
BLAST score
                  1.0e-71
E value
                  378
Match length
                  89
% identity
NCBI Description Glycine max unknown mRNA
                  46831
Seq. No.
                  jC-gmst02400009c05a1
Seq. ID
                  BLASTX
Method
                  g3335378
NCBI GI
BLAST score
                  359
E value
                  4.0e-34
Match length
                  149
                  54
% identity
                  (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                  thaliana]
                  46832
Seq. No.
                  jC-gmst02400009f01a1
Seq. ID
                  BLASTX
Method
                  g4567282
NCBI GI
BLAST score
                  365
E value
                  8.0e-35
Match length
                  89
                  78
% identity
NCBI Description (AC006841) putative DNAJ protein [Arabidopsis thaliana]
Seq. No.
                  46833
                  jC-gmst02400009g07a1
Seq. ID
Method
                  BLASTX
                  g2317902
NCBI GI
BLAST score
                  356
                  7.0e-34
E value
Match length
                  132
% identity
                  62
                  (U89959) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  46834
                  jC-qmst02400010h01d1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g450634
BLAST score
                  81
E value
                  1.0e-37
Match length
                  238
% identity
NCBI Description Soybean GTP binding protein mRNA, complete cds
Seq. No.
                  46835
```

jC-gmst02400011a12a1 Seq. ID

Method BLASTX NCBI GI q2708331 BLAST score 327 E value 2.0e-30 Match length 133 % identity 47



NCBI Description (AF038557) ligand gated channel-like protein [Arabidopsis thaliana]

Seq. No. 46836

Seq. ID jC-gmst02400011b05a1

Method BLASTX
NCBI GI g2853087
BLAST score 182
E value 2.0e-13
Match length 135
% identity 38

NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

Seq. No. 46837

Seq. ID jC-gmst02400011g08d1

Method BLASTX
NCBI GI g3947735
BLAST score 147
E value 2.0e-09
Match length 54
% identity 54

NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No. 46838

Seq. ID jC-gmst02400011h09a1

Method BLASTX
NCBI GI g4567202
BLAST score 380
E value 1.0e-36
Match length 121
% identity 67

NCBI Description (AC007168) putative myo-inositol 1-phosphate synthase

[Arabidopsis thaliana]

Seq. No. 46839

Seq. ID jC-gmst02400014a04a1

Method BLASTN
NCBI GI g602564
BLAST score 64
E value 9.0e-28
Match length 144
% identity 86

NCBI Description C.paradisi (Macf) INO1 gene

Seq. No. 46840

Seq. ID jC-gmst02400014a10d1

Method BLASTX
NCBI GI g4512657
BLAST score 264
E value 5.0e-23
Match length 77
% identity 58

NCBI Description (AC006931) putative APG protein [Arabidopsis thaliana] >gi 4544463 gb AAD22370.1 AC006580 2 (AC006580) putative

APG isolog protein [Arabidopsis thaliana]

Seq. No. 46841



```
jC-gmst02400014b07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3702343
                   321
BLAST score
                  1.0e^{-29}
E value
                  148
Match length
                  52
% identity
                   (AC005397) putative homeotic gene regulator [Arabidopsis
NCBI Description
                  thaliana]
                   46842
Seq. No.
                   jC-gmst02400014d04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3176714
BLAST score
                   232
                   3.0e-19
E value
                   90
Match length
% identity
                   50
NCBI Description
                   (AC002392) putative tRNA-splicing endonuclease positive
                   effector [Arabidopsis thaliana]
                   46843
Seq. No.
                   jC-gmst02400014f11d1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3421109
                   140
BLAST score
                   1.0e-08
E value
Match length
                   33
                   82
% identity
                   (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                   thaliana]
                   46844
Seq. No.
                   jC-gmst02400014g09d1
Seq. ID
Method
                   BLASTX
                   g4539395
NCBI GI
BLAST score
                   142
E value
                   1.0e-08
Match length
                   35
                   74
% identity
                  (AL035526) putative protein [Arabidopsis thaliana]
NCBI Description
                   46845
Seq. No.
                   jC-gmst02400014h03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2281639
BLAST score
                   491
E value
                   1.0e-49
Match length
                   144
% identity
                   67
                   (AF003100) AP2 domain containing protein RAP2.7
NCBI Description
                   [Arabidopsis thaliana]
                   46846
Seq. No.
```

Seq. ID jC-gmst02400015b12a1

Method BLASTX NCBI GI g2833379



```
BLAST score
                  4.0e-32
E value
                  92
Match length
                  71
% identity
                  RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL
NCBI Description
                  PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi_1076397_pir__S51270
                  ribose-phosphate pyrophosphokinase (EC \overline{2}.7.6.1)
                  Arabidopsis thaliana >gi_633140_emb_CAA58717_ (X83764)
                  phosphoribosyl diphosphate synthetase [Arabidopsis
                  thaliana] >gi_3608149 (AC005314) phosphoribosyl diphosphate
                  synthetase [Arabidopsis thaliana]
                  46847
Seq. No.
                  jC-gmst02400015d11a1
Seq. ID
Method
                  BLASTN
                  g602358
NCBI GI
BLAST score
                  64
                  2.0e-27
E value
                  196
Match length
                  89
% identity
NCBI Description P.sativum mRNA for type II chlorophyll a/b binding protein
                   46848
Seq. No.
                   jC-gmst02400015d12a1
Seq. ID
                   BLASTX
Method
                   g3540179
NCBI GI
                   476
BLAST score
                   8.0e-48
E value
Match length
                   164
                   53
% identity
                   (AC004122) putative amino acid permease [Arabidopsis
NCBI Description
                   thaliana]
                   46849
Seq. No.
                   jC-gmst02400015g10a1
Seq. ID
                   BLASTX
Method
                   g4558553
NCBI GI
BLAST score
                   217
                   1.0e-17
E value
                   78
Match length
                   59
% identity
                   (AC007138) putative potassium channel [Arabidopsis
NCBI Description
                   thaliana]
                   46850
Seq. No.
                   jC-gmst02400016b12d1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3860250
BLAST score
                   171
                   4.0e-12
E value
Match length
                   49
% identity
                   65
                   (AC005824) putative chloroplast prephenate dehydratase
```

46851 Seq. No.

NCBI Description

jC-gmst02400016c08d1 Seq. ID

[Arabidopsis thaliana]

Match length

% identity

164 24



```
BLASTX
Method
                  g1518113
NCBI GI
                  166
BLAST score
                  1.0e-11
E value
Match length
                  33
                  91
% identity
                  (U66193) SLL2 [Brassica napus]
NCBI Description
                   46852
Seq. No.
                   jC-gmst02400016c10a1
Seq. ID
                   BLASTX
Method
                   g3157943
NCBI GI
                   261
BLAST score
                   9.0e-23
E value
Match length
                   119
% identity
                   47
                   (AC002131) Contains similarity to BAP31 protein gb_X81816
NCBI Description
                   from Mus musculus. [Arabidopsis thaliana]
                   46853
Seq. No.
                   jC-gmst02400016d01a1
Seq. ID
                   BLASTX
Method
                   q3892057
NCBI GI
BLAST score
                   612
                   8.0e-64
E value
Match length
                   144
% identity
                   54
                   (AC002330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46854
Seq. No.
                   jC-gmst02400016d04a1
Seq. ID
                   BLASTX
Method
                   q4469025
NCBI GI
                   174
BLAST score
                   6.0e-15
E value
Match length
                   74
                                                 - W. Je.
                   58
% identity
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   46855
Seq. No.
                   jC-gmst02400016d09d1
Seq. ID
                   BLASTX
Method
                   q4417287
NCBI GI
                   224
BLAST score
                   3.0e-18
E value
Match length
                   80
                   54
% identity
                   (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46856
Seq. No.
                   jC-qmst02400016f03a1
Seq. ID
                   BLASTX
Method
                   g2292907
NCBI GI
                   388
BLAST score
E value
                   2.0e-37
```



NCBI Description (Y10099) P-glycoprotein homologue [Hordeum vulgare]

Seq. No. 46857

Seq. ID jC-gmst02400016g05a1

Method BLASTN NCBI GI g2961297

BLAST score 42 E value 2.0e-14 Match length 187 % identity 81

NCBI Description Cicer arietinum mRNA for unidentified protein

Seq. No. 46858

Seq. ID jC-gmst02400016h10d1

Method BLASTX
NCBI GI g3176671
BLAST score 218
E value 1.0e-17
Match length 75
% identity 56

NCBI Description (AC004393) Contains similarity to hypothetical gene B0495.7

gb_687822 from C. elegans cosmid gb_U21317. [Arabidopsis

thaliana]

Seq. No. 46859

Seq. ID jC-gmst02400017c08d1

Method BLASTX
NCBI GI g3953471
BLAST score 272
E value 5.0e-24
Match length 72
% identity 62

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 46860

Seq. ID jC-gmst02400018b07a1

Method BLASTX
NCBI GI 94406782
BLAST score 357
E value 6.0e-34
Match length 100
% identity 70

NCBI Description (AC006532) hypothetical protein [Arabidopsis thaliana]

Seq. No. 46861

Seq. ID jC-gmst02400018c03a1

Method BLASTN
NCBI GI g18764
BLAST score 277
E value 1.0e-154
Match length 365
% identity 94

NCBI Description G.max tefS1 gene for elongation factor EF-la

Seq. No. 46862

Seq. ID jC-gmst02400018c04d1

Method BLASTX



NCBI GI q3746060 254 BLAST score 2.0e-22 E value 76 Match length % identity NCBI Description (AC005311) unknown protein [Arabidopsis thaliana] 46863 Seq. No. Seq. ID jC-qmst02400018c11d1 Method BLASTX NCBI GI q3600031 BLAST score 203 E value 6.0e-16 Match length 68 % identity 62 NCBI Description (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolases [Arabidopsis thaliana] 46864 Seq. No. jC-gmst02400018e03a1 Seq. ID Method BLASTN NCBI GI g18551 BLAST score 241 E value 1.0e-133 Match length 293 % identity 96 Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding NCBI Description protein 46865 Seq. No. Seq. ID jC-gmst02400018e10a1 Method BLASTX NCBI GI q3901091 343 BLAST score E value 3.0e-32Match length 86 % identity 69 (AJ006305) arbuscular mycorrhiza protein [Pisum sativum] NCBI Description Seq. No. 46866 Seq. ID jC-gmst02400018f05d1 Method BLASTX NCBI GI g2191144 269 BLAST score 1.0e-23 E value 90 Match length % identity 53 (AF007269) A IG002N01.24 gene product [Arabidopsis NCBI Description

thaliana]

Seq. No. 46867

Seq. ID jC-qmst02400018f06a1

Method BLASTX NCBI GI q2191144 BLAST score 346 E value 1.0e-32 Match length 116

Seq. No.

46873



```
% identity
                  (AF007269) A IG002N01.24 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  46868
Seq. No.
                  jC-gmst02400018g03d1
Seq. ID
                  BLASTX
Method
                  g3600031
NCBI GI
                  191
BLAST score
                  1.0e-14
E value
                  69
Match length
                  61
% identity
                  (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic
NCBI Description
                  acid aldolases [Arabidopsis thaliana]
                   46869
Seq. No.
                   jC-qmst02400018g05a1
Seq. ID
                  BLASTX
Method
                  g2529707
NCBI GI
                   420
BLAST score
                   2.0e-41
E value
                  132
Match length
% identity
                   62
                  (AF001434) Hpast [Homo sapiens]
NCBI Description
                   46870
Seq. No.
                   jC-gmst02400018g12a1
Seq. ID
                   BLASTX
Method
                   q4455217
NCBI GI
                   180
BLAST score
                   8.0e-14
E value
                   66
Match length
                   50
% identity
                   (AL035440) Avr9 elicitor response like protein [Arabidopsis
NCBI Description
                   thaliana]
                   46871
Seq. No.
                   jC-gmst02400018h09d1
Seq. ID
                   BLASTN
Method
                   g170046
NCBI GI
BLAST score
                   44
                   1.0e-15
E value
                   88
Match length
                   96
% identity
NCBI Description Glycine max protein kinase (PK6) mRNA, complete cds
                   46872
Seq. No.
                   jC-gmst02400020a04a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2245138
BLAST score
                   469
                   4.0e-47
E value
                   110
Match length
                   83
% identity
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```



```
jC-gmst02400020b02a1
Seq. ID
                  BLASTN
Method
                  g3264604
NCBI GI
BLAST score
                  73
                  1.0e-32
E value
                  129
Match length
                  89
% identity
                  Zea mays ribosomal protein L25 mRNA, partial cds
NCBI Description
                  46874
Seq. No.
                  jC-gmst02400020dg04d1
Seq. ID
                  BLASTX
Method
                  q3024135
NCBI GI
                  254
BLAST score
                  7.0e-22
E value
Match length
                  91
                   59
% identity
                  PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND
NCBI Description
                   >gi_2224467_dbj_BAA57951_ (AB001684) cell division
                   inhibitor MinD [Chlorella vulgaris]
Seq. No.
                   46875
                   jC-gmst02400020f03a1
Seq. ID
                   BLASTX
Method
                   g3182996
NCBI GI
BLAST score
                   306
E value
                   7.0e-28
                   153
Match length
                   44
% identity
                   TRANSLATION INITIATION FACTOR EIF-2B BETA SUBUNIT (EIF-2B
NCBI Description
                   GDP-GTP EXCHANGE FACTOR) (S20I15) >gi_1117954 (U40756)
                   S20i15 [Fugu rubripes]
                   46876
Seq. No.
                   jC-gmst02400020g07a1
Seq. ID
                   BLASTN
Method
                   g1575730
NCBI GI
                   39
BLAST score
                   4.0e-13
E value
                   119
Match length
 % identity
                   83
                   Glycine max 14-3-3 related protein SGF14D mRNA, complete
NCBI Description
                   cds
                   46877
 Seq. No.
                   jC-gmst02400020g08a1
 Seq. ID
                   BLASTX
 Method
                   g3068717
 NCBI GI
                   310
 BLAST score
                   2.0e-28
 E value
                   90
 Match length
                   67
 % identity
 NCBI Description (AF049236) unknown [Arabidopsis thaliana]
```

46878

BLASTX

jC-gmst02400020g12a1

Seq. No.

Seq. ID

Method



```
g3036796
NCBI GI
                  441
BLAST score
                  1.0e-43
E value
Match length
                  154
% identity
                   60
                   (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3805858_emb_CAA21478_ (AL031986) putative protein
                   [Arabidopsis thaliana]
                   46879
Seq. No.
                   jC-gmst02400023a04d1
Seq. ID
                   BLASTX
Method
                   g3924605
NCBI GI
BLAST score
                   259
                   1.0e-22
E value
Match length
                   60
% identity
                   73
                   (AF069442) putative inhibitor of apoptosis [Arabidopsis
NCBI Description
                   thaliana]
                   46880
Seq. No.
                   jC-gmst02400023d12a1
Seq. ID
                   BLASTX
Method
                   g4262174
NCBI GI
BLAST score
                   536
                   6.0e-55
E value
Match length
                   140
% identity
                   68
                   (AC005508) 9058 [Arabidopsis thaliana]
NCBI Description
                   46881
Seq. No.
                   jC-gmst02400023f01d1
Seq. ID
                   BLASTX
Method
                   g4220480
NCBI GI
                   205
BLAST score
                   4.0e-16
E value
                   95
Match length
% identity
                   41
                   (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46882
Seq. No.
                   jC-gmst02400023f08a1
Seq. ID
                   BLASTX
Method
                   g1652733
NCBI GI
                   398
BLAST score
                   9.0e-39
E value
                   136
Match length
                   57
 % identity
                   (D90908) glycogen operon protein GlgX [Synechocystis sp.]
NCBI Description
                    46883
 Seq. No.
                    jC-gmst02400024b11a1
 Seq. ID
                    BLASTX
 Method
                    g2598575
 NCBI GI
                    106
 BLAST score
                    8.0e-10
 E value
```

Match length



```
% identity
                  (Y15293) MtN21 [Medicago truncatula]
NCBI Description
                  46884
Seq. No.
                  jC-gmst02400024e12a1
Seq. ID
                  BLASTN
Method
                  q296408
NCBI GI
                  1,53
BLAST score
                  9.0e-81
E value
                  245
Match length
                  92
% identity
                  G.max ADR12 mRNA
NCBI Description
                   46885
Seq. No.
                   jC-gmst02400025b11d1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3559805
BLAST score
                   145
                   4.0e-09
E value
                   46
Match length
% identity
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   46886
Seq. No.
                   jC-gmst02400026e08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3858939
                   225
BLAST score
                   2.0e-18
E value
                   129
Match length
                   47
% identity
                   (AL021636) serine/threonine protein kinase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   46887
Seq. No.
                   jC-gmst02400026e09a1
Seq. ID
                   BLASTX
Method
                   g1495251
NCBI GI
                   388
BLAST score
                   1.0e-37
E value
                   104
Match length
                   74
% identity
                   (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   46888
 Seq. No.
                   jC-gmst02400026f07a1
 Seq. ID
                   BLASTX
Method
                   g4432866
NCBI GI
                   112
BLAST score
                   1.0e-18
E value
Match length
                   160
                   36
 % identity
                   (AC006300) putative reverse transcriptase [Arabidopsis
 NCBI Description
                   thaliana]
```

46889

Seq. No.



```
jC-gmst02400027e02a1
Seq. ID
                  BLASTX
Method
                  g1109699
NCBI GI
                  298
BLAST score
                   6.0e-27
E value
                  125
Match length
                   46
% identity
                   (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
                   46890
Seq. No.
                   jC-gmst02400027e02d1
Seq. ID
                   BLASTX
Method
                   g1109697
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
Match length
                   66
% identity
                   58
                   (X83380) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
                   46891
Seq. No.
                   jC-gmst02400027f10a1
Seq. ID
                   BLASTX
Method
                   g3953478
NCBI GI
                   182
BLAST score
                   3.0e-13
E value
                   56
Match length
                   57
% identity
                   (AC002328) F2202.23 [Arabidopsis thaliana]
NCBI Description
                   46892
Seq. No.
                   jC-gmst02400028d12a1
Seq. ID
                   BLASTX
Method
                   g2252840
NCBI GI
                   385
BLAST score
                   3.0e-37
E value
                   125
Match length
                   57
% identity
                   (AF013293) contains regions of similarity to Haemophilus
NCBI Description
                   influenzae permease (SP:P38767) [Arabidopsis thaliana]
                   46893
Seq. No.
                   jC-gmst02400029b12a1
Seq. ID
                   BLASTX
Method
                   q3892056
NCBI GI
BLAST score
                   281
                   1.0e-26
E value
                   79
Match length
                   74
 % identity
                   (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   jC-gmst02400029c01a1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3335375
 BLAST score
                   157
```

2.0e-10

35

E value Match length

% identity 71 NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]

Seq. No. 46895

Seq. ID jC-gmst02400029c07a1

Method BLASTN
NCBI GI g2317899
BLAST score 235
E value 1.0e-129
Match length 343
% identity 92

NCBI Description Glycine max Sali3-2 mRNA, complete cds

Seq. No. 46896

Seq. ID jC-gmst02400029f02a1

Method BLASTX
NCBI GI g2497702
BLAST score 162
E value 6.0e-11
Match length 140
% identity 35

NCBI Description OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR

>gi_2121019_pir__I40710 outer membrane lipoprotein Citrobacter freundii >gi_717136 (U21727) lipocalin

precursor [Citrobacter freundii]

Seq. No. 46897

Seq. ID jC-gmst02400029f08a1

Method BLASTX
NCBI GI g3702317
BLAST score 153
E value 4.0e-10
Match length 52
% identity 56

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

>gi 4559376_gb_AAD23036.1_AC006526_1 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 46898

Seq. ID jC-gmst02400029g02a1

Method BLASTX
NCBI GI g4204268
BLAST score 695
E value 2.0e-73
Match length 148
% identity 81

NCBI Description (AC005223) 62134 [Arabidopsis thaliana]

Seq. No. 46899

Seq. ID jC-gmst02400029g10a1

Method BLASTN
NCBI GI g2317899
BLAST score 151
E value 1.0e-79
Match length 255
% identity 90

NCBI Description Glycine max Sali3-2 mRNA, complete cds

NCBI GI

BLAST score



```
46900
Seq. No.
                  jC-gmst02400029h06d1
Seq. ID
                  BLASTX
Method
                  g3293031
NCBI GI
                  314
BLAST score
                  8.0e-29 ·
E value
Match length
                  91
% identity
                  (AJ007574) amino acid carrier [Ricinus communis]
NCBI Description
                  46901
Seq. No.
                  jC-gmst02400029h09a1
Seq. ID
                  BLASTN
Method
                  g3869075
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
                  88
Match length
                  85
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXK3, complete sequence [Arabidopsis thaliana]
                   46902
Seq. No.
                  jC-gmst02400029h11a1
Seq. ID
                   BLASTX
Method
                   g3168840
NCBI GI
                   217
BLAST score
                   5.0e-18
E value
Match length
                   67
                   61
% identity
                  (U88711) copper homeostasis factor [Arabidopsis thaliana]
NCBI Description
                   46903
Seq. No.
                   jC-gmst02400030a07d1
Seq. ID
                   BLASTX
Method
                   g3297816
NCBI GI
                   527
BLAST score
                   7.0e-54
E value
                   137
Match length
% identity
                   76
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
                   46904
Seq. No.
                   jC-qmst02400030b07a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g456713
                   123
BLAST score
                   6.0e-63
E value
                   171
Match length
% identity
                   27
NCBI Description Glycine max gene for ubiquitin, complete cds
                   46905
Seq. No.
                   jC-qmst02400030b10d1
Seq. ID
                   BLASTX
Method
```

g2146731

190



```
8.0e-15
E value
Match length
                  81
% identity
                  52
                  FK506-binding protein - Arabidopsis thaliana >gi_1354207
NCBI Description
                   (U49453) rof1 [Arabidopsis thaliana]
                  46906
Seq. No.
                  jC-gmst02400030f01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539452
BLAST score
                   602
                  1.0e-62
E value
Match length
                  140
% identity
                   76
                   (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
                   46907
Seq. No.
                   jC-gmst02400030f01d1
Seq. ID
Method
                   BLASTX
                   g3287696
NCBI GI
BLAST score
                   146
                   2.0e-09
E value
                   43
Match length
% identity
                   65
                   (AC003979) Strong similarity to phosphoribosylanthranilate
NCBI Description
                   transferase gb_D86180 from Pisum sativum. This ORF may be
                   part of a larger gene that lies in the overlapping region.
                   [Arabidopsis thaliana]
                   46908
Seq. No.
                   jC-gmst02400030f02a1
Seq. ID
                   BLASTX
Method
                   g3096947
NCBI GI
BLAST score
                   273
E value
                   4.0e-24
                   118
Match length
                   54
% identity
                   (Y16327) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                   46909
Seq. No.
                   jC-gmst02400030h04a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2499945
BLAST score
                   369
                   6.0e-36
E value
Match length
                   124
```

% identity 67

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi_1076363_pir__S46440 orotate

phosphoribosyltransferase (EC 2.4.2.10) /

orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)

pyrE-F [Arabidopsis thaliana]

```
Seq. No.
                  jC-gmst02400031c04a1
Seq. ID
                  BLASTN
Method
                  g2264367
NCBI GI
                  37
BLAST score
                  3.0e-11
E value
                  73
Match length
                  88
% identity
                  Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  46911
Seq. No.
                  jC-gmst02400031d01a1
Seq. ID
                  BLASTX
Method
                  g3775997
NCBI GI
BLAST score
                  612
                  9.0e-64
E value
                  160
Match length
                  75
% identity
                  (AJ010462) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   46912
Seq. No.
                   jC-gmst02400031e11d1
Seq. ID
                   BLASTN
Method
                   g607187
NCBI GI
BLAST score
                   92
                   4.0e-44
E value
                   196
Match length
                   87
% identity
NCBI Description S.hamata mRNA for low affinity sulphate transporter
                   46913
Seq. No.
                   jC-gmst02400031g02a1
Seq. ID
                   BLASTX
Method
                   g3273243
NCBI GI
                   352
BLAST score
                   1.0e-33
E value
Match length
                   87
% identity
                   48
                   (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                   >gi 3273245 dbj_BAA31166_ (AB004814) NLS receptor [Oryza
                   sativa]
                   46914
Seq. No.
                   jC-gmst02400031g10a1
Seq. ID
                   BLASTX
Method
                   q3047089
NCBI GI
                   161
BLAST score
E value
                   5.0e-11
```

64 Match length % identity 50

(AF058826) contains similarity to pseudouridylate NCBI Description

synthases [Arabidopsis thaliana]

46915 Seq. No.

jC-gmst02400032a08a1 Seq. ID

Method BLASTX



```
g1706956
NCBI GI
                   399
BLAST score
                   6.0e-39
E value
                   126
Match length
                   67
% identity
                  (U58283) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   46916
Seq. No.
                   jC-gmst02400032c03d1
Seq. ID
                   BLASTX
Method
                   q4204285
NCBI GI
                   429
BLAST score
                   3.0e-42
E value
Match length
                   126
                   59
% identity
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   46917
Seq. No.
                   jC-gmst02400032e05a1
Seq. ID
                   BLASTX
Method
                   g3063465
NCBI GI
                   350
BLAST score
                   4.0e-33
E value
Match length
                   101
                   72
% identity
                   (AC003981) F22013.27 [Arabidopsis thaliana]
NCBI Description
                   46918
Seq. No.
                   jC-gmst02400032h03a1
Seq. ID
                   BLASTN
Method
                   g607187
NCBI GI
                   166
BLAST score
E value
                   3.0e-88
                   434
Match length
% identity
NCBI Description S.hamata mRNA for low affinity sulphate transporter
Seq. No.
                   46919
                   jC-qmst02400033b03a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4314370
BLAST score
                   173
                   3.0e-12
E value
Match length
                   54
                   74
 % identity
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46920
 Seq. No.
                   jC-gmst02400033c03d1
 Seq. ID
Method
                   BLASTX
                   g3046700
 NCBI GI
                   199
 BLAST score
                   3.0e-15
E value
Match length
                   74
                   55
 % identity
 NCBI Description (AJ005261) cytidine deaminase [Arabidopsis thaliana]
```



% identity

NCBI Description

>gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
[Arabidopsis thaliana] >gi_4191787 (AC005917) putative
cytidine deaminase [Arabidopsis thaliana]

```
46921
Seq. No.
                  jC-gmst02400033e06a1
Seq. ID
Method
                  BLASTN
                  q607904
NCBI GI
BLAST score
                  35
E value
                  2.0e-10
                  83
Match length
                  86
% identity
                  Solanum chacoense PI 320287 abscisic stress ripening
NCBI Description
                  protein mRNA, partial cds
                   46922
Seq. No.
                   jC-gmst02400033f06a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2275210
                   315
BLAST score
                   5.0e-29
E value
                   142
Match length
                   46
% identity
                   (AC002337) peptidyl-prolyl cis-trans isomerase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   46923
Seq. No.
                   jC-qmst02400033h02a1
Seq. ID
Method
                   BLASTX
                   g2829870
NCBI GI
                   295
BLAST score
                   1.0e-26
E value
                   147
Match length
% identity
                   51
                  (ACO02396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46924
                   jC-qmst02400034c08d2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3402749
BLAST score
                   177
                   6.0e-13
E value
                   90
Match length
                   16
% identity
                   (AL031187) putative protein [Arabidopsis thaliana]
NCBI Description
                   46925
Seq. No.
                   jC-gmst02400034d06d2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076634
BLAST score
                   325
                   4.0e-30
E value
Match length
                   81
```

kinase [Nicotiana tabacum]

protein-serine/threonine kinase NPK15 - common tobacco

>gi 505146 dbj BAA06538 (D31737) protein-serine/threonine



```
46926
Seq. No.
                  jC-gmst02400036b10a1
Seq. ID
                  BLASTN
Method
                  g1053215
NCBI GI
                  244
BLAST score
                  1.0e-135
E value
                  268
Match length
                   98
% identity
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                  nuclear gene encoding chloroplast protein, complete cds
                   46927
Seq. No.
                   jC-gmst02400036d06d2
Seq. ID
Method
                   BLASTX
                   g2511576
NCBI GI
                   165
BLAST score
                   1.0e-11
E value
                   46
Match length
                   67
% identity
                   (Y13177) multicatalytic endopeptidase [Arabidopsis
NCBI Description
                   thaliana]
                   46928
Seq. No.
                   jC-gmst02400037f04a1
Seq. ID
                   BLASTX
Method
                   g3702314
NCBI GI
                   358
BLAST score
                   3.0e - 34
E value
                   104
Match length
                   66
% identity
                   (AC002535) similar to SWI/SNF complex subunit BAF170
NCBI Description
                   [Arabidopsis thaliana]
                   46929
Seq. No.
                   jC-gmst02400039b01a1
Seq. ID
Method
                   BLASTX
                   q3805956
NCBI GI
                   451
BLAST score
                   6.0e-45
E value
                   106
Match length
                   74
% identity
                   (Y13769) laccase [Populus balsamifera subsp. trichocarpa]
NCBI Description
                   46930
Seq. No.
                   jC-gmst02400039e01a1
Seq. ID
                   BLASTX
Method
                   q4567209
NCBI GI
BLAST score
                   199
E value
                   3.0e-30
Match length
                   105
% identity
                   64
                   (AC007168) hypothetical protein [Arabidopsis thaliana]
```

NCBI Description

Seq. No. jC-gmst02400039e04a1 Seq. ID

Method BLASTX

```
a3367517
NCBI GI
                  481
BLAST score
                  2.0e-48
E value
                  153
Match length
                  52
% identity
                  (AC004392) Similar to F4I1.26 putative beta-glucosidase
NCBI Description
                  gi_3128187 from A. thaliana BAC gb_AC004521. ESTs
                  gb_N97083, gb_F19868 and gb_F15482 come from this gene.
                  [Arabidopsis thaliana]
                  46932
Seq. No.
                  jC-gmst02400040a07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2853072
                  294
BLAST score
                  1.0e-26
E value
                  76
Match length
                  74
% identity
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]
                  46933
Seq. No.
                  jC-gmst02400040c11d1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3341687
BLAST score
                  141
                  1.0e-08
E value
                  44
Match length
                   66
% identity
                  (AC003672) putative ras protein [Arabidopsis thaliana]
NCBI Description
                   46934
Seq. No.
                   jC-gmst02400040e02a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g313723
BLAST score
                   75
E value
                   6.0e - 34
Match length
                   155
                   87
% identity
NCBI Description P.sativum hemC mRNA for hydroxymethylbilane synthase
                   46935
Seq. No.
                   jC-gmst02400040f10a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g602564
BLAST score
                   80
                   4.0e-37
E value
Match length
                   248
                   83
% identity
NCBI Description C.paradisi (Macf) INO1 gene
```

Seq. No. 46936

Seq. ID jC-gmst02400041h05a1

Method BLASTN
NCBI GI g1399304
BLAST score 48
E value 3.0e-18
Match length 48



thaliana]

% identity

NCBI Description

```
% identity
                  Glycine max phosphoinositide-specific phospholipase C P13
NCBI Description
                  mRNA, complete cds
                  46937
Seq. No.
                  jC-gmst02400042c08a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4567248
                  256
BLAST score
                  3.0e-22
E value
                  108
Match length
                   47
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46938
Seq. No.
                   jC-gmst02400042g06a1
Seq. ID
                  BLASTX
Method
                   g4249411
NCBI GI
                   355
BLAST score
                   9.0e-34
E value
                   100
Match length
                   67
% identity
                   (AC006072) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46939
                   jC-gmst02400043a06a1
Seq. ID
                   BLASTX
Method
                   g3785997
NCBI GI
                   330
BLAST score
                   9.0e-31
E value
                   120
Match length
                   55
% identity
                  (AC005499) putative annexin [Arabidopsis thaliana]
NCBI Description
                   46940
Seq. No.
                   jC-gmst02400043b02a1
Seq. ID
Method
                   BLASTX
                   q3738302
NCBI GI
                   224
BLAST score
E value
                   2.0e-18
                   58
Match length
                   69
% identity
                   (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4249398 (AC006072) putative tubby protein [Arabidopsis
                   thaliana]
                   46941
Seq. No.
                   jC-qmst02400043c05a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3033381
BLAST score
                   600
                   2.0e-62
E value
                   139
Match length
```

(AC004238) putative UDP-galactose-4-epimerase [Arabidopsis

```
Seq. No.
                  jC-qmst02400043c06a1
Seq. ID
                  BLASTX
Method
                  q4104561
NCBI GI
BLAST score
                  397
                  1.0e-38
E value
                  124
Match length
                  62
% identity
NCBI Description (AF036960) subtilisin-like protease [Glycine max]
                  46943
Seq. No.
                  jC-gmst02400043c09a1
Seq. ID
                  BLASTX
Method
                  g4539383
NCBI GI
                  218
BLAST score
                  1.0e-17
E value
                  109
Match length
                  35
% identity
                  (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  46944
Seq. No.
                  jC-gmst02400044c04a1
Seq. ID
                  BLASTX
Method
                  g2213629
NCBI GI
                  377
BLAST score
                  2.0e-49
E value
                  145
Match length
% identity
                   61
                  (AC000103) F21J9.21 [Arabidopsis thaliana]
NCBI Description
                   46945
Seq. No.
                   jC-gmst02400044d06d1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g131385
                   172
BLAST score
                   2.0e-12
E value
Match length
                   42
                   74
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN)
                   46946
Seq. No.
                   jC-gmst02400044f04a1
Seq. ID
                   BLASTN
Method
                   g3885514
NCBI GI
                   49
BLAST score
E value
                   6.0e-19
                   89
Match length
% identity
NCBI Description Medicago sativa clone MS56 unknown mRNA
```

Seq. No. 46947

Seq. ID jC-gmst02400044g01d1

Method BLASTN NCBI GI g949872



```
BLAST score
                  1.0e-140
E value
                  305
Match length.
                  96
% identity 🏂
NCBI Description G.max DNA for EF-Tu chloroplast specific protein
                   46948
Seq. No.
                   jC-gmst02400045d06a1
Seq. ID
                  BLASTX
Method
                   g3021279
NCBI GI
                   102
BLAST score
                   7.0e-09
E value
                   88
Match length
```

% identity 43
NCBI Description (AL022347) serine/threonine kinase [Arabidopsis thaliana]

 Seq. No.
 46949

 Seq. ID
 jC-gmst02400046b11a1

 Method
 BLASTN

 NCBI GI
 g21002

 BLAST score
 55

 E value
 1.0e-22

Match length 121 % identity 9

NCBI Description Bean DNA for glycine-rich cell wall protein GRP 1.8

Seq. No. 46950

Seq. ID jC-gmst02400046g11d1

Method BLASTX
NCBI GI g3046695
BLAST score 174
E value 1.0e-12
Match length 74
% identity 51

NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

Seq. No. 46951

Seq. ID jC-gmst02400046g12d1

Method BLASTX
NCBI GI g3786009
BLAST score 192
E value 1.0e-14
Match length 49
% identity 76

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 46952

Seq. ID jC-gmst02400046h03a1

Method BLASTN
NCBI GI g1277163
BLAST score 112
E value 3.0e-56
Match length 193
% identity 91

NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds

Seq. No. 46953

Seq. ID Method



~ ·

```
jC-gmst02400047c11a1
Seq. ID
                  BLASTX
Method
                  q3776564
NCBI GI
                  456
BLAST score
                  2.0e-45
E value
                  165
Match length
                  55
% identity
                  (AC005388) Similar to hypothetical protein T1D16.16
NCBI Description
                  gi_3075397 from A. thaliana BAC gb_AC004484. [Arabidopsis ...
                  thaliana]
                  46954
Seq. No.
                  jC-gmst02400047d06a1
Seq. ID
                  BLASTX
Method
                  g309673
NCBI GI
                  162
BLAST score
                  1.0e-11
E value
                  62
Match length
                  66
% identity
                  (L19651) light harvesting protein [Pisum sativum]
NCBI Description
                  46955
Seq. No.
                  jC-gmst02400047e12a1
Seq. ID
                  BLASTX
Method
                  g3913439
NCBI GI
                  193
BLAST score
                  7.0e-15
E value
                   43
Match length
                   86
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi_1498080 (U64927) S-adenosylmethionine
                   decarboxylase [Ipomoea nil]
                   46956
Seq. No.
                   jC-gmst02400047f02d1
Seq. ID
                   BLASTN
Method
                   g3510345
NCBI GI
BLAST score
                   82
                   3.0e-38
E value
Match length
                   214
% identity
                   85
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNJ8, complete sequence [Arabidopsis thaliana]
                   46957
Seq. No.
                   jC-gmst02400047f08a1
Seq. ID
                   BLASTN
Method
                   q1438878
NCBI GI
BLAST score
                   236
                   1.0e-130
E value
Match length
                   311
                   95
% identity
NCBI Description Glycine max choline kinase GmCKlp mRNA, complete cds
Seq. No.
```

jC-qmst02400047f09a1

BLASTX



```
g3913420
NCBI GI
                  530
BLAST score
                  4.0e-54
E value
Match length
                  128
% identity
                  77
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >qi 1421752 (U60592) S-adenosylmethionine
                  decarboxylase [Pisum sativum]
                   46959
Seq. No.
                   jC-gmst02400047g05a1
Seq. ID
                  BLASTX
Method
                   g4115382
NCBI GI
BLAST score
                   204
                   5.0e-27
E value
Match length
                   156
% identity
                   47
                  (AC005967) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46960
Seq. No.
                   jC-qmst02400048g04a1
Seq. ID
Method
                   BLASTX
                   g3702340
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
                   43
Match length
% identity
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46961
Seq. No.
                   jC-gmst02400049a07a1
Seq. ID
                   BLASTX
Method
                   q4234953
NCBI GI
                   279
BLAST score
                   9.0e-25
E value
                   139
Match length
% identity
                  (AF098970) NBS-LRR-like protein cD7 [Phaseolus vulgaris]
NCBI Description
                   46962
Seq. No.
Seq. ID
                   jC-gmst02400049c07a1
                   BLASTX
Method
                   q3540180
NCBI GI
                   498
BLAST score
                   2.0e-50
E value
                   154
Match length
 % identity
                   (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   46963
 Seq. No.
                   jC-gmst02400049c07d1
 Seq. ID
                   BLASTX
 Method
                   g3540180
 NCBI GI
                   220
 BLAST score
                   8.0e-18
 E value
                   50
 Match length
```

% identity





```
(AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  46964
Seq. No.
                  jC-gmst02400049g04d1
Seq. ID
                  BLASTN
Method
                  g4490734
NCBI GI
BLAST score
                  83
E value
                  1.0e-38
Match length
                  214
                  85
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
                                                                       (ESSA
NCBI Description
                  project)
                  46965
Seq. No.
                  jC-gmst02400049h07d1
Seq. ID
Method
                  BLASTX
                  g1171577
NCBI GI
BLAST score
                  239
                  4.0e-20
E value
                  88
Match length
                  57
% identity
                  (X95343) hypersensitivity-related gene [Nicotiana tabacum]
NCBI Description
                  46966
Seq. No.
                  jC-gmst02400050c01d1
Seq. ID
Method
                  BLASTX
                  g4512705
NCBI GI
                  160
BLAST score
                  7.0e-11
E value
Match length
                  70
                  57
% identity
                   (AC006569) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   46967
                   jC-gmst02400050d01a1
Seq. ID
Method
                   BLASTX
                   g4510383
NCBI GI
                   357
BLAST score
E value
                   7.0e-34
                   110
Match length
                   69
% identity
                   (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   46968
                   jC-gmst02400050f06a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3402754
BLAST score
                   424
                   1.0e-41
E value
Match length
                   146
                   57
% identity
                  (AL031187) putative protein [Arabidopsis thaliana]
```

Seq. No. 46969

NCBI Description

jC-gmst02400050f11a1 Seq. ID

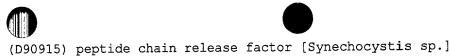
Method BLASTX

% identity

42



```
q2160756
NCBI GI
                   288
BLAST score
                   1.0e-25
E value
                   170
Match length
                   39
% identity
                  (U96879) CLV1 receptor kinase [Arabidopsis thaliana]
NCBI Description
                   46970
Seq. No.
                   jC-gmst02400050h08a1
Seq. ID
                   BLASTX
Method
                   g4544389
NCBI GI
                   385
BLAST score
                   4.0e-37
E value
Match length
                   153
% identity
                   56
                  (AC007047) putative homeodomain protein [Arabidopsis
NCBI Description
                   thaliana]
                   46971
Seq. No.
                   jC-gmst02400051c05a1
Seq. ID
                   BLASTX
Method
                   g4262153
NCBI GI
BLAST score
                   178
                   5.0e-13
E value
                   121
Match length
                   37
% identity
                   (AC005275) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   46972
Seq. No.
                   jC-gmst02400051d03a1
Seq. ID
                   BLASTX
Method
                   g2270994
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
                   82
Match length
                   57
% identity
                   (AF004809) Ca+2-binding EF hand protein [Glycine max]
NCBI Description
                   46973
Seq. No.
                   jC-gmst02400051e08d1
Seq. ID
                   BLASTX
Method
                   g3695392
NCBI GI
BLAST score
                   220
                   8.0e-18
E value
Match length
                   62
                   63
% identity
                   (AF096371) No definition line found [Arabidopsis thaliana]
NCBI Description
                   46974
Seq. No.
Seq. ID
                   jC-qmst02400051f02d1
                   BLASTX
Method
                   q1653665
NCBI GI
                   176
BLAST score
                   1.0e-12
E value
Match length
                   86
```



NCBI Description



```
46975
Seq. No.
                  jC-gmst02400052a05a1
Seq. ID
                  BLASTX
Method
                  g3377850
NCBI GI
BLAST score
                  156
                  3.0e-10
E value
                  39
Match length
                  85
% identity
                  (AF076274) contains simlarity to Canis familiaris signal
NCBI Description
                  peptidase complex 25 kDa subunit (GB:U12687) [Arabidopsis
                  thaliana]
                   46976
Seq. No.
                   jC-gmst02400052d05a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1706955
BLAST score
                  83
                   4.0e-39
E value
                  183
Match length
                   86
% identity
                  Gossypium hirsutum cellulose synthase (celA1) mRNA,
NCBI Description
                   complete cds
                   46977
Seq. No.
                   jC-gmst02400052g10a1
Seq. ID
                   BLASTN
Method
                   g18551
NCBI GI
BLAST score
                   398
                   0.0e + 00
E value
                   402
Match length
                   100
% identity
                   Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
                   46978
Seq. No.
                   jC-gmst02400053a04d1
Seq. ID
                   BLASTX
Method
                   q3885327
NCBI GI
                   168
BLAST score
                   8.0e-12
E value
                   50
Match length
                   60
% identity
                   (AC005623) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46979
Seq. No.
                   jC-gmst02400053f09d1
Seq. ID
Method
                   BLASTN
                   q1055367
NCBI GI
BLAST score
                   79
                   1.0e-36
E value
                   279
Match length
                   87
% identity
                   Glycine max ribulose-1,5-bisphosphate carboxylase small
NCBI Description
```

subunit mRNA, complete cds

- 7



```
46980
Seq. No.
                  jC-gmst02400054a10a1
Seq. ID
                  BLASTX
Method
                  g4538939
NCBI GI
                  423
BLAST score
                  1.0e-41
E value
                  141
Match length
                  62
% identity
                  (AL049483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  46981
Seq. No.
                  jC-gmst02400054c05a1
Seq. ID
Method
                  BLASTX
                  g2979554
NCBI GI
                  373
BLAST score
                  1.0e-35
E value
                  99
Match length
                   69
% identity
NCBI Description (AC003680) CDC4 like protein [Arabidopsis thaliana]
                   46982
Seq. No.
                   jC-gmst02400054c12a1
Seq. ID
Method
                   BLASTX
                   g3402704
NCBI GI
BLAST score
                   214
                   5.0e-17
E value
                   140
Match length
                   33
% identity
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
                   46983
Seq. No.
                   jC-gmst02400054d01d1
Seq. ID
Method
                   BLASTN
                   q576506
NCBI GI
BLAST score
                   47
E value
                   3.0e-17
                   123
Match length
                   85
% identity
                  Pisum sativum outer membrane protein (IAP75) mRNA, complete
NCBI Description
                   cds
                   46984
Seq. No.
Seq. ID
                   jC-gmst02400054g04a1
Method
                   BLASTX
                   g4559333
NCBI GI
BLAST score
                   193
                   1.0e-14
E value
Match length
                   94
                   53
% identity
                  (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
                   46985
Seq. No.
                   jC-gmst02400054h07a1
Seq. ID
Method
                   BLASTX
```

g3831442

256

NCBI GI

BLAST score

```
4 0e=22
```

E value 4.0e-22
Match length 103
% identity 42

NCBI Description (AC005819) homeobox-leucine zipper protein [Arabidopsis

thaliana]

Seq. No. 46986

Seq. ID jC-gmst02400055b06a1

Method BLASTX
NCBI GI g2288887
BLAST score 233
E value 1.0e-19
Match length 96
% identity 62

NCBI Description (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis

thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate

diphosphate decarboxylase [Arabidopsis thaliana]

>gi 3786002 (AC005499) mevalonate diphosphate decarboxylase

[Arabidopsis thaliana]

Seq. No. 46987

Seq. ID jC-gmst02400055f11a1

Method BLASTX
NCBI GI g3695392
BLAST score 296
E value 9.0e-27
Match length 146
% identity 48

NCBI Description (AF096371) No definition line found [Arabidopsis thaliana]

Seq. No. 46988

Seq. ID jC-gmst02400055g03a1

Method BLASTX
NCBI GI g2351099
BLAST score 361
E value 2.0e-34
Match length 129
% identity 51

NCBI Description (AB006812) endonuclease III homologue [Mus musculus]

>gi_2407946_emb_CAA70866_ (Y09688) endonuclease III
homologue 1 [Mus musculus] >gi_3219302_dbj_BAA28846_
(AB009371) homologue of endonuclease III [Mus musculus]

Seq. No. 46989

Seq. ID jC-gmst02400056a05a1

Method BLASTX
NCBI GI g2149955
BLAST score 261
E value 4.0e-44
Match length 126
% identity 72

NCBI Description (U97023) putative aquaporin-1 [Phaseolus vulgaris]

Seq. No. 46990

Seq. ID jC-gmst02400056b08a1

Method BLASTX NCBI GI g3150406



```
BLAST score
                  8.0e-21
E value
                  112
Match length
                   46
% identity
                  (AC004165) putative indole-3-acetate
NCBI Description
                  beta-glucosyltransferase [Arabidopsis thaliana]
                   46991
Seq. No.
                   jC-gmst02400056e11d1
Seq. ID
                  BLASTN
Method
                   g558924
NCBI GI
                   102
BLAST score
                   4.0e-50
E value
Match length
                   230
% identity
                   86
                  Lupinus albus geranylgeranyl pyrophosphate synthase (ggps1)
NCBI Description
                  mRNA, complete cds
                   46992
Seq. No.
                   jC-gmst02400056f07d1
Seq. ID
                   BLASTX
Method
                   g3152583
NCBI GI
                   199
BLAST score
                   2.0e-15
E value
                   49
Match length
                   69
% identity
                   (AC002986) Contains similarity to inhibitor of apoptosis
NCBI Description
                   protein gb_U45881 from D. melanogaster. [Arabidopsis
                   thaliana]
                   46993
Seq. No.
                   jC-gmst02400057a03a1
Seq. ID
                   BLASTX
Method
                   g2245115
NCBI GI
                   188
BLAST score
                   5.0e-14
E value
                   79
Match length
% identity
                   51
                   (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   46994
Seq. No.
                   jC-gmst02400057a09a1
Seq. ID
                   BLASTX
Method
                   q2947063
NCBI GI
BLAST score
                   306
E value
                   7.0e-28
                   145
Match length
                   50
% identity
                   (AC002521) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   46995
Seq. No.
                   jC-qmst02400057b04a1
Seq. ID
                   BLASTX
```

Method BLASTX
NCBI GI g2827992
BLAST score 373
E value 4.0e-36



```
Match length
                  66
% identity
                  (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
NCBI Description
                  46996
Seq. No.
                  jC-gmst02400057c02a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2498979
                  147
BLAST score
                  3.0e-09
E value
                  68
Match length
                  43
% identity
                  TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT
NCBI Description
                   (TAFII-150) (TAFII150) >gi_627172_pir__A54063 TATA-binding
                  protein-associated factor II - fruit fly (Drosophila sp.)
                  >gi_541665_emb_CAA55830_ (X79243) dTAF II 150 [Drosophila
                  melanogaster]
                   46997
Seq. No.
                   jC-gmst02400057e02a1
Seq. ID
                   BLASTX
Method
                   g4220482
NCBI GI
                   459
BLAST score
                   1.0e-45
E value
                   162
Match length
                   55
% identity
                  (AC006069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   46998
Seq. No.
                   jC-gmst02400057g10a1
Seq. ID
                   BLASTX
Method
                   g3176660
NCBI GI
                   277
BLAST score
E value
                   2.0e-24
Match length
                   65
                   77
% identity
                   (AC004393) Similar to ERECTA receptor protein kinase
NCBI Description
                   gb_U47029 from A. thaliana. [Arabidopsis thaliana]
                   46999
Seq. No.
                   iC-qmst02400057h07a1
Seq. ID
                   BLASTX
Method
                   g2980782
NCBI GI
                   548
BLAST score
E value
                   3.0e-56
                   161
Match length
% identity
                   (AL022198) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47000
Seq. No.
                   jC-gmst02400058c07a1
Seq. ID
Method
                   BLASTX
```

7583

q4406763

7.0e-25

280

84

65

NCBI GI BLAST score

E value

Match length

% identity

```
(AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                   47001
Seq. No.
                   jC-gmst02400058e04d1
Seq. ID
                   BLASTX
Method
                  q1914683
NCBI GI
                   267
BLAST score
                   2.0e-23
E value
                   87
Match length
                   63
% identity
                  (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
                   47002
Seq. No.
                   jC-gmst02400058f08a1
Seq. ID
                   BLASTX
Method
                   g3063445
NCBI GI
                   329
BLAST score
                   7.0e-31
E value
                   107
Match length
                   52
% identity
                   (AC003981) F22013.7 [Arabidopsis thaliana]
NCBI Description
                   47003
Seq. No.
                   jC-gmst02400058f08d1
Seq. ID
                   BLASTX
Method
                   g3063445
NCBI GI
                   264
BLAST score
                   5.0e-23
E value
                   96
Match length
                   57
% identity
                   (AC003981) F22013.7 [Arabidopsis thaliana]
NCBI Description
                   47004
Seq. No.
                   jC-gmst02400058g12a1
Seq. ID
                   BLASTX
Method
                   q3426048
NCBI GI
                   278
BLAST score
                   8.0e-25
E value
                   97
Match length
                   58
% identity
                   (AC005168) putative hydroxymethylglutaryl-CoA lyase
NCBI Description
                   precursor [Arabidopsis thaliana]
                   47005
 Seq. No.
                   jC-gmst02400060c11a1
 Seq. ID
                   BLASTX
Method
                   g2735256
NCBI GI
                   156
BLAST score
                   3.0e-10
 E value
                   78
Match length
 % identity
                   (U89683) protein kinase [Lycopersicon esculentum]
 NCBI Description
```

7584

47006

BLASTX q3860247

jC-gmst02400060e06a1

Seq. No.

Seq. ID Method

NCBI GI

% identity

NCBI Description

43



```
BLAST score
                  1.0e-32
E value
                  72
Match length
                  88
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47007
                  jC-gmst02400060g08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2924728
BLAST score
                  57
E value
                   3.0e-23
Match length
                   199
                   90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXH1, complete sequence [Arabidopsis thaliana]
                   47008
Seq. No.
                   jC-qmst02400060h04a1
Seq. ID
                   BLASTX
Method
                   q4455275
NCBI GI
                   269
BLAST score
E value
                   1.0e-23
Match length
                   132
% identity
                   (AL035527) putative protein [Arabidopsis thaliana]
NCBI Description
                   47009
Seq. No.
                   jC-qmst02400061e01a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2160544
                   564
BLAST score
                   4.0e-58
E value
Match length
                   168
% identity
                   (U63652) ent-kaurene synthase A [Pisum sativum]
NCBI Description
                   47010
Seq. No.
                   jC-qmst02400061g07a1
Seq. ID
                   BLASTX
Method
                   g4210449
NCBI GI
                   417
BLAST score
                   3.0e-41
E value
Match length
                   102
                   79
% identity
                   (AB016471) ARR1 protein [Arabidopsis thaliana]
NCBI Description
                   47011
Seq. No.
                   jC-gmst02400062b08a1
Seq. ID
                   BLASTX
Method
                   g3183401
NCBI GI
                   289
BLAST score
                   7.0e-26
E value
Match length
                   159
```

(AL031180) protease, possible pheromone response

PUTATIVE ZINC-PROTEASE C2E11.12C >gi 3395558 emb_CAA20142_



[Schizosaccharomyces pombe]

```
      Seq. No.
      47012

      Seq. ID
      jC-gmst02400062d02d1

      Method
      BLASTX

      NCBI GI
      g1911822

      BLAST score
      200

      E value
      2.0e-15

      Match length
      82
```

Match length 82 % identity 50

NCBI Description (S83425) glycosylasparaginase alpha beta {EC 3.5.1.26} [Spodoptera frugiperda, Sf9, Peptide, 320 aa] [Spodoptera

1

frugiperda]

Seq. No. 47013

Seq. ID jC-gmst02400062d04d1

Method BLASTX
NCBI GI g3080375
BLAST score 150
E value 9.0e-10
Match length 64
% identity 48

NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. 47014

Seq. ID jC-gmst02400062e12a1

Method BLASTX
NCBI GI g2529685
BLAST score 379
E value 2.0e-36
Match length 79
% identity 94

NCBI Description (AC002535) putative dimethyladenosine transferase

[Arabidopsis thaliana]

Seq. No. 47015

Seq. ID jC-gmst02400062f04d1

Method BLASTX
NCBI GI g1708924
BLAST score 179
E value 3.0e-13
Match length 39
% identity 87

NCBI Description MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT

MALIC ENZYME) (NADP-ME) >gi 515759 (L34836) malate

dehydrogenase (NADP+) [Vitis vinifera]

Seq. No. 47016

Seq. ID jC-gmst02400063b04a1

Method BLASTN
NCBI GI g169360
BLAST score 122
E value 6.0e-62
Match length 283
% identity 88

NCBI Description P.vulgaris PVPK-1 protein, complete cds



```
Seq. No.
                  jC-gmst02400063b10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220529
BLAST score
                  360
                  2.0e-34
E value
                  107
Match length
% identity
                  64
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  47018
Seq. No.
                  jC-gmst02400063c04d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827709
BLAST score
                  346
E value
                  1.0e-32
Match length
                  136
% identity
                  27
                  (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                  47019
Seq. No.
                  jC-gmst02400063d06a1
Seq. ID
Method
                  BLASTN
                                 *
NCBI GI
                  q4324966
BLAST score
                  224
E value
                  1.0e-123
Match length
                  248
% identity
                  98
NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds
                  47020
Seq. No.
Seq. ID
                  jC-gmst02400063g02a1
Method
                  BLASTX
NCBI GI
                  g2342724
BLAST score
                  450
                  6.0e-49
E value
Match length
                  162
                  64
% identity
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                  jC-gmst02400063h11d1
Method
                  BLASTX
NCBI GI
                  q2160180
BLAST score
                  140
E value
                  1.0e-08
Match length
                  30
% identity
                  80
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47022
                  jC-gmst02400064g12d1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g584825
```

233

45

2.0e-19

BLAST score

E value Match length

```
% identity
                  B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
NCBI Description
                  >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus
                  carota]
                  47023
Seq. No.
                  jC-gmst02400064h11d1
Seq. ID
                  BLASTX
Method
                  q2344891
NCBI GI
                  238
BLAST score
                  6.0e-20
E value
                  110
Match length
                  43
% identity
                  (AC002388) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  47024
Seq. No.
                  jC-gmst02400065a02d1
Seq. ID
                  BLASTX
Method
                  q3935183
NCBI GI
                  177
BLAST score
                  8.0e-13
E value
                  92
Match length
                  47
% identity
                  (AC004557) F17L21.26 [Arabidopsis thaliana]
NCBI Description
                   47025
Seq. No.
                   jC-gmst02400065a08d1
Seq. ID
                   BLASTX
Method
                   q2244759
NCBI GI
                   365
BLAST score
                   7.0e-35
E value
                   72
Match length
                   89
% identity
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
NCBI Description
                   47026
Seq. No.
                   jC-gmst02400065d05a2
Seq. ID
                   BLASTX
Method
                   a1707998
NCBI GI
                   485
BLAST score
                   7.0e-49
E value
                   124
Match length
                   79
 % identity
                   SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481944 pir__S40218 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - potato
                   >gi_438247_emb_CAA81082_ (Z25863) glycine
                   hydroxymethyltransferase [Solanum tuberosum]
```

Seq. No. 47027

Seq. ID jC-gmst02400065d11a2

Method BLASTX
NCBI GI g3367520
BLAST score 406
E value 5.0e-41
Match length 128



% identity 68

NCBI Description (AC004392) Similar to protein kinase APK1A,

tyrosine-serine-threonine kinase gb D12522 from A.

thaliana. [Arabidopsis thaliana]

Seq. No.

Seq. ID jC-gmst02400065d11d1

47028

Method BLASTX
NCBI GI g4580398
BLAST score 304
E value 1.0e-27
Match length 101
% identity 58

NCBI Description (AC007171) putative protein kinase APKIA [Arabidopsis

thaliana]

Seq. No.

47029

Seq. ID jC-gmst02400065h09d1

Method BLASTX
NCBI GI g585338
BLAST score 214
E value 2.0e-17
Match length 58
% identity 76

NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)

>gi 391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza

sativa]

Seq. No.

47030

Seq. ID jC-gmst02400065h10d1

Method BLASTX
NCBI GI g3212610
BLAST score 175
E value 1.0e-12
Match length 53
% identity 60

NCBI Description Chain A, Sulfite Oxidase From Chicken Liver

>gi_3212611_pdb_1SOX_B Chain B, Sulfite Oxidase From

Chicken Liver

Seq. No. 47031

Seq. ID jC-gmst02400066b04a2

Method BLASTX
NCBI GI g3687223
BLAST score 318
E value 2.0e-34
Match length 136
% identity 64

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47032

Seq. ID jC-gmst02400066b11d1

Method BLASTX
NCBI GI g4510363
BLAST score 146
E value 2.0e-09
Match length 38

% identity NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis thaliana] Seq. No. 47033 jC-qmst02400066d12a2 Seq. ID Method BLASTN NCBI GI q2443750 BLAST score 34 E value 2.0e-09 Match length 54 91 % identity NCBI Description Arabidopsis thaliana fumarase (FUM1) gene, complete cds 47034 Seq. No. jC-qmst02400066e09a2 Seq. ID Method BLASTX NCBI GI q3142298 BLAST score 160 7.0e-11 E value Match length 123 % identity 34 NCBI Description (AC002411) Strong similarity to protein SBT1 gb X98929 from Lycopersicum esculentum. [Arabidopsis thaliana] Seq. No. 47035 Seq. ID jC-qmst02400066e09d1 Method BLASTX NCBI GI g1483177 BLAST score 280 E value 4.0e-25 Match length 112 50 % identity (D86598) antifreeze-like protein (af70) [Picea abies] NCBI Description Seq. No. 47036 jC-gmst02400066h08a2 Seq. ID

Method BLASTX
NCBI GI g3329366
BLAST score 151
E value 8.0e-10
Match length 38
% identity 79

NCBI Description (AF031243) nodule-specific protein N1j70 [Lotus japonicus]

Seq. No. 47037

Seq. ID jC-gmst02400066h10a2

Method BLASTX
NCBI GI g2098707
BLAST score 194
E value 8.0e-15
Match length 76
% identity 53

NCBI Description (U82974) pectinesterase [Citrus sinensis]

Seq. No. 47038

Seq. ID jC-gmst02400066h10d1

Match length

NCBI Description

% identity

101 49

```
Method
NCBI GI
                   q2098709
                   249
BLAST score
E value
                   2.0e-21
                   64
Match length
% identity
                   (U82975) pectinesterase [Citrus sinensis]
NCBI Description
Seq. No.
                   jC-gmst02400067a08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4263790
BLAST score
                   382
                   5.0e-37
E value
                   153
Match length
                   63
% identity
                  (AC006068) putative ch-TOG protein [Arabidopsis thaliana]
NCBI Description
                   47040
Seq. No.
                   jC-gmst02400067d07a1
Seq. ID
                   BLASTN
Method
                   g456713
NCBI GI
BLAST score
                   462
E value
                   0.0e + 00
                   474
Match length
                   29
% identity
                   Glycine max gene for ubiquitin, complete cds
NCBI Description
                   47041
Seq. No.
                   jC-gmst02400067e01a1
Seq. ID
                   BLASTX
Method
                   q1518540
NCBI GI
                   736
BLAST score
E value
                   3.0e-78
                   163
Match length
% identity
                   82
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                   47042
                   jC-qmst02400067f06d1
Seq. ID
Method
                   BLASTX
                   g3643607
NCBI GI
BLAST score
                   235
E value
                   8.0e-20
                   52
Match length
% identity
                   88
                   (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                   47043
Seq. No.
                   jC-qmst02400067f07d1
Seq. ID
                   BLASTX
Method
                   q2529686
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
```

(AC002535) putative G-beta-repeat containing protein, 5'



partial [Arabidopsis thaliana]

```
Seq. No.
                   47044
Seq. ID
                   jC-gmst02400069a02a1
Method
                   BLASTN
                   g456567
NCBI GI
BLAST score
                   78
                   6.0e-36
E value
Match length
                   149
% identity
                   91
                  Pisum sativum ubiquitin conjugating enzyme (UBC4), complete
NCBI Description
Seq. No.
                   47045
                   jC-gmst02400069c09d1
Seq. ID
                   BLASTX
Method
                   g2146731
NCBI GI
BLAST score
                   165
E value
                   6.0e-12
Match length
                   46
                   67
% identity
                  FK506-binding protein - Arabidopsis thaliana >gi_1354207
NCBI Description
                   (U49453) rof1 [Arabidopsis thaliana]
                   47046
Seq. No.
Seq. ID
                   jC-qmst02400069e01d1
Method
                   BLASTX
NCBI GI
                   q466160
BLAST score
                   219
                   7.0e-18
E value
                   50
Match length
                   84
% identity
                  HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                   >gi 630771 pir S44903 ZK652.3 protein - Caenorhabditis
                   elegans >gi 289769 (L14429) putative [Caenorhabditis
                   elegans]
                   47047
Seq. No.
                   jC-gmst02400069g02d1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3452136
BLAST score
                   60
                   2.0e-25
E value
                   84
Match length
                   93
% identity
                  Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                   partial
                   47048
Seq. No.
                   jC-gmst02400069h05a1
Seq. ID
Method
                   BLASTN
                   g1053215
NCBI GI
BLAST score
                   390
E value
                   0.0e + 00
Match length
                   412
% identity
                   99
```

NCBI Description Glycine max chlorophyll a/b-binding protein (cab3) mRNA,

NCBI Description



nuclear gene encoding chloroplast protein, complete cds

```
Seq. No.
                   jC-gmst02400069h08a1
Seq. ID
                  BLASTX
Method
                  g2274993
NCBI GI
BLAST score
                   228
                   1.0e-18
E value
                   81
Match length
% identity
                   (AJ000230) unnamed protein product [Hordeum vulgare]
NCBI Description
Seq. No.
                   jC-gmst02400069h10a1
Seq. ID
                   BLASTN
Method
                   g170065
NCBI GI
                   411
BLAST score
                   0.0e + 00
E value
                   439
Match length
                   18
% identity
                   Soybean (G.max) proline-rich cell wall protein (SbPRP2)
NCBI Description
                   gene, complete cds
                   47051
Seq. No.
                   jC-gmst02400070h11a1
Seq. ID
                   BLASTX
Method
                   q3461835
NCBI GI
                   684
BLAST score
                   4.0e-72
E value
                   178
Match length
                   72
% identity
                   (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi_3927840 (AC005727) putative protein kinase [Arabidopsis
                   thaliana]
                   47052
Seq. No.
                   jC-qmst02400071b02a1
Seq. ID
Method
                   BLASTX
                   g3746069
NCBI GI
                   128
BLAST score
E value
                   3.0e-10
Match length
                   113
                   37
% identity
                   (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
                   47053
 Seq. No.
                   jC-gmst02400071b11a1
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   g3004564
                   560
 BLAST score
                   9.0e-58
 E value
                   142
 Match length
                   75
 % identity
                   (AC003673) putative receptor Ser/Thr protein kinase
```

[Arabidopsis thaliana]

```
470
```

Seq. No. 47054

Seq. ID jC-gmst02400071b12a1

Method BLASTX
NCBI GI g2129651
BLAST score 542
E value 2.0e-55
Match length 166
% identity 65

NCBI Description myosin heavy chain ATM2 - Arabidopsis thaliana (fragment)

>gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis

thaliana]

Seq. No. 47055

Seq. ID jC-gmst02400071f11a1

Method BLASTN
NCBI GI g18834
BLAST score 190
E value 1.0e-102
Match length 474
% identity 85

NCBI Description H.brasiliensis HMGR1 mRNA for 3-hydroxy-3-methylglutaryl

coenzyme A reductase

Seq. No. 47056

Seq. ID jC-gmst02400071h04a1

Method BLASTN

NCBI GI g938299

BLAST score 34

E value 4.0e-10

Match length 54

% identity 91

NCBI Description V.ungiculata mRNA for unknown protein (A3 gene)

Seq. No. 47057

Seq. ID jC-gmst02400072a02a1

Method BLASTX
NCBI GI g1717755
BLAST score 405
E value 2.0e-39
Match length 116
% identity 66

NCBI Description TROPINONE REDUCTASE HOMOLOG (P29X) >gi 539028_pir__C48674

tropinone reductase homolog - jimsonweed >gi_424158 (L20475) 29kDa protein; high homology to aa sequence of

tropinone reductases [Datura stramonium]

Seq. No. 47058

Seq. ID jC-gmst02400072a06a1

Method BLASTX
NCBI GI g2462749
BLAST score 196
E value 4.0e-15
Match length 57
% identity 63

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]



```
Seq. No.
                  jC-gmst02400072h11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3236249
BLAST score
                  130
                  5.0e-11
E value
                  65
Match length
                  52
% identity
NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]
                  47060
Seq. No.
                  jC-gmst02400073a12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462763
BLAST score
                  329
                  1.0e-30
E value
Match length
                  112
% identity
                  59
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  47061
Seq. No.
Seq. ID
                  jC-gmst02400073d03a1
Method
                  BLASTN
NCBI GI
                  q1008880
BLAST score
                  99
E value
                  3.0e-48
Match length
                  201
% identity
                  90
                  Phaseolus vulgaris eukaryotic initiation factor 5 (eIF-5)
NCBI Description
                  gene, complete cds
Seq. No.
                  47062
Seq. ID
                  jC-gmst02400073d04a1
                  BLASTX
Method
                  g3461817
NCBI GI
BLAST score
                  585
                  1.0e-60
E value
Match length
                  171
% identity
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
                  47063
Seq. No.
                  jC-gmst02400073f05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2088659
BLAST score
                  289
E value
                  6.0e-26
Match length
                  77
                  77
% identity
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]
                  47064
Seq. No.
```

Seq. ID jC-gmst02400073g07a1

Method BLASTX NCBI GI g4220445 BLAST score 226



E value 2.0e-18 Match length 119 % identity 5

NCBI Description (AC006216) Similar to gi_3004555 F19F24.14 salt inducible protein homolog from Arabidopsis thaliana BAC gb_AC003673.

[Arabidopsis thaliana]

Seq. No. 47065

Seq. ID jC-gmst02400074a05a1

Method BLASTX
NCBI GI g4206209
BLAST score 636
E value 1.0e-66
Match length 136
% identity 82

NCBI Description (AF071527) putative glucan synthase component [Arabidopsis

thaliana] >gi 4263042 gb AAD15311 (AC005142) putative

1

glucan synthase component [Arabidopsis thaliana]

Seq. No. 47066

Seq. ID jC-qmst02400074b03d1

Method BLASTN
NCBI GI g1370204
BLAST score 38
E value 6.0e-12

Match length 91 % identity 91

NCBI Description L.japonicus mRNA for small GTP-binding protein, RAN1B

Seq. No. 47067

Seq. ID jC-gmst02400074b10d1

Method BLASTX
NCBI GI g4469025
BLAST score 181
E value 2.0e-13
Match length 45
% identity 69

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 47068

Seq. ID jC-qmst02400074d05a1

Method BLASTX
NCBI GI g4539414
BLAST score 197
E value 5.0e-17
Match length 135
% identity 53

NCBI Description (AL049524) putative subtilisin-like protease [Arabidopsis

thaliana]

Seq. No. 47069

Seq. ID jC-gmst02400074h03d1

Method BLASTX
NCBI GI g3445238
BLAST score 511
E value 5.0e-52
Match length 131



```
% identity
                  (AL022347) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3451059_emb_CAA20455.1_ (AL031326) putative protein
                  [Arabidopsis thaliana]
                  47070
Seq. No.
                  jC-gmst02400075f10d1
Seq. ID
                  BLASTX
Method
                  g2760612
NCBI GI
                  190
BLAST score
                  3.0e-14
E value
                  78
Match length
                  46
% identity
                   (AB002414) cyclophilin-type peptidyl-prolyl cis-trans
NCBI Description
                  isomerase [Halobacterium cutirubrum]
                  47071
Seq. No.
                   jC-gmst02400076a04d1
Seq. ID
                  BLASTX
Method
                  g3702328
NCBI GI
                   242
BLAST score
                   2.0e-20
E value
                   53
Match length
                   81
% identity
                  (AC005397) putative cytochrome b5 [Arabidopsis thaliana]
NCBI Description
                   47072
Seq. No.
                   jC-gmst02400076a08a1
Seq. ID
                   BLASTX
Method
                   g3860321
NCBI GI
                   269
BLAST score
                   1.0e-23
E value
                   82
Match length
                   70
% identity
                   (AJ012687) beta-galactosidase [Cicer arietinum]
NCBI Description
                   47073
Seq. No.
                   jC-gmst02400076b12a1
Seq. ID
                   BLASTX
Method
                   q4490735
NCBI GI
                   436
BLAST score
                   4.0e-43
E value
                   128
Match length
                   63
% identity
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   47074
Seq. No.
                   jC-gmst02400076c01a1
Seq. ID
                   BLASTN
Method
                   q1173641
NCBI GI
BLAST score
                   286
                   1.0e-160
E value
                   431
Match length
                   96
 % identity
NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds
```

47075

Seq. No.



```
jC-gmst02400076c06a1
Seq. ID
                  BLASTN
Method
                  a18764
NCBI GI
                  429
BLAST score
                  0.0e+00
E value
                  437
Match length
                  100
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                  47076
Seq. No.
                   jC-gmst02400076g11a1
Seq. ID
                  BLASTN
Method
                  g4098318
NCBI GI
                   185
BLAST score
                   1.0e-99
E value
                   385
Match length
                   87
% identity
NCBI Description Triticum aestivum beta-tubulin 1 (tubb1) mRNA, complete cds
                   47077
Seq. No.
                   jC-gmst02400076h04a1
Seq. ID
                   BLASTX
Method
                   g3096920
NCBI GI
                   411
BLAST score
                   4.0e-40
E value
                   88
Match length
                   85
% identity
                   (AL023094) putative ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   47078
Seq. No.
                   jC-gmst02400076h09a1
Seq. ID
                   BLASTX
Method
                   q3176689
NCBI GI
                   348
BLAST score
                   7.0e-33
E value
                   146
Match length
                   48
% identity
                   (AC003671) Contains similarity to ubiquitin
NCBI Description
                   carboxyl-terminal hydrolase 14 gb_Z35927 from S.
                   cerevisiae. [Arabidopsis thaliana]
                   47079
 Seq. No.
                   jC-gmst02400077a11a1
 Seq. ID
 Method
                   BLASTX
                   g3252807
 NCBI GI
                    141
 BLAST score
                    1.0e-08
 E value
 Match length
                    133
                    32
 % identity
                   (AC004705) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    47080
```

Seq. No.

jC-gmst02400077c03a1 Seq. ID

Method BLASTX g3805845 NCBI GI 528 -BLAST score



E value Match length 129 % identity

(AL031986) putative protein [Arabidopsis thaliana] NCBI Description

47081 Seq. No.

jC-gmst02400077c05a1 Seq. ID

BLASTX Method g2270994 NCBI GI 410 BLAST score 3.0e-40E value 134 Match length 55 % identity

(AF004809) Ca+2-binding EF hand protein [Glycine max] NCBI Description

47082 Seq. No.

jC-gmst02400077c05d1 Seq. ID

Method BLASTX g2270994 NCBI GI 184 BLAST score 6.0e-14 E value 62 Match length

55 % identity

(AF004809) Ca+2-binding EF hand protein [Glycine max] NCBI Description

47083 Seq. No.

jC-gmst02400077c12d1 Seq. ID

BLASTN Method q1944190 NCBI GI 295 BLAST score 1.0e-165 E value 299 Match length 100 % identity

NCBI Description Glycine max mRNA for nodulin 35, complete cds

47084 Seq. No.

jC-qmst02400077f12a1 Seq. ID

BLASTX Method g2149640 NCBI GI BLAST score 192 2.0e-14 E value 141 Match length % identity

(U91995) Argonaute protein [Arabidopsis thaliana] NCBI Description

47085 Seq. No.

jC-gmst02400078a07a1 Seq. ID

Method BLASTX q2114104 NCBI GI BLAST score 517 E value 9.0e-53 130 Match length 74 % identity

(AB003590) sulfate transporter [Arabidopsis thaliana] NCBI Description

>gi 2114106 dbj BAA20085_ (AB003591) sulfate transporter

[Arabidopsis thaliana]

NCBI GI



```
Seq. No.
                   jC-gmst02400078d06d1
Seq. ID
                   BLASTX
Method
                   g2459412
NCBI GI
                   309
BLAST score
                   2.0e-28
E value
                   130
Match length
% identity
                   47
                  (AC002332) putative G9a protein [Arabidopsis thaliana]
NCBI Description
                   47087
Seq. No.
                   jC-qmst02400078d07a1
Seq. ID
                   BLASTN
Method
                   q3869065
NCBI GI
                   48
BLAST score
                   6.0e-18
E value
                   96
Match length
% identity
                   88
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K24M7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   47088
                   jC-qmst02400078f03d1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q525331
                   42
BLAST score
                   3.0e-14
E value
                   122
Match length
                   84
% identity
                   Pisum sativum Alaska alpha-tubulin (TubA1) gene, complete
NCBI Description
                   cds
                   47089
Seq. No.
                   jC-gmst02400078g06a1
Seq. ID
Method
                   BLASTX
                   g2864618
NCBI GI
                   210
BLAST score
                   1.0e-16
E value
                   75
Match length
% identity
                  (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
                   47090
Seq. No.
                   jex700903039.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3241923
                   39
BLAST score
                   9.0e-13
E value
                   47
Match length
                   96
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MMN10, complete sequence [Arabidopsis thaliana]
                    47091
 Seq. No.
 Seq. ID
                    jex700903134.h1
                   BLASTN
 Method
```

g1778371

```
BLAST score
E value
                   1.0e-29
Match length
                   117
% identity
                   91
NCBI Description
                   Glycine max asparagine synthetase 1 (AS1) mRNA, complete
Seq. No.
                   47092
Seq. ID
                   jex700903280.h1
Method
                   BLASTX
NCBI GI
                   q4432821
BLAST score
                   281
E value
                   2.0e-25
Match length
                   79
% identity
NCBI Description
                  (AC006593) putative transmembrane protein [Arabidopsis
                   thaliana]
Seq. No.
                   47093
                   jex700903293.h1
Seq. ID
Method_
                   BLASTX
NCBI GI
                   q2765093
BLAST score
                   157
E value
                   6.0e-11
Match length
                   73
% identity
                   51
NCBI Description (Y10983) putative cytochrome P450 [Glycine max]
Seq. No.
                   47094
Seq. ID
                   jex700903384.h1
Method
                  BLASTX
NCBI GI
                   q4262186
BLAST score
                   163
E value
                  8.0e-12
Match length
                   43
% identity
                  70
NCBI Description
                  (AC005508) Highly similar to cullin 3 [Arabidopsis
                  thaliana]
Seq. No.
                  47095
Seq. ID
                  jex700903424.h1
Method
                  BLASTX
NCBI GI
                  g3158476
BLAST score
                  282
E value
                  2.0e-25
Match length
                  67
% identity
                  82
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  47096
Seq. ID
                  jex700903441.h1
Method
```

BLASTX NCBI GI g2541876 BLAST score 153 2.0e-10 E value Match length 64 % identity 53

```
(D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                  [Nicotiana tabacum]
                  47097
Seq. No.
                  jex700903448.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1695691
BLAST score
                  104
                  1.0e-51
E value
Match length
                  184
                  89
% identity
NCBI Description Pisum sativum mRNA for diminuto, complete cds
                  47098
Seq. No.
                  jex700903459.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3047117
BLAST score
                  210
                  4.0e-17
E value
Match length
                  59
                  75
% identity
                  (AF058919) similar to ATP-dependent RNA helicases
NCBI Description
                  [Arabidopsis thaliana]
                  47099
Seq. No.
Seq. ID
                  jex700903567.h1
                  BLASTX
Method
NCBI GI
                  g3482977
                  185
BLAST score
                  1.0e-17
E value
Match length
                  57
                  86
% identity
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
                  47100
Seq. No.
Seq. ID
                  jex700903587.h1
                  BLASTX
Method
NCBI GI
                  q2244981
BLAST score
                  145
                  2.0e-18
E value
```

Match length 71 % identity

NCBI Description (Z97340) similarity to proline-rich protein APG -

Arabidopsis [Arabidopsis thaliana]

47101 Seq. No.

Seq. ID jex700903616.hl

Method BLASTX NCBI GI g3935167 BLAST score 199 E value 7.0e-16 Match length 43 % identity

(AC004557) F17L21.10 [Arabidopsis thaliana] NCBI Description

47102 Seq. No.

jex700903632.h1 Seq. ID



```
Method
NCBI GI
                  g1171161
BLAST score
                  181
E value
                  9.0e-14
Match length
                  67
% identity
                  51
NCBI Description
                  (U41472) pectate lyase homolog [Medicago sativa]
                  47103
Seq. No.
Seq. ID
                  jex700903633.h1
Method
                  BLASTN
NCBI GI
                  g2282583
BLAST score
                  72
                  2.0e-32
E value
                  163
Match length
% identity
                  90
                  Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete
NCBI Description
                  47104
Seq. No.
Seq. ID
                  jex700903639.hl
Method
                  BLASTN
NCBI GI
                  q516853
BLAST score
                  40
                  2.0e-13
E value
Match length
                  60
% identity
NCBI Description
                  Soybean SUBI-2 gene for ubiquitin, complete cds
Seq. No.
                  47105
                  jex700903657.h1
Seq. ID
Method
                  BLASTN
                  g2598656
NCBI GI
BLAST score
                  103
E value
                  5.0e-51
Match length
                  135
% identity
                  94
                  Vicia faba mRNA for elongation factor 1-alpha (EF1-a)
NCBI Description
                  47106
Seq. No.
                  jex700903754.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1477565
BLAST score
                  170
                  2.0e-12
E value
Match length
                  80
% identity
NCBI Description
                  (U50078) p532 [Homo sapiens]
                  >gi 4557026 ref NP 003913.1 pHERC1 hect (homologous to the
                  E6-AP (UBE3A) carboxyl terminus) domain and RCC1
                   (CHC1)-like domain (RLD)
```

Seq. No.

47107

80

jex700903821.h1 Seq. ID

Method BLASTN NCBI GI g3378649

BLAST score



```
E value
Match length
                   160
                   88
% identity
```

M.sativa mRNA translated from abscisic activated gene NCBI Description

Seq. No. 47108

jex700903843.h1 Seq. ID

BLASTX Method q2708743 NCBI GI 160 BLAST score 2.0e-11 E value 72 Match length 32 % identity

(AC003952) putative Tal-1-like reverse transcriptase NCBI Description

[Arabidopsis thaliana]

Seq. No.

47109

Seq. ID jex700903859.h1

Method BLASTN NCBI GI g1262439 BLAST score 98 5.0e-48 E value 237 Match length 86 % identity

NCBI Description Glycine max lipoxygenase (vlxC) mRNA, complete cds

Seq. No.

jex700903967.h1 Seq. ID

BLASTX Method NCBI GI g3702332 152 BLAST score 2.0e-10 E value Match length 72 39 % identity

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.

47111

47110

Seq. ID jex700904050.h1

BLASTN Method NCBI GI q4468192 BLAST score 111 E value 9.0e-56 Match length 139 % identity 95

NCBI Description Glycine max mRNA for inosine monophosphate dehydrogenase

Seq. No.

47112

Seq. ID jex700904070.h1

Method BLASTN NCBI GI g18551 BLAST score 55 3.0e-22 E value Match length 171 % identity 87

Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding NCBI Description

protein



Seq. No. 47113

Seq. ID jex700904089.h1

Method BLASTX
NCBI GI g2642159
BLAST score 187
E value 7.0e-19
Match length 80
% identity 62

NCBI Description (AC003000) putative mannose-1-phosphate guanyltransferase

[Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose

pyrophosphorylase [Arabidopsis thaliana] >gi_4151925

(AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No. 47114

Seq. ID jex700904115.h1

Method BLASTX
NCBI GI g4455232
BLAST score 96
E value 1.0e-08
Match length 64
% identity 58

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 47115

Seq. ID jex700904153.h1

Method BLASTX
NCBI GI g546360
BLAST score 140
E value 5.0e-11
Match length 67
% identity 61

NCBI Description (S70187) ferric leghemoglobin reductase, FLbR [Glycine

max=soybeans, Merr, nodules, Peptide, 523 aa] [Glycine max]

Seq. No. 47116

Seq. ID jex700904154.h1

Method BLASTX
NCBI GI g3047095
BLAST score 172
E value 8.0e-13
Match length 47
% identity 68

NCBI Description (AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 72.39) [Arabidopsis thaliana]

Seq. No. 47117

Seq. ID jex700904174.h1

Method BLASTX
NCBI GI g3080420
BLAST score 229
E value 2.0e-19
Match length 80
% identity 53

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 47118



```
jex700904181.h1
Seq. ID
                  BLASTX
Method
                  g2828296
NCBI GI
BLAST score
                  244
                  3.0e-21
E value
Match length
                  61
                  75
% identity
                  (AL021687) RNase L inhibitor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47119
                  jex700904217.h1
Seq. ID
                  BLASTX
Method
                  g4138265
NCBI GI
                  444
BLAST score
E value
                  2.0e-44
Match length
                  91
% identity
                  82
                  (AJ006228) Avr9 elicitor response protein [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                   47120
                   jex700904230.h1
Seq. ID
Method
                  BLASTX
                  g4432867
NCBI GI
BLAST score
                  243
E value
                   6.0e-21
Match length
                  88
% identity
                   49
                  (AC006300) putative dnaJ-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   47121
                   jex700904271.hl
Seq. ID
                   BLASTX
Method
                   g2344898
NCBI GI
BLAST score
                   227
                   5.0e-19
E value
Match length
                   39
                   100
% identity
                  (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis
NCBI Description
                   thaliana]
                   47122
Seq. No.
                   jex700904295.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g242461
                   48
BLAST score
                   4.0e-18
E value
Match length
                   80
% identity
                   90
                  loxA=lipoxygenase [Glycine max=soybeans, Merr.cv.Williams,
NCBI Description
                   mRNA, 1897 nt]
```

Seq. No. 47123

Seq. ID jex700904303.h1

Method BLASTX NCBI GI g1750376



```
BLAST score
                  2.0e-30
E value
                  85
Match length
% identity
                  78
                  (U80808) ubiquitin activating enzyme [Arabidopsis thaliana]
NCBI Description
                  >qi 3150409 (AC004165) ubiquitin activating enzyme (UBA1)
                  [Arabidopsis thaliana]
                  47124
Seq. No.
                  jex700904319.h1
Seq. ID
                  BLASTX
Method
                  g2979556
NCBI GI
BLAST score
                  176
                  4.0e-13
E value
Match length
                  72
% identity
                  50
                  (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
                  47125
Seq. No.
                  jex700904341.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4218120
                  293
BLAST score
                  7.0e-27
E value
Match length
                  83
% identity
                  66
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  47126
Seq. No.
                   jex700904427.hl
Seq. ID
Method
                  BLASTX
                  q4262240
NCBI GI
                  289
BLAST score
E value
                  2.0e-26
Match length
                  83
                   64
% identity
                  (AC006200) putative stress protein [Arabidopsis thaliana]
NCBI Description
                   47127
Seq. No.
                   jex700904457.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1890331
BLAST score
                  335
                  9.0e-32
E value
Match length
                  83
                   69
% identity
                  (Y10275) L-3-phosphoserine phosphatase [Homo sapiens]
NCBI Description
Seq. No.
                   47128
                   jex700904466.hl
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4263722
BLAST score 111
E value 3.0e-12
Match length 73
% identity 51

Method

NCBI GI

BLASTX g3128228





```
(AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47129
                  jex700904477.h1
Seq. ID
Method
                  BLASTN
                  q3559806
NCBI GI
BLAST score
                  87
                  2.0e-41
E value
Match length
                  239
% identity
                  84
                 Arabidopsis thaliana mRNA for nuclear protein HCF136
NCBI Description
                  47130
Seq. No.
                  jex700904543.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g398598
BLAST score
                  67
                  2.0e-29
E value
Match length
                  123
% identity
                  89
NCBI Description A.hypochondriacus Lhcb2*Ah1 mRNA
Seq. No.
                   47131
                   jex700904554.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510397
BLAST score
                   287
E value
                   4.0e-26
Match length
                   86
% identity
                   67
                  (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
NCBI Description
                   47132
Seq. No.
                   jex700904559.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2887500
BLAST score
                   189
                   1.0e-14
E value
Match length
                   38
                   82
% identity
                  (AC002339) putative AP2 domain-containing protein
NCBI Description
                   [Arabidopsis thaliana]
                   47133
Seq. No.
                   jex700904584.h1
Seq. ID
Method
                   BLASTX
                   g2194119
NCBI GI
                   278
BLAST score
                   4.0e-25
E value
Match length
                   85
% identity
                  (AC002062) No definition line found [Arabidopsis thaliana]
NCBI Description
                   47134
Seq. No.
                   jex700904595.h1
Seq. ID
```



BLAST score 214 E value 1.0e-17 Match length 45 % identity 89

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 47135

Seq. ID jex700904638.hl

Method BLASTX
NCBI GI g3033399
BLAST score 215
E value 1.0e-17
Match length 82
% identity 6

NCBI Description (AC004238) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47136

Seq. ID jex700904654.hl

Method BLASTX
NCBI GI 94544399
BLAST score 133
E value 3.0e-16
Match length 79
% identity 58

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 47137

Seq. ID jex700904655.h1

Method BLASTN
NCBI GI g21016
BLAST score 64
E value 4.0e-28
Match length 100
% identity 91

NCBI Description P.vulgaris loxA gene for lipoxygenase

Seq. No. 47138

Seq. ID jex700904656.h1

Method BLASTN
NCBI GI g1173641
BLAST score 55
E value 3.0e-22
Match length 198
% identity 85

NCBI Description Glycine max lipoxygenase (lox7) mRNA, complete cds

Seq. No. 47139

Seq. ID jex700904660.h1

Method BLASTX
NCBI GI g3335351
BLAST score 162
E value 1.0e-11
Match length 52
% identity 16



NCBI Description (AC004512) Similar to ERECTA receptor protein kinase

gb D83257 from A. thaliana. ESTs gb_T41629 and gb_AA586072

come from this gene. [Arabidopsis thaliana]

Seq. No. 47140

٠.

Seq. ID jex700904696.hl

Method BLASTX
NCBI GI g4063760
BLAST score 271
E value 3.0e-24
Match length 82
% identity 60

NCBI Description (AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq. No. 47141

Seq. ID jex700904768.hl

Method BLASTN
NCBI GI g170091
BLAST score 165
E value 6.0e-88
Match length 248
% identity 92

NCBI Description Glycine max vegetative storage protein (vspB) gene,

complete cds

Seq. No. 47142

Seq. ID jex700904776.h1

Method BLASTX
NCBI GI g3337350
BLAST score 173
E value 3.0e-27
Match length 82

% identity 82

NCBI Description (AC004481) putative permease [Arabidopsis thaliana]

Seq. No. 47143

Seq. ID jex700904781.h1

Method BLASTX
NCBI GI g4512698
BLAST score 208
E value 5.0e-35
Match length 81
% identity 83

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47144

Seq. ID jex700904787.h1

Method BLASTN
NCBI GI g2662346
BLAST score 86
E value 8.0e-41

Match length 165 % identity 89

NCBI Description Oryza sativa mRNA for EF-1 alpha, complete cds

Seq. No. 47145

Seq. ID jex700904810.h1

7610



```
Method
                  BLASTN
NCBI GI
                  g2264311
BLAST score
                  61
                  7.0e-26
E value
                  141
Match length
                  86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLN1, complete sequence [Arabidopsis thaliana]
                  47146
Seq. No.
                  jex700904856.hl
Seq. ID
Method
                  BLASTX
                  g4325339
NCBI GI
BLAST score
                  396
E value
                  7.0e-39
Match length
                  89
% identity
                  74
                  (AF128392) No definition line found [Arabidopsis thaliana]
NCBI Description
                  47147
Seq. No.
                  jex700904884.h1
Seq. ID
                  BLASTX
Method
                  q4539452
NCBI GI
BLAST score
                  243
                  5.0e-21
E value
Match length
                  80
                   57
% identity
                  (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
                   47148
Seq. No.
                   jex700904885.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2245073
                   38
BLAST score
                   4.0e-12
E value
Match length
                   111
                   90
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   47149
Seq. No.
                   jex700904910.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4432855
BLAST score
                   240
E value
                   1.0e-20
Match length
                   64
                   78
% identity
                  (AC006300) unknown protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 47150

Seq. ID jex700904913.hl

BLASTX Method q4490737 NCBI GI BLAST score 177 E value 3.0e-13



```
Match length
% identity
                  32
                  (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                  47151
Seq. No.
                  jex700904949.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g533256
BLAST score
                  166
                  4.0e-12
E value
                  49
Match length
                  59
% identity
                  (L27101) pectinesterase [Petunia inflata]
NCBI Description
                  47152
Seq. No.
                  jex700904960.h1
Seq. ID
                  BLASTX
Method
                  g2997613
NCBI GI
BLAST score
                  280
                  1.0e-25
E value
Match length
                  84
                  69
% identity
                  (AF035438) CUM1 [Cucumis sativus]
NCBI Description
Seq. No.
                  47153
                  jex700904976.h1
Seq. ID
Method
                  BLASTX
                  g1213629
NCBI GI
                  199
BLAST score
E value
                  8.0e-19
                  64
Match length
                  72
% identity
                  (X95991) pectinesterase [Prunus persica]
NCBI Description
Seq. No.
                  47154
                   jex700904978.h1
Seq. ID
Method
                  BLASTX
                  q3426038
NCBI GI
                   259
BLAST score
E value
                   7.0e-23
Match length
                  82
                   66
% identity
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   47155
Seq. No.
                   jex700905031.h1
Seq. ID
Method
                  BLASTX
```

q3482973 NCBI GI BLAST score 268 7.0e-24 E value Match length 85 72 % identity

(AL031369) putative protein [Arabidopsis thaliana] NCBI Description

47156 Seq. No.

jex700905035.h1 Seq. ID

Method BLASTX



```
q1165322
NCBI GI
BLAST score
                  143
                  2.0e-09
E value
Match length
                  39
% identity
                  72
                  (U44838) extensin [Glycine max]
NCBI Description
                  47157
Seq. No.
                  jex700905286.h1
Seq. ID
Method
                  BLASTX
                  g3643599
NCBI GI
                  209
BLAST score
                  7.0e-21
E value
                  70
Match length
% identity
                  73
                  (AC005395) putative trytophanyl-tRNA synthetase
NCBI Description
                   [Arabidopsis thaliana]
                   47158
Seq. No.
                   jex700905306.h1
Seq. ID
Method
                   BLASTX
                   q3377797
NCBI GI
BLAST score
                   259
                   8.0e-23
E value
Match length
                   66
% identity
                   79
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
                   47159
Seq. No.
                   jex700905312.h1
Seq. ID
Method
                   BLASTX
                   g4105697
NCBI GI
BLAST score
                   263
E value
                   3.0e-23
                   72
Match length
% identity
                   69
NCBI Description (AF049870) thaumatin-like protein [Arabidopsis thaliana]
                   47160
Seq. No.
                   jex700905352.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3892046
BLAST score
                   330
E value
                   4.0e-31
Match length
                   87
% identity
                   74
```

NCBI Description (AC002330) predicted protein destination factor

[Arabidopsis thaliana]

Seq. No. 47161

Seq. ID jex700905368.h1

Method BLASTX NCBI GI g3004565



BLAST score 2.0e-09 E value Match length 34 79 % identity

(AC003673) putative protein kinase [Arabidopsis thaliana] NCBI Description

47162 Seq. No.

jex700905420.h1 Seq. ID

Method BLASTX NCBI GI g4544422 BLAST score 214 1.0e-17 E value Match length 77 % identity 58

NCBI Description (AC006955) putative fimbrin [Arabidopsis thaliana]

Seq. No.

47163

jex700905480.h1 Seq. ID

Method BLASTN g21002 NCBI GI BLAST score 33 3.0e-09 E value Match length 45 % identity 17

NCBI Description Bean DNA for glycine-rich cell wall protein GRP 1.8

47164 Seq. No.

jex700905490.h1 Seq. ID

Method BLASTN NCBI GI g1518539 BLAST score 164 2.0e-87 E value Match length 172 99 % identity

NCBI Description Glycine max UDP-glucose dehydrogenase mRNA, complete cds

47165 Seq. No.

jex700905495.h1 Seq. ID

Method BLASTN NCBI GI g1575730 BLAST score 151 1.0e-79 E value 155 Match length 99 % identity

Glycine max 14-3-3 related protein SGF14D mRNA, complete NCBI Description

47166 Seq. No.

jex700905517.h1 Seq. ID

Method BLASTX NCBI GI g4262141 179 BLAST score 2.0e-13 E value Match length 56 % identity 61

NCBI Description (AC005275) hypothetical protein [Arabidopsis thaliana]

Method

NCBI GI BLAST score BLASTX g3250679

123



```
47167
Seq. No.
                  jex700905586.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469020
                  361
BLAST score
                  8.0e-35
E value
                  85
Match length
                  78
% identity
                  (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  47168
Seq. No.
                  jex700905626.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2317902
BLAST score
                  194
                  3.0e-15
E value
Match length
                  62
% identity
                  53
                  (U89959) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47169
Seq. No.
                   jex700905673.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2826842
BLAST score
                  317
E value
                  1.0e-29
Match length
                  80
% identity
                  71
NCBI Description (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]
Seq. No.
                   47170
                   jex700905679.h1
Seq. ID
                  BLASTX
Method
                  g2244866
NCBI GI
BLAST score
                   215
                   9.0e-18
E value
                   66
Match length
% identity
                   65
                 (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47171
                   jex700905683.h1
Seq. ID
                   BLASTX
Method
                   g3128168
NCBI GI
                   189
BLAST score
                   1.0e-14
E value
Match length
                   76
                   50
% identity
                  (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
                   47172
Seq. No.
                   jex700905717.h1
Seq. ID
```



```
E value
                   2.0e-11
Match length
                   46
                   72
% identity
NCBI Description
```

(AL024486) putative protein [Arabidopsis thaliana]

47173 Seq. No.

jex700905821.h1 Seq. ID

Method BLASTX g1209703 NCBI GI 194 BLAST score 2.0e-31 E value Match length 86 % identity 78

(U40489) maize gl1 homolog [Arabidopsis thaliana] NCBI Description

Seq. No. 47174

jex700905840.hl Seq. ID

Method BLASTX g3004555 NCBI GI BLAST score 185 E value 8.0e-30 Match length 123 % identity 23

(AC003673) similar to salt inducible protein [Arabidopsis NCBI Description

thaliana]

47175 Seq. No.

Seq. ID jex700905866.h1

Method BLASTX NCBI GI g3643607 BLAST score 192 2.0e-32 E value Match length 84 59 % identity

(AC005395) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

47176

jex700905928.h1 Seq. ID

Method BLASTN NCBI GI g21306 BLAST score 46 6.0e-17 E value Match length 118 85 % identity

S.oleracea mRNA for photosystem II 22kDa protein NCBI Description

Seq. No.

47177 jex700905940.h1 Seq. ID

Method BLASTN g310575 NCBI GI BLAST score 53

E value 4.0e-21 Match length 193 85 % identity

Glycine max nodulin-26 mRNA, complete cds NCBI Description

Seq. No. 47178

7616

```
jex700905990.h1
Seq. ID
                  BLASTX
Method
                  g3413424
NCBI GI
BLAST score
                  150
                  4.0e-10
E value
                  75
Match length
                  47
% identity
                  (AJ006309) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47179
                  jex700906021.h1
Seq. ID
Method
                  BLASTN
                  g457572
NCBI GI
BLAST score
                  122
E value
                   3.0e-62
Match length
                  253
% identity
                   91
                  V.angularis mRNA for endo-xyloglucan transferase, complete
NCBI Description
Seq. No.
                   47180
                   jex700906046.hl
Seq. ID
Method
                   BLASTX
                   g2760837
NCBI GI
                   385
BLAST score
E value
                   1.0e-37
Match length
                   87
% identity
                  79
NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
                   47181
Seq. No.
                   jex700906065.h1
Seq. ID
                   BLASTX
Method
                   g4530126
NCBI GI
BLAST score
                   143
                   3.0e-09
E value
Match length
                   56
                   48
% identity
                  (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
Seq. No.
                   47182
                   jex700906170.h1
Seq. ID
```

Method BLASTX
NCBI GI g3341694
BLAST score 145
E value 1.0e-09
Match length 69
% identity 57

NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]

Seq. No. 47183

Seq. ID jex700906181.h1

Method BLASTX
NCBI GI g2979543
BLAST score 285
E value 6.0e-26



Match length 80 % identity 78

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.

47184 jex700906193.h1

Method BLASTX
NCBI GI g4314359
BLAST score 301
E value 8.0e-28
Match length 78
% identity 74

NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

47185

Seq. ID jex700906279.h1

Method BLASTX
NCBI GI g2464855
BLAST score 214
E value 1.0e-17
Match length 50
% identity 74

NCBI Description (Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No.

47186

Seq. ID jex700906296.h1

Method BLASTX
NCBI GI g3334259
BLAST score 261
E value 4.0e-23
Match length 85
% identity 62

NCBI Description WD-40 REPEAT PROTEIN MSI4 >gi 2599092 (AF028711) WD-40

repeat protein MSI4 [Arabidopsis thaliana]

Seq. No. 47187

Seq. ID jex700906317.h1

Method BLASTX
NCBI GI g3193293
BLAST score 237
E value 3.0e-20
Match length 75
% identity 57

NCBI Description (AF069298) contains a short region of similarity to another

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

Seq. No. 47188

Seq. ID jex700906435.h1

Method BLASTX
NCBI GI g3600036
BLAST score 374
E value 3.0e-36
Match length 91
% identity 75

NCBI Description (AF080119) contains similarity to protein kinase domains



```
47189
Seq. No.
                   jex700906445.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3176097
                  80
BLAST score
                   3.0e-37
E value
                  224
Match length
% identity
                   83
                  Medicago truncatula mRNA for annexin
NCBI Description
                   47190
Seq. No.
                   jex700906471.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2865427
BLAST score
                   120
                   1.0e-10
E value
                   85
Match length
% identity
                   41
                  (AF039372) polyprotein [Arabidopsis thaliana]
NCBI Description
                   47191
Seq. No.
                   jex700906487.hl
Seq. ID
                   BLASTX
Method
                   g3152731
NCBI GI
BLAST score
                   297
                   3.0e-27
E value
Match length
                   60
% identity
                   95
                  (AF056325) myo-inositol 1-phosphate synthase; INO1 [Hordeum
NCBI Description
                   vulgare]
                   47192
Seq. No.
                   jex700906508.h1
Seq. ID
                   BLASTX
Method
                   g2961352
NCBI GI
                   285
BLAST score
                   7.0e-26
E value
Match length
                   69
% identity
                   72
NCBI Description (AL022140) putative protein [Arabidopsis thaliana]
                   47193
Seq. No.
                   jex700906556.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g575603
BLAST score
                   \bar{1}71
                   1.0e-12
E value
Match length
                   65
% identity
                   48
NCBI Description
                  (D42064) cationic peroxidase isozyme 38K precursor
                   [Nicotiana tabacum]
```

Seq. No. 47194

Seq. ID jex700906681.h1

Method BLASTX NCBI GI g2829901



```
BLAST score
                  4.0e-21
E value
Match length
                  59
% identity
                  81
                  (AC002311) putative 10kd chaperonin [Arabidopsis thaliana]
NCBI Description
                  47195
Seq. No.
                  jex700906701.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1009234
BLAST score
                  258
                  8.0e-23
E value
Match length
                  55
% identity
                  89
NCBI Description
                  (L38829) SUP2 gene product [Nicotiana tabacum]
Seq. No.
                  47196
                  jex700906703.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2979562
BLAST score
                  298
E value
                  2.0e-27
Match length
                  89
% identity
                  (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3386623 (AC004665) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                   47197
                   jex700906770.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3096910
                   374
BLAST score
                   3.0e-36
E value
Match length
                   86
                   78
% identity
                  (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   47198
Seq. No.
                   jex700906783.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4468986
                   172
BLAST score
                   1.0e-12
E value
Match length
                   73
% identity
                   45
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47199
```

jex700906814.h1 Seq. ID

Method BLASTN q1431628 NCBI GI 36 BLAST score 6.0e-11 E value Match length 36

100 % identity



NCBI Description V.radiata mRNA for pectinacetylesterase

Seq. No. 47200

Seq. ID jex700906911.hl

Method BLASTN g2369713 NCBI GI

BLAST score 79 1.0e-36 E value Match length 175 % identity 89

Beta vulgaris cDNA for elongation factor NCBI Description

Seq. No.

47201 jex700906914.h1 Seq. ID

Method BLASTX NCBI GI g2462134 BLAST score 230 E value 2.0e-19 Match length 85

% identity 51

NCBI Description (Y13368) reverse transcriptase [Beta vulgaris]

Seq. No. 47202

jex700906936.hl Seq. ID

Method BLASTX NCBI GI g3668088 BLAST score 219 E value 4.0e-18 85 Match length 58 % identity

(AC004667) G9a-like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 47203

jex700906985.h1 Seq. ID

Method BLASTX NCBI GI g3152590 BLAST score 214 E value 1.0e-17 Match length 71 % identity 62

(AC002986) Similar to protein serine/threonine kinase NPK15 NCBI Description gb D31737 from Nicotiana tabacum. [Arabidopsis thaliana]

47204 Seq. No.

jex700906991.hl Seq. ID

Method BLASTX NCBI GI g4191782 406 BLAST score 4.0e-40 E value Match length 83 % identity 87

(AC005917) WD-40 repeat protein [Arabidopsis thaliana] NCBI Description

47205 Seq. No.

jex700907016.hl Seq. ID

Method BLASTN NCBI GI q886099

7621



```
BLAST score 189
E value 1.0e-102
Match length 221
% identity 96
```

NCBI Description Glycine max putative water channel protein (Pip1) mRNA,

complete cds

Seq. No. 47206

Seq. ID jex700907090.h1

Method BLASTX
NCBI GI g2961085
BLAST score 159
E value 2.0e-12
Match length 83
% identity 57

NCBI Description (AF037228) transcription factor [Arabidopsis thaliana]

Seq. No. 47207

Seq. ID jex700907168.h1

Method BLASTX
NCBI GI g2827516
BLAST score 176
E value 4.0e-13
Match length 54
% identity 65

NCBI Description (AL021633) DNA topoisomerase like- protein [Arabidopsis

thaliana]

Seq. No.

47208

Seq. ID jex700907169.h1

Method BLASTX
NCBI GI g4490736
BLAST score 170
E value 2.0e-12
Match length 55
% identity 38

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No.

47209

Seq. ID jex700907255.h1

Method BLASTX
NCBI GI g2827546
BLAST score 170
E value 2.0e-12
Match length 57
% identity 53

NCBI Description (AL021635) cytochrome P450 like protein [Arabidopsis

thaliana]

Seq. No. 47210

Seq. ID jex700907259.h1

Method BLASTX
NCBI GI g4006886
BLAST score 274
E value 1.0e-24
Match length 59
% identity 86



```
(Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47211
Seq. ID
                  jex700907266.h1
Method
                  BLASTX
                  g3341443
NCBI GI
BLAST score
                  161
                  2.0e-11
E value
Match length
                  64
                  45
% identity
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                  47212
Seq. No.
Seq. ID
                  jex700907362.h1
Method
                  BLASTX
NCBI GI
                  q3560529
BLAST score
                  154
                  1.0e-10
E value
Match length
                  43
                  74
% identity
                  (AF039598) light harvesting chlorophyll A/B binding protein
NCBI Description
                   [Prunus persica]
                  47213
Seq. No.
Seq. ID
                   jex700907364.h1
Method
                  BLASTX
                  g3152568
NCBI GI
BLAST score
                  284
E value
                   1.0e-25
                   78
Match length
% identity
                   69
                  (AC002986) Similar to hypothetical protein product
NCBI Description
                   gb_Z97337 from A. thaliana. EST gb_H76597 comes from this
                   gene. [Arabidopsis thaliana]
                   47214
Seq. No.
                   jex700907410.h1
Seq. ID
                   BLASTN
Method
                   g558542
NCBI GI
                   86
BLAST score
                   5.0e-41
E value
                   159
Match length
                   100
% identity
                  G.max (Evans) mRNA for zinc-finger protein (C-terminal)
NCBI Description
                   47215
Seq. No.
                   jex700907452.h1
Seq. ID
                   BLASTN
Method
                   g1053215
NCBI GI
BLAST score
                   42
                   5.0e-15
E value
Match length
                   86
                   87
% identity
                 Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
```

Seq. No. 47216

nuclear gene encoding chloroplast protein, complete cds

```
jex700907496.h1
Seq. ID
                  BLASTX
Method
                  g3193308
NCBI GI
                  155
BLAST score
                  1.0e-10
E value
                  86
Match length
                  38
% identity
                  (AF069300) similar to Medicago truncatula MtN2 (GB:Y15293)
NCBI Description
                  [Arabidopsis thaliana]
                  47217
Seq. No.
                  jex700907592.h1
Seq. ID
```

Seq. ID jex/0090/592.

Method BLASTX

NCBI GI g2911067

BLAST score 160

E value 6.0e-20

Match length 76

% identity 68

NCBI Description (AL021960) UV-damaged DNA-binding protein-like

[Arabidopsis thaliana]

 Seq. No.
 47218

 Seq. ID
 jex700907612.h1

 Method
 BLASTX

 NCBI GI
 g3941436

 BLAST score
 163

NCBI GI g3941436
BLAST score 163
E value 1.0e-11
Match length 38
% identity 74

NCBI Description (AF062872) putative transcription factor [Arabidopsis

thaliana]

Seq. No.

47219

Seq. ID jex700907616.hl

Method BLASTX
NCBI GI g3021348
BLAST score 144
E value 1.0e-09
Match length 50
% identity 64

NCBI Description (AJ004961) ribosomal protein L18 [Cicer arietinum]

Seq. No.

47220

Seq. ID jex700907628.h1

Method BLASTX
NCBI GI g417544
BLAST score 163
E value 2.0e-11
Match length 68
% identity 62

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5)

>gi_320209_pir__A60695 photosystem I chain II precursor cucumber >gi_625966_pir__JQ2132 photosystem I complex 20K
protein precursor - cucumber >gi_227772_prf__1710320A

photosystem I 20kD protein [Cucumis sativus]

Method

NCBI GI

BLAST score

BLASTN

113

g310575



```
47221
Seq. No.
                  jex700907641.hl
Seq. ID
                  BLASTX
Method
                  g3924611
NCBI GI
                  302
BLAST score
                  6.0e-28
E value
                  82
Match length
                  72
% identity
                  (AF069442) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  47222
Seq. No.
                   jex700907667.hl
Seq. ID
                  BLASTX
Method
                  g1421741
NCBI GI
BLAST score
                   253
                   4.0e-22
E value
                   69
Match length
                   65
% identity
                  (U54770) cytochrome P450 homolog [Lycopersicon esculentum]
NCBI Description
                   47223
Seq. No.
                   jex700907694.h1
Seq. ID
                   BLASTN
Method
                   g684941
NCBI GI
                   83
BLAST score
                   5.0e-39
E value
                   159
Match length
% identity
                   88
NCBI Description Medicago sativa S-adenosyl-L-methionine:trans-caffeoyl-CoA
                   3-O-methyltransferase (CCOMT) mRNA, complete cds
                   47224
Seq. No.
                   jex700907728.h1
Seq. ID
                   BLASTX
Method
                   g4558673
NCBI GI
                   315
BLAST score
                   2.0e-29
E value
Match length
                   78
                   71
% identity
                  (AC007063) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47225
Seq. No.
                   jex700907805.h1
Seq. ID
                   BLASTX
Method
                   g3941448
NCBI GI
                   318
BLAST score
                   8.0e-30
E value
Match length
                   63
% identity
                   (AF062878) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   47226
Seq. No.
                   jex700907851.h1
Seq. ID
```



E value Match length 260 % identity

Glycine max nodulin-26 mRNA, complete cds NCBI Description

Seq. No.

47227

Seq. ID

jex700907867.hl

Method NCBI GI BLAST score E value

BLASTX g4263722 346

5.0e-33 Match length 83 % identity 83

(AC006223) putative glucan synthase [Arabidopsis thaliana] NCBI Description

Seq. No.

47228

Seq. ID

jex700907870.hl

Method BLASTX g2129929 NCBI GI 386 BLAST score E value 9.0e-38 Match length 81 90 % identity

NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 -

tomato >gi_1049068 (U28403) RNA polymerase II subunit 2

[Solanum lycopersicum]

Seq. No.

47229

Seq. ID

jex700907926.h1

Method BLASTX g4510339 NCBI GI 257 BLAST score 1.0e-22 E value Match length 72 % identity 69

(AC006921) putative ABC transporter protein [Arabidopsis NCBI Description

thaliana]

Seq. No.

47230

Seq. ID

jex700907943.h1

Method BLASTX NCBI GI g2842493 BLAST score 211 E value 3.0e-17 Match length 78 53 % identity

NCBI Description (AL021749) predicted protein [Arabidopsis thaliana]

Seq. No.

47231

Seq. ID

jex700907950.h1

Method BLASTX NCBI GI g1903347 BLAST score 294 6.0e-27 E value Match length 79 75 % identity

NCBI Description (AC000104) EST gb ATTS5672 comes from this gene.



[Arabidopsis thaliana]

Seq. No. 47232 jex700907963.h1 Seq. ID Method BLASTX NCBI GI g2062172 BLAST score 372 E value 4.0e-36 77 Match length 86 % identity (AC001645) unknown protein [Arabidopsis thaliana] NCBI Description 47233 Seq. No. Seq. ID jex700908134.h1 Method BLASTN g3063391 NCBI GI BLAST score 96 9.0e-47 E value 157 Match length % identity 96 Vigna radiata mRNA for Ca2+/H+ exchanger, complete cds NCBI Description 47234 Seq. No. jex700908153.h1 Seq. ID Method BLASTX NCBI GI g3219269 BLAST score 153 2.0e-10 E value Match length 38 79 % identity (AB015314) MAP kinase kinase 3 [Arabidopsis thaliana] NCBI Description 47235 Seq. No. jex700908183.h1 Seq. ID Method BLASTX NCBI GI g4006888 BLAST score 173 E value 9.0e-13 Match length 54 56 % identity NCBI Description (Z99708) putative protein [Arabidopsis thaliana] 47236 Seq. No. jex700908201.h1 Seq. ID Method BLASTX g2739044 NCBI GI 152 BLAST score 3.0e-10 E value Match length 55 76 % identity (AF024651) polyphosphoinositide binding protein Ssh1p NCBI Description [Glycine max]

Seq. No. 47237

Seq. ID jex700908285.h1

Method BLASTX NCBI GI g3236249



```
BLAST score
                  7.0e-13
E value
Match length
                  35
                  89
% identity
                  (AC004684) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  47238
Seq. No.
                  jex700908301.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4580394
BLAST score
                  379
                  7.0e-37
E value
Match length
                  87
% identity
                  79
NCBI Description
                  (AC007171) putative fatty acid elongase [Arabidopsis
                  thaliana]
                  47239
Seq. No.
                  jex700908308.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2104536
                  289
BLAST score
                  2.0e-26
E value
Match length
                  82
% identity
                  67
                  (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                  47240
Seq. No.
Seq. ID
                  jex700908322.h1
Method
                  BLASTX
NCBI GI
                  q3914472
BLAST score
                  245
E value
                  3.0e-21
Match length
                  59
% identity
                  80
NCBI Description
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
                  >gi_322764_pir__S32021 photosystem II 10K protein - common
                  tobacco >gi 22669 emb CAA49693 (X70088) NtpII10 [Nicotiana
                  tabacum]
Seq. No.
                  47241
                  jex700908326.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3176686
                  171
BLAST score
                  2.0e-12
E value
Match length
                  49
```

% identity 69

(AC003671) Similar to high affinity potassium transporter, NCBI Description

HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 47242

Seq. ID jex700908337.h1

Method BLASTN NCBI GI q4102599



BLAST score 67 E value 2.0e-29 Match length 135 % identity 87

NCBI Description Arabidopsis thaliana ARF6 (ARF6) mRNA, complete cds

Seq. No. 47243

Seq. ID jex700908340.h1

Method BLASTX
NCBI GI g3885328
BLAST score 173
E value 9.0e-13
Match length 35
% identity 94

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 47244

Seq. ID jex700908343.h1

Method BLASTN
NCBI GI g2505873
BLAST score 37
E value 1.0e-11
Match length 85
% identity 86

NCBI Description Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus

Seq. No. 47245

Seq. ID jex700908371.h1

Method BLASTX
NCBI GI g4191779
BLAST score 354
E value 5.0e-34
Match length 82
% identity 85

NCBI Description (AC005917) putative recA protein [Arabidopsis thaliana]

Seq. No. 47246

Seq. ID jex700908402.h1

Method BLASTN
NCBI GI g3021374
BLAST score 144
E value 2.0e-75
Match length 180
% identity 96

NCBI Description Glycine max mRNA for profilin, PRO1

Seq. No. 47247

Seq. ID jex700908463.h1

Method BLASTX
NCBI GI g1502430
BLAST score 264
E value 1.0e-23
Match length 67
% identity 73

NCBI Description (U62331) phosphate transporter [Arabidopsis thaliana] >gi 2564661 (AF022872) phosphate transporter [Arabidopsis

% identity

74





thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770) phosphate transporter, AtPT2 [Arabidopsis thaliana]

47248 Seq. No. jex700908508.h1 Seq. ID Method BLASTN g904153 NCBI GI BLAST score 154 2.0e-81 E value 189 Match length 96 % identity Glycine max FAD2-2 microsomal omega-6 desaturase mRNA, NCBI Description complete cds 47249 Seq. No. jex700908523.h1 Seq. ID BLASTX Method g629602 NCBI GI 223 BLAST score 1.0e-18 E value 80 Match length 57 % identity probable imbibition protein - wild cabbage NCBI Description >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea] 47250 Seq. No. jex700908531.hl Seq. ID Method BLASTX NCBI GI q2245084 BLAST score 150 4.0e-10 E value 73 Match length 48 % identity (Z97343) hypothetical protein [Arabidopsis thaliana] NCBI Description 47251 Seq. No. jex700908561.h1 Seq. ID Method BLASTX g4469008 NCBI GI BLAST score 157 5.0e-11 E value Match length 68 % identity 51 (AL035602) UDP rhamnose--anthocyanidin-3-glucoside NCBI Description rhamnosyltransferase-like protein [Arabidopsis thaliana] 47252 Seq. No. jex700908615.hl Seq. ID Method BLASTX NCBI GI q2459445 BLAST score 140 7.0e-09 E value Match length 34

NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis

% identity

40



thaliana]

```
47253
Seq. No.
                  jex700908661.hl
Seq. ID
                  BLASTX
Method
                  g3914472
NCBI GI
                  245
BLAST score
                  3.0e-21
E value
                  59
Match length
                  80
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
NCBI Description
                  >gi_322764_pir__S32021 photosystem II 10K protein - common
                  tobacco >gi 22669 emb_CAA49693_ (X70088) NtpII10 [Nicotiana
                  tabacum]
                  47254
Seq. No.
                  jex700908667.h1
Seq. ID
                  BLASTX
Method
                  g1236114
NCBI GI
BLAST score
                  210
                  4.0e-17
E value
Match length
                  81
% identity
                  47
                  (U34843) D123 [Rattus norvegicus]
NCBI Description
                  47255
Seq. No.
                  jex700908686.h1
Seq. ID
                  BLASTX
Method
                  g4580471
NCBI GI
BLAST score
                  231
                  8.0e-20
E value
Match length
                  82
                  70
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   47256
Seq. No.
                   jex700908750.h1
Seq. ID
Method
                   BLASTX
                   q1168189
NCBI GI
BLAST score
                   148
                   5.0e-12
E value
Match length
                   63
                   68
% identity
                  14-3-3-LIKE PROTEIN A (VFA-1433A) >gi 1076542_pir_ S52899
NCBI Description
                   14-3-3 brain protein homolog - fava bean
                   >gi_695765_emb_CAA88415_ (Z48504) 14-3-3 brain protein
                   homolog [Vicia faba]
Seq. No.
                   47257
                   jex700908794.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3152599
BLAST score
                   391
E value
                   2.0e-38
                   81
Match length
```

NCBI Description (AC002986) Strong similarity to lupeol synthase gb_U49919



100

% identity

NCBI Description

and cycloartenol synthase gb_U02555 from A. thaliana (the third gene with similar homology). [Arabidopsis thaliana]

47258 Seq. No. jex700908834.h1 Seq. ID Method BLASTX g2642157 NCBI GI BLAST score 229 1.0e-19 E value Match length 70 63 % identity (AC003000) ankyrin-like protein [Arabidopsis thaliana] NCBI Description 47259 Seq. No. jex700908852.h1 Seq. ID BLASTN Method g2656025 NCBI GI 38 BLAST score 4.0e-12 E value Match length 114 % identity 83 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MCD7 Seq. No. 47260 jex700908932.h1 Seq. ID Method BLASTN g3985949 NCBI GI BLAST score 34 9.0e-10 E value Match length 60 97 % identity Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MOB24, complete sequence [Arabidopsis thaliana] 47261 Seq. No. jex700908935.h1 Seq. ID Method BLASTX q3877951 NCBI GI BLAST score 180 1.0e-13 E value Match length 63 % identity 30 (Z81555) predicted using Genefinder [Caenorhabditis NCBI Description elegans] 47262 Seq. No. jex700909040.h1 Seq. ID Method BLASTN NCBI GI q1053215 BLAST score 104 E value 2.0e-51 Match length 104

Glycine max chlorophyll a/b-binding protein (cab3) mRNA,

nuclear gene encoding chloroplast protein, complete cds



Seq. No. 47263

Seq. ID jex700909087.h1

Method BLASTX
NCBI GI g1706325
BLAST score 198
E value 1.0e-15
Match length 69
% identity 57

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_476286 (U07339)

pyruvate decarboxylase 1 [Oryza sativa] >gi_1098559

(U26660) pyruvate decarboxylase [Oryza sativa]

Seq. No. 47264

Seq. ID jex700909120.h1

Method BLASTX
NCBI GI g2136100
BLAST score 159
E value 4.0e-11
Match length 73
% identity 49

NCBI Description replication factor C large subunit - human >gi 410218

(L23320) replication factor C large subunit [Homo sapiens] >gi_4506485_ref_NP_002904.1_pRFC1_ replication factor C

(activator $\overline{1}$) $1^{-}(1\overline{4}5kD)$

Seq. No. 47265

Seq. ID jex700909215.h1

Method BLASTX
NCBI GI g2498329
BLAST score 141
E value 6.0e-09
Match length 89
% identity 37

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__\$65571

pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

Seq. No. 47266

Seq. ID jex700909263.h1

Method BLASTN
NCBI GI g2739045
BLAST score 226
E value 1.0e-124
Match length 233
% identity 100

NCBI Description Glycine max polyphosphoinositide binding protein Ssh2p

(SSH2) mRNA, complete cds

Seq. No. 47267

Seq. ID jex700909286.h1

Method BLASTN NCBI GI g3445196



BLAST score E value 9.0e-41 Match length 206 85 % identity

Arabidopsis thaliana chromosome II BAC T20K9 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

47268 Seq. No.

Seq. ID jex700909288.h1

Method BLASTX NCBI GI q2252841 BLAST score 260 E value 5.0e-23 Match length 93 % identity 62

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

47269 Seq. No.

jex700909350.h1 Seq. ID

Method BLASTX NCBI GI g3785972 BLAST score 224 E value 9.0e-35 Match length 88 % identity 92

NCBI Description (AC005560) putative auxin transport protein [Arabidopsis

thaliana] >gi_4262249_gb_AAD14542_ (AC006200) putative

auxin transport protein [Arabidopsis thaliana]

Seq. No. 47270

jex700909366.h1 Seq. ID

Method BLASTX NCBI GI q3329368 BLAST score 153 E value 2.0e-10 Match length 43

% identity

NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 47271

jex700909423.h1 Seq. ID

Method BLASTX g3080740 NCBI GI BLAST score 405 7.0e-40 E value 92 Match length % identity 79

NCBI Description (U77366) pasticcino 1-D [Arabidopsis thaliana]

Seq. No. 47272

jex700909457.h1 Seq. ID

BLASTX Method NCBI GI q4455350 BLAST score 204 E value 2.0e-16 Match length 53 % identity 66





```
(AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  47273
Seq. No.
                  jex700909505.h1
Seq. ID
                  BLASTX
Method
                  q4519671
NCBI GI
BLAST score
                  186
E value
                  3.0e-14
                  80
Match length
                  49
% identity
                  (AB017693) transfactor [Nicotiana tabacum]
NCBI Description
                  47274
Seq. No.
Seq. ID
                  jex700909564.h1
Method
                  BLASTX
                  g1871185
NCBI GI
                  354
BLAST score
                  5.0e-34
E value
Match length
                  82
% identity
                  76
                  (U90439) seven in absentia isolog [Arabidopsis thaliana]
NCBI Description
                  47275
Seq. No.
                  jex700909586.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g769773
BLAST score
                  32
                  1.0e-08
E value
                  118
Match length
                  88
% identity
                  C.laevigatus chloroplast rbcL gene for
NCBI Description
                  ribulose-1,5-biphosphate-carboxylase and promoter region
                  47276
Seq. No.
                  jex700909620.h1
Seq. ID
Method
                  BLASTN
                  g256142
NCBI GI
                  193
BLAST score
                  1.0e-104
E value
Match length
                  233
% identity
                  96
                  cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                  Prize, mRNA, 1450 nt]
                  47277
Seq. No.
                   jex700909626.h1
Seq. ID
Method
                  BLASTX
                  g1652848
NCBI GI
BLAST score
                  188
                  2.0e-18
E value
Match length
                  80
% identity
                   62
                  (D90909) DNA photolyase [Synechocystis sp.]
NCBI Description
```

Seq. No. 47278

Seq. ID jex700909658.h1

Method BLASTN



```
NCBI GI
                  q1814402
BLAST score
                  2.0e-31
E value
                  158
Match length
% identity
                  Mesembryanthemum crystallinum methionine synthase (MetE)
NCBI Description
                  mRNA, complete cds
                  47279
Seq. No.
                  jex700909695.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4104930
BLAST score
                  62
                  2.0e-26
E value
Match length
                  118
                  88
% identity
                  Arabidopsis thaliana auxin response factor 8 (ARF8) mRNA,
NCBI Description
                  complete cds
                  47280
Seq. No.
                  jex700909712.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1438878
BLAST score
                  90
                  3.0e-43
E value
Match length
                  90
                  100
% identity
NCBI Description Glycine max choline kinase GmCK1p mRNA, complete cds
Seq. No.
                  47281
                   jex700909788.h1
Seq. ID
Method
                  BLASTX
                  g2444180
NCBI GI
BLAST score
                  201
                  4.0e-16
E value
Match length
                  51
% identity
                   69
                  (U94785) unconventional myosin [Helianthus annuus]
NCBI Description
Seq. No.
                   47282
                   jex700909860.h1
Seq. ID
Method
                   BLASTX
                  g2832717
NCBI GI
                   400
BLAST score
E value
                   2.0e-39
                   77
Match length
% identity
                  (AJ003114) alkaline/neutral invertase [Lolium temulentum]
NCBI Description
                   47283
Seq. No.
                   jex700909904.hl
Seq. ID
Method
                   BLASTX
```

NCBI GI q4538967 BLAST score 255 E value 2.0e-22 Match length 68 % identity 72



```
(AL049488) major intrinsic protein (MIP)-like [Arabidopsis
NCBI Description
                  thaliana]
                  47284
Seq. No.
                  jex700909970.h1
Seq. ID
                  BLASTX
Method
                  g3482929
NCBI GI
                  144
BLAST score
                  2.0e-09
E value
Match length
                  25
                  100
% identity
                  (AC003970) Putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  47285
                  jex700909988.h1
Seq. ID
                  BLASTX
Method
                  q1707642
NCBI GI
BLAST score
                  330
                  3.0e-31
E value
Match length
                  82
                  76
% identity
NCBI Description (Y07748) TMK [Oryza sativa]
                  47286
Seq. No.
                  jex700910061.h1
Seq. ID
Method
                  BLASTN
                  g2511690
NCBI GI
                  59
BLAST score
                  1.0e-24
E value
Match length
                  146
                  90
% identity
NCBI Description Phaseolus vulgaris Moldavian encoding cysteine proteinase
                  precursor (clone cp41)
                   47287
Seq. No.
                   jex700910067.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3688173
BLAST score
                  98
                   6.0e-09
E value
Match length
                  73
                   47
% identity
NCBI Description
                  (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   47288
                   jex700910090.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1170619
BLAST score
                   210
E value
                   1.0e-24
                   96
Match length
```

76 % identity KINESIN-LIKE PROTEIN A >gi_479594_pir__S34830

NCBI Description

kinesin-related protein katA - Arabidopsis thaliana >gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

NCBI Description

47294

jsh701063749.h1

Seq. No.

Seq. ID





>gi_2911084_emb_CAA17546_ (AL021960) kinesin-related protein katA [Arabidopsis thaliana]

```
47289
Seq. No.
                  jsh701063710.h1
Seq. ID
                  BLASTN
Method
                  g349436
NCBI GI
BLAST score
                  32
                  1.0e-08
E value
                  40
Match length
% identity
                  95
                  Carrot EP1 mRNA, complete cds
NCBI Description
Seq. No.
                  47290
                  jsh701063718.h1
Seq. ID
                  BLASTX
Method
                  g4262236
NCBI GI
                  141
BLAST score
                  1.0e-19
E value
Match length
                  91
% identity
                  51
                   (AC006200) putative ribose 5-phosphate isomerase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  47291
                   jsh701063728.h1
Seq. ID
Method
                  BLASTX
                  g4490321
NCBI GI
BLAST score
                  261
                  5.0e-23
E value
Match length
                   62
                   81
% identity
                  (AJ011604) nitrate transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47292
                   jsh701063743.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4185738
BLAST score
                   116
                   2.0e-14
E value
Match length
                   83
                 - 47
% identity
                  (AF079998) putative glutamate receptor [Arabidopsis
NCBI Description
                   thaliana]
                   47293
Seq. No.
                   jsh701063748.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4038481
                   218
BLAST score
E value
                   6.0e-18
                   47
Match length
% identity
                   83
```

7638

(AL021713) DNA binding-like protein [Arabidopsis thaliana]



```
Method BLASTN
NCBI GI g3452136
BLAST score 197
E value 1.0e-107
Match length 228
% identity 98
```

NCBI Description Glycine max mRNA for glucose-6-phosphate-dehydrogenase,

partial

 Seq. No.
 47295

 Seq. ID
 jsh701063804.h1

 Method
 BLASTN

 NCBI GI
 g2304954

 BLAST score
 283

 E value
 1.0e-158

Match length 283 % identity 100

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No. 47296

Seq. ID jsh701063811.h1

Method BLASTX
NCBI GI g4559333
BLAST score 156
E value 1.0e-10
Match length 88
% identity 42

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 47297

Seq. ID jsh701063830.h1

Method BLASTX
NCBI GI g3914403
BLAST score 190
E value 1.0e-14
Match length 43
% identity 79

NCBI Description PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II) (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II)

>gi_2370335_emb_CAA73866_ (Y13466) protoporphyrinogen oxidase [Nicotiana tabacum] >gi_3929920_dbj_BAA34712_ (AB020500) mitochondrial protoporphyrinogen oxidase

[Nicotiana tabacum] >gi 4105188 (AF044129)

protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]

Seq. No. 47298

Seq. ID jsh701063860.h1

Method BLASTN
NCBI GI g18764
BLAST score 262
E value 1.0e-146
Match length 276
% identity 99

NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No. 47299

Seq. ID jsh701063906.h1



```
BLASTN
Method
                  g3522932
NCBI GI
BLAST score
                  108
                  7.0e-54
E value
                  212
Match length
                  88
% identity
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  47300
Seq. No.
                  jsh701063923.hl
Seq. ID
                  BLASTN
Method
                  g3378649
NCBI GI
BLAST score
                  76
                  8.0e-35
E value
Match length
                  160
% identity
                  87
                  M.sativa mRNA translated from abscisic activated gene
NCBI Description
                  47301
Seq. No.
                  jsh701063939.h1
Seq. ID
                  BLASTN
Method
                  g2244991
NCBI GI
BLAST score
                  64
                  1.0e-27
E value
Match length
                  160
% identity
                  85
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  47302
Seq. No.
                   jsh701063970.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2293006
BLAST score
                  157
                  7.0e-11
E value
Match length
                  58
% identity
                   53
                  (AJ000977) hypothetical protein [Rhodobacter sphaeroides]
NCBI Description
Seq. No.
                   47303
                   jsh701064011.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3152614
BLAST score
                   216
E value
                   8.0e-18
Match length
                   60
                   68
% identity
                  (AC004482) unknown protein [Arabidopsis thaliana]
NCBI Description
                   47304
```

Seq. No.

jsh701064095.h1 Seq. ID ,

Method BLASTX NCBI GI q3337361

BLAST score 230 E value 2.0e-19 Match length 83



```
% identity
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                  47305
Seq. No.
                  jsh701064128.hl
Seq. ID
                  BLASTX
Method
                  g1781299
NCBI GI
                  159
BLAST score
                  4.0e-11
E value
                  70
Match length
                  49
% identity
                  (Y09506) transformer-SR ribonucleoprotein [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  47306
                  jsh701064164.h1
Seq. ID
                  BLASTN
Method
                  q166935
NCBI GI
                  100
BLAST score
                  4.0e-49
E value
                  212
Match length
                  87
% identity
NCBI Description A.thaliana ubiquitin extension protein (UBQ6) gene,
                  complete cds
                  47307
Seq. No.
                  jsh701064165.h1
Seq. ID
                  BLASTN
Method
                  q170089
NCBI GI
BLAST score
                  112
                  2.0e-56
E value
                  164
Match length
                  92
% identity
NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds
                  47308
Seq. No.
                  jsh701064191.hl
Seq. ID
                  BLASTN
Method
                  g310575
NCBI GI
                  82
BLAST score
                  2.0e-38
E value
                  219
Match length
% identity
                  87
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                  47309
Seq. No.
                  jsh701064205.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g18764
BLAST score
                  160
```

6.0e-85 E value Match length 224 93 % identity

NCBI Description G.max tefS1 gene for elongation factor EF-1a

47310 Seq. No.

jsh701064249.hl Seq. ID

Match length

% identity

82

90



```
BLASTN
Method
                  q4336435
NCBI GI
BLAST score
                  42
E value
                  1.0e-14
Match length
                  66
                  91
% identity
                  Lotus japonicus protein phosphatase type 2C (PP2C2) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  47311
                  jsh701064256.h1
Seq. ID
Method
                  BLASTX
                  g3327394
NCBI GI
BLAST score
                  162
E value
                  2.0e-11
Match length
                  54
% identity
                  56
                  (AC004483) putative RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47312
Seq. ID
                  jsh701064263.h1
Method
                  BLASTN
                  g473604
NCBI GI
BLAST score
                   60
                   3.0e-25
E value
Match length
                   110
% identity
                   85
                  Zea mays W-22 histone H2B mRNA, complete cds
NCBI Description
                   47313
Seq. No.
                   jsh701064353.hl
Seq. ID
Method
                   BLASTX
                   q3341443
NCBI GI
BLAST score
                   223
                   1.0e-18
E value
Match length
                   79
% identity
                   54
                  (AJ223074) acid phosphatase [Glycine max]
NCBI Description
                   47314
Seq. No.
                   jsh701064520.h1
Seq. ID
                   BLASTN
Method
                   q169899
NCBI GI
BLAST score
                   69
                   6.0e-31
E value
Match length
                   125
% identity
                   89
                  G.max 31 kDa protein mRNA, 3' end
NCBI Description
                   47315
Seq. No.
                   jsh701064532.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g19565
BLAST score
                   50
E value
                   1.0e-19
```

7642





NCBI Description M.liliiflora GADPH mRNA for glycolytic

glyceraldehyde-3-phosphate

dehydrogenase

Seq. No. 47316

Seq. ID jsh701064544.h1

Method BLASTN
NCBI GI g2905771
BLAST score 102
E value 1.0e-50
Match length 122
% identity 97

NCBI Description Glycine max glyceraldehyde-3 phosphate dehydrogenase

(GAPDH) mRNA, partial cds

Seq. No. 47317

Seq. ID jsh701064545.h1

Method BLASTN
NCBI GI g296408
BLAST score 56
E value 4.0e-23
Match length 116
% identity 87

NCBI Description G.max ADR12 mRNA

Seq. No. 47318

Seq. ID jsh701064669.h1

Method BLASTX
NCBI GI g3914555
BLAST score 212
E value 2.0e-17
Match length 49
% identity 88

NCBI Description PUTATIVE RIBOSOME-BINDING FACTOR A, CHLOROPLAST PRECURSOR

>gi 3096942_emb_CAA18852.1_ (AL023094) putative protein

[Arabidopsis thaliana]

Seq. No. 47319

Seq. ID jsh701064730.h1

Method BLASTN
NCBI GI g1053048
BLAST score 84
E value 1.0e-39
Match length 223
% identity 93

NCBI Description Glycine max histone H3 gene, partial cds, clone S3

Seq. No. 47320

Seq. ID jsh701064742.h1

Method BLASTN
NCBI GI g2304954
BLAST score 121
E value 1.0e-61
Match length 212
% identity 92

NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds

Seq. No. 47321



```
jsh701064751.h1
Seq. ID
                  BLASTX
Method
                  g2245098
NCBI GI
BLAST score
                  291
                  2.0e-26
E value
                  78
Match length
                  72
% identity
                  (Z97343) ribosomal protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47322
                  jsh701064780.hl
Seq. ID
                  BLASTX
Method
                  g100226
NCBI GI
BLAST score
                  166
E value
                  7.0e-12
Match length
                  92
% identity
                  37
                  hypothetical protein - tomato >gi_19275_emb_CAA78112_
NCBI Description
                   (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi 445619 prf 1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                  47323
Seq. No.
                  jsh701064804.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3269297
BLAST score
                  149
E value
                   6.0e-10
Match length
                  47
% identity
                  57
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                  47324
Seq. No.
                   jsh701064931.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1675195
                  107
BLAST score
                   3.0e-53
E value
Match length
                  217
                  88
% identity
                  Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,
NCBI Description
                  complete cds
                   47325
Seq. No.
                   jsh701064934.h1
Seq. ID
                  BLASTX
Method
                   g2062167
NCBI GI
                   105
BLAST score
                   4.0e-10
E value
Match length
                   83
% identity
                   45
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 47326

Seq. ID jsh701065031.h1

Method BLASTN



```
g1808591
NCBI GI
                  108
BLAST score
                  7.0e-54
E value
Match length
                  176
                  90
% identity
NCBI Description C.arietinum mRNA for SAM-synthetase
                  47327
Seq. No.
                  jsh701065034.hl
Seq. ID
                  BLASTN
Method
                  g1336096
NCBI GI
                  54
BLAST score
                  1.0e-21
E value
                  164
Match length
% identity
                  84
                  Pisum sativum pyruvate dehydrogenase Elbeta mRNA, nuclear
NCBI Description
                  gene encoding mitochondrial protein, complete cds
                  47328
Seq. No.
                  jsh701065080.h1
Seq. ID
Method
                  BLASTN
                  q169988
NCBI GI
BLAST score
                  96
                  1.0e-46
E value
Match length
                  211
                  87
% identity
                  Glycine max NADP-specific isocitrate dehydrogenase (idh1)
NCBI Description
                  mRNA, 3' end
                  47329
Seq. No.
                  jsh701065109.h1
Seq. ID
                  BLASTN
Method
                  q3641869
NCBI GI
                   78
BLAST score
                   5.0e-36
E value
                   98
Match length
                   95
% identity
                  Cicer arietinum epicotyl EST, clone Can133
NCBI Description
                   47330
Seq. No.
                   jsh701065167.h1
Seq. ID
Method
                   BLASTX
                   g2980806
NCBI GI
                   207
BLAST score
                   1.0e-16
E value
                   71
Match length
% identity
                   26
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   47331
Seq. No.
                   jsh701065237.h1
Seq. ID
```

Method BLASTN g170053 NCBI GI BLAST score 164 2.0e-87 E value Match length 168 % identity 99



```
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
                  47332
Seq. No.
                  jsh701065346.h1
Seq. ID
                  BLASTX
Method
                  g3142294
NCBI GI
                  242
BLAST score
                  7.0e-21
E value
                  58
Match length
% identity
                  81
                  (AC002411) Strong similarity to initiation factor eIF-2,
NCBI Description
                  gb U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and
                  gb N37529 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  47333
                  jsh701065355.h1
Seq. ID
                  BLASTX
Method
                  q2497539
NCBI GI
                  153
BLAST score
                  2.0e-10
E value
Match length
                  82
                  54
% identity
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703
NCBI Description
                   (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
Seq. No.
                   47334
                   jsh701065481.h1
Seq. ID
Method
                  BLASTN
                  q170069
NCBI GI
BLAST score
                   63
                  3.0e-27
E value
                  111
Match length
                   90
% identity
                  Soybean calmodulin (SCaM-1) mRNA, complete cds
NCBI Description
                   47335
Seq. No.
                   jsh701065532.h1
Seq. ID
                   BLASTX
Method
                   g466160
NCBI GI
                   186
BLAST score
E value
                   3.0e-14
                   46
Match length
```

78 % identity

HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III NCBI Description >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis

elegans]

47336 Seq. No.

jsh701065583.h1 Seq. ID

Method BLASTX NCBI GI q3510251 BLAST score 161 1.0e-11 E value Match length 51 61 % identity

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]



```
47337
Seq. No.
                  jsh701065649.hl
Seq. ID
Method
                  BLASTX
                  g2262143
NCBI GI
                  107
BLAST score
                   7.0e-11
E value
                   62
Match length
                   69
% identity
                   (AC002330) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   47338
Seq. No.
                   jsh701065693.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2055227
BLAST score
                   42
                   2.0e-14
E value
                   132
Match length
% identity
                   87
                  Glycine max mRNA for SRC1, complete cds
NCBI Description
                   47339
Seq. No.
                   jsh701065703.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g255407
BLAST score
                   96
E value
                   7.0e-47
Match length
                   204
                   11
% identity
                   repetitive proline-rich protein {cDNA clone 1A10-2}
NCBI Description
                   [Glycine max=soybeans, axes germinated for 31 hours, mRNA,
                   943 nt]
                   47340
Seq. No.
                   jsh701065829.h1
Seq. ID
Method
                   BLASTX
                   g2895866
NCBI GI
BLAST score
                   256
                   2.0e-22
E value
                   79
Match length
                   63
% identity
                   (AF045770) methylmalonate semi-aldehyde dehydrogenase
NCBI Description
                   [Oryza sativa]
                   47341
Seq. No.
                   jsh701065883.h1
Seq. ID
                   BLASTN
Method
                   g296444
NCBI GI
                   258
BLAST score
                   1.0e-143
E value
Match length
                   274
                   99
% identity
```

Seq. No. 47342

Seq. ID jsh701065944.h1

NCBI Description G.max ADR6 mRNA



```
BLASTN
Method
NCBI GI
                  q288187
BLAST score
                  58
                  3.0e-24
E value
Match length
                  162
                  84
% identity
NCBI Description V.unguiculata cysteine proteinase inhibitor mRNA
                  47343
Seq. No.
                  jsh701065945.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g118011
BLAST score
                  140
E value
                  2.0e-12
Match length
                  64
                  67
% identity
                  CYTOCHROME C >gi_625189_pir__CCRZ cytochrome c - rice
NCBI Description
                  >gi_169786 (M63704) cytochrome c [Oryza sativa]
                  >gi 218249 dbj BAA02159 (D12634) 'cytochrome C' [Oryza
                  sativa]
                  47344
Seq. No.
                  jsh701066041.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  175
                  3.0e-23
E value
Match length
                  75
                  70
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                  47345
Seq. No.
                  jsh701066056.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1336081
BLAST score
                  201
                  1.0e-109
E value
Match length
                  277
                  94
% identity
                  Glycine max var. Century ascorbate peroxidase 2 (APx2)
NCBI Description
                  mRNA, complete cds
                  47346
Seq. No.
                  jsh701066157.h1
Seq. ID
Method
                  BLASTX
                  g2529677
NCBI GI
                  143
BLAST score
                  2.0e-09
E value
Match length
                  38
```

76 % identity

(AC002535) kinesin-like protein, heavy chain [Arabidopsis NCBI Description

thaliana]

Seq. No.

47347

BLASTN

g349436

Seq. ID

jsh701066172.h1

Method NCBI GI



```
BLAST score
                   1.0e-08
E value
Match length
                   40
% identity
                   95
                  Carrot EP1 mRNA, complete cds
NCBI Description
                   47348
Seq. No.
                   jsh701066192.h1
Seq. ID
                   BLASTX
Method
                   g3608153
NCBI GI
                   253
BLAST score
                   3.0e-22
E value
                   58
Match length
                   79
% identity
                   (AC005314) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47349
Seq. No.
                   jsh701066275.h1
Seq. ID
                   BLASTX
Method
                   g3033384
NCBI GI
BLAST score
                   272
                   3.0e-24
E value
Match length
                   63
                   79
% identity
                   (AC004238) putative CTP synthase [Arabidopsis thaliana]
NCBI Description
                   47350
Seq. No.
                   jsh701066313.h1
Seq. ID
Method
                   BLASTN
                   g2304954
NCBI GI
                   124
BLAST score
                   1.0e-63
E value
                   200
Match length
                   91
% identity
NCBI Description Glycine max aluminum induced sali5-4a mRNA, complete cds
                   47351
Seq. No.
                   jsh701066322.hl
Seq. ID
Method
                   BLASTX
                   g2213425
NCBI GI
BLAST score
                   153
                   9.0e-19
E value
                   61
Match length
                   49
% identity
                   (Z97064) hypothetical protein [Citrus x paradisi]
NCBI Description
                   47352
Seq. No.
                   jsh701066326.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3941454
BLAST score
                   281
                   2.0e-25
E value
                   59
Match length
                   85
% identity
                   (AF062881) putative transcription factor [Arabidopsis
NCBI Description
```

thaliana]



```
47353
Seq. No.
                  jsh701066355.h1
Seq. ID
Method
                  BLASTN
                  g2317899
NCBI GI
                  88
BLAST score
                  3.0e-42
E value
                  128
Match length
                  93
% identity
NCBI Description Glycine max Sali3-2 mRNA, complete cds
                  47354
Seq. No.
                  jsh701066357.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2055227
BLAST score
                  36
                  3.0e-11
E value
Match length
                  64
                  89
% identity
NCBI Description Glycine max mRNA for SRC1, complete cds
                  47355
Seq. No.
                  jsh701066361.h1
Seq. ID
                  BLASTN
Method
                  g18764
NCBI GI
BLAST score
                  78
                  5.0e-36
E value
                  222
Match length
                  84
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-la
                  47356
Seq. No.
                  jsh701066368.h1
Seq. ID
                  BLASTN
Method
                  g4193387
NCBI GI
BLAST score
                  55
                  3.0e-22
E value
Match length
                  214
                  81
% identity
                  Hevea brasiliensis translationally controlled tumor protein
NCBI Description
                   (TCTP) mRNA, complete cds
                   47357
Seq. No.
                   jsh701066415.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4249414
BLAST score
                   165
                   9.0e-12
E value
                   57
Match length
                   58
% identity
                   (AC006072) unknown protein [Arabidopsis thaliana]
NCBI Description
                   47358
Seq. No.
```

Seq. ID jsh701066427.h1

Method BLASTX
NCBI GI g3096919
BLAST score 305
E value 3.0e-28



Match length 75 % identity 73

NCBI Description (AL023094) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 47359

Seq. ID jsh701066474.h1

Method BLASTX
NCBI GI 94185511
BLAST score 166
E value 6.0e-12
Match length 45
% identity 69

NCBI Description (AF102822) actin depolymerizing factor 4 [Arabidopsis

thaliana]

Seq. No. 47360

Seq. ID jsh701066558.h1

Method BLASTN
NCBI GI g2852444
BLAST score 36
E value 6.0e-11
Match length 92
% identity 85

NCBI Description Salix bakko mRNA for SUI1 homolog, complete cds

Seq. No. 47361

Seq. ID jsh701066583.h1

Method BLASTN
NCBI GI g303900
BLAST score 150
E value 5.0e-79
Match length 254
% identity 30

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No. 47362

Seq. ID jsh701066618.h1

Method BLASTN
NCBI GI g2055227
BLAST score 46
E value 7.0e-17
Match length 66
% identity 92

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No. 47363

Seq. ID jsh701066659.h1

Method BLASTN
NCBI GI g1675195
BLAST score 82
E value 2.0e-38
Match length 172
% identity 88

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

```
Seq. No.
                   47364
                  jsh701066736.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q296444
BLAST score
                  279
                  1.0e-156
E value
Match length
                  279
                  100
% identity
NCBI Description
                  G.max ADR6 mRNA
                   47365
Seq. No.
                   jsh701066768.h1
Seq. ID
Method
                  BLASTX
                   g2498706
NCBI GI
BLAST score
                   356
                   4.0e-34
E value
                  87
Match length
% identity
                   68
                  ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103
NCBI Description
                   (U40269) atOrc2p [Arabidopsis thaliana] >gi 3236239
                   (AC004684) origin recognition complex protein [Arabidopsis
                   thaliana]
                   47366
Seq. No.
                   jsh701066867.h1
Seq. ID
Method
                  BLASTN
                   g169834
NCBI GI
BLAST score
                   56
                   7.0e-23
E value
Match length
                   60
% identity
                   98
```

Rye 26S rRNA 3' end and 18S rRNA, 5' end NCBI Description

47367 Seq. No. jsh701066906.h1 Seq. ID Method BLASTX g3763920 NCBI GI BLAST score 343 E value 1.0e-32 Match length 85

% identity

(AC004450) hypothetical protein [Arabidopsis thaliana] NCBI Description

47368 Seq. No.

jsh701066956.h1 Seq. ID

Method BLASTX g3702317 NCBI GI BLAST score 169 3.0e-12 E value Match length 48

% identity 73

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

>gi_4559376_gb_AAD23036.1_AC006526_1 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 47369

Seq. ID jsh701067044.h1



```
Method
                  BLASTX
NCBI GI
                  g1531758
BLAST score
                  164
                  7.0e-12
E value
                  40
Match length
                  75
% identity
                  (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
NCBI Description
                  unknown protein [Arabidopsis thaliana]
                  47370
Seq. No.
                  jsh701067133.hl
Seq. ID
                  BLASTN
Method
                  g169097
NCBI GI
BLAST score
                  54
                  1.0e-21
E value
Match length
                  198
                  82
% identity
                  Pea histone H2A mRNA
NCBI Description
                  47371
Seq. No.
                  jsh701067188.hl
Seq. ID
Method
                  BLASTX
                  g4512685
NCBI GI
                  357
BLAST score
E value
                  3.0e-34
Match length
                  83
                  83
% identity
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)
                  hypothetical protein [Arabidopsis thaliana]
                  47372
Seq. No.
                  jsh701067266.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1370204
BLAST score
                  125
                  5.0e-64
E value
Match length
                  197
% identity
                  91
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAN1B
                  47373
Seq. No.
                   jsh701067292.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                   g441205
BLAST score
                   90
                   2.0e-43
E value
                  158
Match length
% identity
                   91
NCBI Description Soybean lox1gm4 gene encoding lipxygenase L-4
Seq. No.
                   47374
                   jsh701067353.h1
Seq. ID
```

Method BLASTN
NCBI GI g4001539
BLAST score 168
E value 1.0e-89



Match length 252 % identity 92

NCBI Description Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete

sequence [Homo sapiens]

Seq. No. 47375

Seq. ID jsh701067440.h1

Method BLASTX
NCBI GI g1890352
BLAST score 231
E value 2.0e-28
Match length 90
% identity 37

NCBI Description (X91398) transcription factor L2 [Arabidopsis thaliana]

Seq. No. 47376

Seq. ID jsh701067442.h1

Method BLASTN
NCBI GI g1184120
BLAST score 90
E value 4.0e-43
Match length 230
% identity 85

NCBI Description Vigna radiata clone MII-3 auxin-induced protein mRNA,

complete cds

Seq. No. 47377

Seq. ID jsh701067453.h1

Method BLASTN
NCBI GI g218128
BLAST score 65
E value 3.0e-28
Match length 121
% identity 88

NCBI Description Rice mRNA for succinyl-CoA sythetase (475 gene), partial

sequence

Seq. No. 47378

Seq. ID jsh701067484.h1

Method BLASTN
NCBI GI g1675195
BLAST score 73
E value 5.0e-33
Match length 235
% identity 84

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

Seq. No. 47379

Seq. ID jsh701067486.h1

Method BLASTN
NCBI GI g436968
BLAST score 43
E value 4.0e-15
Match length 47
% identity 98

NCBI Description Betula papyrifera small ribosomal subunit RNA (18S rRNA)



```
47380
Seq. No.
                  jsh701067524.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g296408
BLAST score
                  258
E value
                  1.0e-143
Match length
                  289
                  98
% identity
NCBI Description
                  G.max ADR12 mRNA
                  47381
Seq. No.
                  jsh701067553.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218128
BLAST score
                  38
E value
                   4.0e-12
Match length
                  106
                   85
% identity
                  Rice mRNA for succinyl-CoA sythetase (475 gene), partial
NCBI Description
                   sequence
                   47382
Seq. No.
Seq. ID
                   jsh701067586.hl
Method
                   BLASTX
NCBI GI
                   q4455338
BLAST score
                   254
                   4.0e-22
E value
                   62
Match length
% identity
                   73
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47383
                   jsh701067709.hl
Seq. ID
                   BLASTX
Method
                   g3168840
NCBI GI
BLAST score
                   150
                   3.0e-10
E value
Match length
                   37
                   76
% identity
                  (U88711) copper homeostasis factor [Arabidopsis thaliana]
NCBI Description
                   47384
Seq. No.
                   jsh701067860.h1
Seq. ID
                   BLASTX
Method
                   g401213
NCBI GI
BLAST score
                   144
                   1.0e-09
E value
                   40
Match length
                   72
% identity
                   ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi 166792
NCBI Description
                   (M96073) phosphoribosylanthranilate transferase
                   [Arabidopsis thaliana] >gi_445600_prf__1909347A
```

Seq. No. 47385

thaliana]

phosphoribosylanthranilate transferase [Arabidopsis



```
jsh701067910.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g296408
BLAST score
                  250
E value
                  1.0e-138
Match length
                  286
                  98
% identity
NCBI Description G.max ADR12 mRNA
                  47386
Seq. No.
Seq. ID
                  jsh701067933.h1
                  BLASTN
Method
                  g170091
NCBI GI
                  206
BLAST score
                  1.0e-112
E value
Match length
                  306
% identity
                  92
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
Seq. No.
                  47387
Seq. ID
                  jsh701067965.h1
                  BLASTX
Method
NCBI GI
                  g2253442
                  211
BLAST score
                   3.0e-18
E value
Match length
                   90
% identity
                   58
NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca]
Seq. No.
                   47388
Seq. ID
                   jsh701067979.h1
Method
                   BLASTN
                   g296408
NCBI GI
BLAST score
                   188
                   1.0e-101
E value
Match length
                   264
                   93
% identity
NCBI Description G.max ADR12 mRNA
Seq. No.
                   47389
                   jsh701068125.h1
Seq. ID
Method
                   BLASTN
                   q296408
NCBI GI
                   217
BLAST score
                   1.0e-119
E value
                   245
Match length
% identity
                   97
NCBI Description G.max ADR12 mRNA
                   47390
Seq. No.
```

jsh701068148.hl Seq. ID

BLASTN Method g169974 NCBI GI BLAST score 183 1.0e-98 E value Match length 259

NCBI Description



```
% identity
                  Glycine max vspA gene, complete cds
NCBI Description
Seq. No.
                  47391
                  jsh701068156.h1
Seq. ID
Method
                  BLASTN
                  g170029
NCBI GI
BLAST score
                  142
E value
                  3.0e-74
Match length
                  242
% identity
                  90
                  Glycine max cv. Dare nodulin 26 gene fragment
NCBI Description
                  47392
Seq. No.
                  jsh701068182.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4056457
BLAST score
                  244
                   4.0e-21
E value
                   59
Match length
                  73
% identity
                  (AC005990) ESTs gb 234051 and gb F13722 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
                   47393
Seq. No.
Seq. ID
                   jsh701068213.hl
Method
                  BLASTN
NCBI GI
                   g2564044
BLAST score
                   53
E value
                   4.0e-21
Match length
                   180
                   89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19P17, complete sequence [Arabidopsis thaliana]
                   47394
Seq. No.
Seq. ID
                   jsh701068221.h1
Method
                   BLASTX
                   g4539324
NCBI GI
BLAST score
                   140
E value
                   8.0e-09
                   74
Match length
% identity
                   47
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
                   47395
Sea. No.
                   jsh701068223.h1
Seq. ID
Method
                   BLASTX
                   g2129933
NCBI GI
                   364
BLAST score
                   4.0e-35
E value
Match length
                   74
% identity
                   86
```

[Lycopersicon esculentum]

myb-related transcription factor TMH27 - tomato

>gi_1167484_emb_CAA64614_ (X95296) transcription factor



```
47396
Seq. No.
                  jsh701068325.h1
Seq. ID
Method
                  BLASTX
                  q3176709
NCBI GI
BLAST score
                  190
E value
                   1.0e-14
                   88
Match length
% identity
                   (AC002392) putative anthranilate
NCBI Description
                   N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis
                   thaliana]
                   47397
Seq. No.
Seq. ID
                   jsh701068344.h1
                   BLASTX
Method
NCBI GI
                   q4468813
BLAST score
                   265
E value
                   2.0e-23
                   57
Match length
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
                   47398
Seq. No.
                   jsh701068367.hl
Seq. ID
                   BLASTN
Method
                   g3702737
NCBI GI
BLAST score
                   32
                   1.0e-08
E value
                   56
Match length
% identity
                   89
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSN2, complete sequence [Arabidopsis thaliana]
                   47399
Seq. No.
                   jsh701068370.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3452136
BLAST score
                   236
E value
                   1.0e-130
Match length
                   252
                   99
% identity
                   Glycine max mRNA for glucose-6-phosphate-dehydrogenase,
NCBI Description
                   partial
                   47400
Seq. No.
                   jsh701068377.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4510338
BLAST score
                   42
                   2.0e-14
E value
```

Match length 134 % identity 83

Arabidopsis thaliana chromosome II BAC F2H17 genomic NCBI Description

sequence, complete sequence

47401 Seq. No.

jsh701068420.h1 Seq. ID



```
BLASTX
Method
NCBI GI
                  g3128228
BLAST score
                  185
                  4.0e-14
E value
                  39
Match length
% identity
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                  thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
                  47402
Seq. No.
                  jsh701068446.h1
Seq. ID
Method
                  BLASTN
                  g170091
NCBI GI
                  155
BLAST score
                  6.0e-82
E value
Match length
                  254
                  90
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                   47403
Seq. No.
                   jsh701068476.h1
Seq. ID
                  BLASTX
Method
                  g1076715
NCBI GI
BLAST score
                  209
                   6.0e-17
E value
Match length
                  70
                   54
% identity
                  abscisic acid-induced protein HVA22 - barley >gi_404589
NCBI Description
                   (L19119) A22 [Hordeum vulgare]
Seq. No.
                   47404
                   jsh701068548.h1
Seq. ID
                   BLASTX
Method
                   q4514716
NCBI GI
BLAST score
                   138
E value
                   1.0e-08
                   60
Match length
                   38
% identity
                  (AB017533) EPc [Nicotiana tabacum]
NCBI Description
Seq. No.
                   47405
Seq. ID
                   jsh701068579.hl
                   BLASTN
Method
NCBI GI
                   q170071
BLAST score
                   264
E value
                   1.0e-147
Match length
                   268
                   100
% identity
                  Soybean calmodulin (SCaM-2) mRNA, complete cds
NCBI Description
Seq. No.
                   47406
                   jsh701068629.h1
Seq. ID
                   BLASTX
Method
```

g3057150

276

NCBI GI

BLAST score

% identity

NCBI Description



```
8.0e-25
E value
Match length
                  68
% identity
                  (AF059037) chaperonin 10 [Arabidopsis thaliana]
NCBI Description
                  47407
Seq. No.
                  jsh701068634.h1
Seq. ID
                  BLASTX
Method
                  q3834316
NCBI GI
                  276
BLAST score
                   2.0e-29
E value
Match length
                  90
                   68
% identity
                   (AC005679) Similar to gb X16648 pathogenesis related
NCBI Description
                  protein from Hordeum vulgare. EST gb Z18206 comes from
                  this gene. [Arabidopsis thaliana]
                   47408
Seq. No.
                   jsh701068650.h1
Seq. ID
                   BLASTX
Method
                   q3876012
NCBI GI
BLAST score
                   151
E value
                   2.0e-10
                   62
Match length
                   56
% identity
                   (Z50873) Similarity to N.crassa ADP/ATP carrier protein
NCBI Description
                   (SW:ADT NEUCR) [Caenorhabditis elegans]
                   47409
Seq. No.
Seq. ID
                   jsh701068661.hl
                   BLASTN
Method
                   q18764
NCBI GI
BLAST score
                   40
E value
                   1.0e-13
                   84
Match length
                   88
% identity
                  G.max tefS1 gene for elongation factor EF-1a
NCBI Description
                   47410
Seq. No.
Seq. ID
                   jsh701068860.h1
Method
                   BLASTX
NCBI GI
                   q2342725
BLAST score
                   176
E value
                   3.0e-13
Match length
                   43
                   77
% identity
                  (AC002341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47411
                   jsh701068895.h1
Seq. ID
Method
                   BLASTX
                   g3551958
NCBI GI
BLAST score
                   152
E value
                   2.0e-10
                   46
Match length
                   59
```

(AF082032) senescence-associated protein 12 [Hemerocallis



hybrid cultivar]

```
      Seq. No.
      47412

      Seq. ID
      jsh701068964.h1

      Method
      BLASTN

      NCBI GI
      g1850792

      BLAST score
      46
```

BLAST score 46 E value 6.0e-17 Match length 141 % identity 83

NCBI Description A.thaliana atl1 gene

Seq. No. 47413

Seq. ID jsh701068992.h1

Method BLASTN
NCBI GI g169897
BLAST score 274
E value 1.0e-153
Match length 298
% identity 98

NCBI Description G.max 28 kDa protein, complete cds

Seq. No. 47414

Seq. ID jsh701069104.h1

Method BLASTN
NCBI GI g2642237
BLAST score 87
E value 1.0e-41
Match length 87
% identity 100

NCBI Description Glycine max endoplasmic reticulum HSC70-cognate binding

protein precursor (BIP) mRNA, complete cds

Seq. No. 47415

Seq. ID jsh701069131.h1

Method BLASTN
NCBI GI g169899
BLAST score 39
E value 5.0e-13
Match length 99
% identity 86

NCBI Description G.max 31 kDa protein mRNA, 3' end

Seq. No. 47416

Seq. ID jsh701069165.h1

Method BLASTN
NCBI GI g255576
BLAST score 52
E value 1.0e-20
Match length 76
% identity 92

NCBI Description small auxin up RNA gene cluster: orf 6B [Glycine

max=soybeans, cv. Wayne, Genomic, 665 nt]

Seq. No. 47417

Seq. ID jsh701069241.h1

Method BLASTX



NCBI GI g4335745 BLAST score 132 E value 5.0e-10 Match length 66 % identity 58

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 47418

Seq. ID jsh701069305.h1

Method BLASTN
NCBI GI g18644
BLAST score 127
E value 3.0e-65
Match length 213
% identity 92

NCBI Description Soybean mRNA for HMG-1 like protein

Seg. No. 47419

Seq. ID jsh701069313.h1

Method BLASTX
NCBI GI g3386604
BLAST score 192
E value 6.0e-15
Match length 53
% identity 66

NCBI Description (AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No. 47420

Seq. ID jsh701069326.h1

Method BLASTX
NCBI GI g3122357
BLAST score 224
E value 6.0e-23
Match length 81
% identity 67

NCBI Description PUTATIVE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS

PROTEIN B) >gi_2494127 (AC002376) Contains similarity to

Mycobacterium LIPB gene (gb_Q104041). [Arabidopsis

thaliana]

Seq. No. 47421

Seq. ID jsh701069393.h1

Method BLASTN
NCBI GI g644492
BLAST score 82
E value 2.0e-38
Match length 166
% identity 87

NCBI Description Corn elongation factor lalpha gene, complete cds

Seq. No.

Seq. ID jsh701069406.h1

47422

Method BLASTN
NCBI GI g296442
BLAST score 158



```
E value
Match length
                  158
                  100
% identity
NCBI Description G.max ADR11 mRNA
Seq. No.
                  47423
                  jsh701069424.h1
Seq. ID
                  BLASTX
Method
                  q719291
NCBI GI
                  194
BLAST score
E value
                   3.0e-15
                   45
Match length
% identity
                   71
                   (U19134) unknown [Arabidopsis thaliana]
NCBI Description
                   >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]
Seq. No.
                   47424
Seq. ID
                   jsh701069451.hl
                   BLASTN
Method
                   q456713
NCBI GI
                   126
BLAST score
E value
                   1.0e-64
                   253
Match length
                   40
% identity
NCBI Description Glycine max gene for ubiquitin, complete cds
                   47425
Seq. No.
                   jsh701069454.hl
Seq. ID
                   BLASTN
Method
NCBI GI
                   q170091
BLAST score
                   38
                   1.0e-12
E value
Match length
                   110
% identity
                   Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                   complete cds
                   47426
Seq. No.
                   jsh701069455.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4580461
BLAST score
                   404
E value
                   8.0e-40
Match length
                   87
% identity
                   (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47427
                   jsh701069486.h1
Seq. ID
                   BLASTN
Method
                   g170089
NCBI GI
BLAST score
                   104
E value
                   8.0e-52
Match length
                   147
                   94
% identity
```

NCBI Description G.max vegetative storage protien mRNA (VSP27), complete cds



```
47428
Seq. No.
Seq. ID
                  jsh701069510.h1
                  BLASTX
Method
                  g4218120
NCBI GI
BLAST score
                  173
E value
                  1.0e-12
                  90
Match length
                  40
% identity
                  (AL035353) Proline-rich APG-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  47429
Seq. No.
Seq. ID
                  jsh701069545.h1
                  BLASTN
Method
                  g18764
NCBI GI
BLAST score
                  37
E value
                  1.0e-11
                   69
Match length
% identity
                  G.max tefS1 gene for elongation factor EF-1a
NCBI Description
                   47430
Seq. No.
                   jsh701069573.hl
Seq. ID
                   BLASTN
Method
                   g2055227
NCBI GI
                   38
BLAST score
                   4.0e-12
E value
Match length
                   66
                   89
% identity
                  Glycine max mRNA for SRC1, complete cds
NCBI Description
                   47431
Seq. No.
Seq. ID
                   jsh701069584.hl
Method
                   BLASTN
NCBI GI
                   g303743
BLAST score
                   51
E value
                   5.0e-20
Match length
                   63
                   95
% identity
                   Pea mRNA for GTP-binding protein, complete cds
NCBI Description
                   47432
Seq. No.
                   jsh701069624.hl
Seq. ID
                   BLASTN
Method
                   q3522932
NCBI GI
                   108
BLAST score
                   7.0e-54
E value
Match length
                   212
% identity
                   88
                   Arabidopsis thaliana chromosome II BAC F14M4 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

 Seq. No.
 47433

 Seq. ID
 jsh701069642.h1

 Method
 BLASTN

NCBI GI g170087 BLAST score 33



96

% identity

NCBI Description

```
3.0e-09
E value
                  52
Match length
% identity
                  92
                  G.max vegetative storage protein mRNA (VSP25 gene)
NCBI Description
                  47434
Seq. No.
                  jsh701069643.h1
Seq. ID
                  BLASTX
Method
                  q4115388
NCBI GI
BLAST score
                  239
                  2.0e-20
E value
Match length
                  77
% identity
                  57
                   (AC005967) putative prolylcarboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
                   47435
Seq. No.
                   jsh701069730.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1053215
BLAST score
                   170
E value
                   7.0e-91
Match length
                   270
                   92
% identity
                  Glycine max chlorophyll a/b-binding protein (cab3) mRNA,
NCBI Description
                   nuclear gene encoding chloroplast protein, complete cds
                   47436
Seq. No.
Seq. ID
                   jsh701069768.h1
Method
                   BLASTX
                   q2462929
NCBI GI
BLAST score
                   118
                   2.0e-12
E value
Match length
                   77
% identity
                   55
                  (Y12295) glutathione transferase [Arabidopsis thaliana]
NCBI Description
                   47437
Seq. No.
                   jsh701069779.hl
Seq. ID
                   BLASTN
Method
NCBI GI
                   q469247
BLAST score
                   37
E value
                   1.0e-11
                   93
Match length
% identity
                   86
                   Helianthus annuus ribosomal protein S3a mRNA, complete cds
NCBI Description
Seq. No.
                   47438
                   jsh701069789.hl
Seq. ID
                   BLASTN
Method
                   g1399379
NCBI GI
BLAST score
                   80
                   4.0e-37
E value
Match length
                   96
```

methyltransferase mRNA, complete cds

Glycine max S-adenosyl-L-methionine:delta24-sterol-C-

Seq. ID

Method

NCBI GI



```
47439
Seq. No.
                  jsh701069791.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g170091
BLAST score
                  261
                  1.0e-145
E value
                  288
Match length
                   98
% identity
                  Glycine max vegetative storage protein (vspB) gene,
NCBI Description
                  complete cds
                   47440
Seq. No.
                   jsh701069803.h1
Seq. ID
                   BLASTN
Method
                   g170067
NCBI GI
BLAST score
                   166
                   2.0e-88
E value
                   166
Match length
                   81
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                   gene, complete cds
                   47441
Seq. No.
                   jsh701069857.h1
Seq. ID
                   BLASTX
Method
                   g3860333
NCBI GI
                   212
BLAST score
                   3.0e-17
E value
                   75
Match length
% identity
                  (AJ012693) basic blue copper protein [Cicer arietinum]
NCBI Description
                   47442
Seq. No.
                   jsh701069859.hl
Seq. ID
                   BLASTN
Method
                   q170089
NCBI GI
BLAST score
                   210
                   1.0e-115
E value
                   274
Match length
                   94
% identity
                  G.max vegetative storage protien mRNA (VSP27), complete cds
NCBI Description
Seq. No.
                   47443
Seq. ID
                   jsh701069934.h2
                   BLASTN
Method
                   q3063540
NCBI GI
BLAST score
                   32
                   9.0e-09
E value
                   52
Match length
                   19
% identity
                   Trypanosoma cruzi CL Brener cosmid 1b21 chromosome
NCBI Description
Seq. No.
                   47444
```

jsh701069979.h2

BLASTX

g3063450



```
BLAST score
                  1.0e-16
E value
                  61
Match length
                  72
% identity
                  (AC003981) F22013.12 [Arabidopsis thaliana]
NCBI Description
                  47445
Seq. No.
Seq. ID
                  jsh701070020.h2
                  BLASTX
Method
                  q3201618
NCBI GI
BLAST score
                  295
                  5.0e-27
E value
                  71
Match length
% identity
                  73
                  (AC004669) Sop2p-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47446
Seq. ID
                  jsh701070053.h2
                  BLASTN
Method
NCBI GI
                  q452360
BLAST score
                  117
E value
                   3.0e-59
                  245
Match length
                  89
% identity
                  V.faba mRNA for guanine nucleotide regulatory protein
NCBI Description
                   (807bp)
                   47447
Seq. No.
                   jsh701070093.h2
Seq. ID
Method
                   BLASTX
                   q4006900
NCBI GI
BLAST score
                   157
E value
                   2.0e-14
Match length
                   83
% identity
                   (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47448
                   jsh701070143.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3128228
BLAST score
                   308
E value
                   1.0e-28
Match length
                   65
% identity
                   91
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
                   47449
Seq. No.
                   jsh701070166.hl
Seq. ID
                   BLASTN
Method
```

Method BLASTN
NCBI GI g256142
BLAST score 264
E value 1.0e-147
Match length 268
% identity 100



NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

Seq. No. 47450

Seq. ID jsh701070207.h1

Method BLASTN
NCBI GI g3452136
BLAST score 136
E value 1.0e-70
Match length 152
% identity 99

NCBI Description Glycine max mRNA for glucose-6-phosphate-dehydrogenase,

partial

Seq. No. 47451

Seq. ID jsh701070243.h1

Method BLASTX
NCBI GI g544018
BLAST score 225
E value 7.0e-19
Match length 82
% identity 50

NCBI Description NITRATE/CHLORATE TRANSPORTER >gi_1076359_pir__A45772

nitrate-inducible nitrate transporter - Arabidopsis thaliana >gi_166668 (L10357) CHL1 [Arabidopsis thaliana] >gi_3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb_L10357 from A. thaliana. ESTs gb_H37533 and gb_R29790, gb_T46117, gb_T46068, gb_T75688,

gb_R29817, gb_R29862, gb_Z34634 and gb_Z34258 come from

this gene. [Arabidopsis thaliana]

Seq. No. 47452

Seq. ID jsh701070250.h1

Method BLASTN
NCBI GI g1532162
BLAST score 41
E value 6.0e-14

Match length 53 % identity 94

NCBI Description Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3,

AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14

genes, partial cds, AT.I.24-7, ascorbate peroxidase

(ATHAPX1), EF-lalpha-A1, -A2 and -A3 (EF-lalpha) and AT.I

Seq. No. 47453

Seq. ID jsh701070283.h1

Method BLASTN
NCBI GI g18764
BLAST score 243
E value 1.0e-134
Match length 247
% identity 100

NCBI Description G.max tefS1 gene for elongation factor EF-1a

Seq. No. 47454

Seq. ID jsh701070343.h1

Method BLASTX



```
q1709347
NCBI GI
                  133
BLAST score
                   3.0e-14
E value
                  87
Match length
                   48
% identity
                  SERINE/THREONINE-PROTEIN KINASE NRK2 (SERINE/THREONINE
NCBI Description
                   KINASE 2) >gi_348245 (L20321) protein serine/threonine
                   kinase [Homo sapiens] >gi_4507277_ref_NP_003148.1_pSTK2_
                   serine/threonine kinase
                   47455
Seq. No.
                   jsh701070390.h1
Seq. ID
                   BLASTX
Method
                   q3927894
NCBI GI
                   107
BLAST score
                   1.0e-08
E value
Match length
                   83
                   47
% identity
NCBI Description (Y17192) peroxidase [Cucurbita pepo]
                   47456
Seq. No.
Seq. ID
                   jsh701070393.h1
                   BLASTN
Method
                   q3641835
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   114
Match length
                   83
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
NCBI Description
                   (ESSAII project)
Seq. No.
                   47457
Seq. ID
                   jsh701070405.hl
                   BLASTN
Method
                   q3021374
NCBI GI
                   99
BLAST score
                   2.0e-48
E value
Match length
                   227
% identity
NCBI Description Glycine max mRNA for profilin, PRO1
Seq. No.
                   47458
Seq. ID
                   jsh701070435.h1
Method
                   BLASTX
                   q886100
NCBI GI
BLAST score
                   202
```

9.0e-27 E value 67 Match length % identity

(U27347) putative water channel protein; plasmalemma NCBI Description intrinsic protein; similar to Arabidopsis Pip2a gene

product, PIR Accession Number S44084 [Glycine max]

47459 Seq. No.

jsh701070436.h1 Seq. ID

BLASTN Method q3982595 NCBI GI



```
BLAST score
                  1.0e-115
E value
Match length
                  262
                  95
% identity
                  Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
NCBI Description
Seq. No.
                  47460
Seq. ID
                  jsh701070439.h1
                  BLASTN
Method
                  g4193387
NCBI GI
                  71
```

BLAST score 71
E value 8.0e-32
Match length 139
% identity 88
NCRI Description Heyes b

NCBI Description Hevea brasiliensis translationally controlled tumor protein

(TCTP) mRNA, complete cds

Seq. No. 47461 jsh701070451.h1 Seq. ID BLASTX Method g3894169 NCBI GI 292 BLAST score 1.0e-26 E value 88 Match length 64 % identity

NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 47462

 Seq. ID
 jsh701070453.h1

 Method
 BLASTX

 NCBI GI
 g603074

 BLAST score
 169

 E value
 2.0e-12

Match length 74 % identity 45

NCBI Description (U18197) ATP:citrate lyase [Homo sapiens]

Seq. No. 47463
Seq. ID jsh701070488.h1

Method BLASTX
NCBI GI g2055228
BLAST score 169
E value 6.0e-21
Match length 74
% identity 74

NCBI Description (AB000129) SRC1 [Glycine max]

Seq. No. 47464

Seq. ID kl1701202303.h1

Method BLASTN
NCBI GI g2674202
BLAST score 107
E value 2.0e-53
Match length 215
% identity 87

NCBI Description Arabidopsis thaliana CLP protease regulatory subunit CLPX mRNA, nuclear gene encoding chloroplast protein, complete

Seq. No.

Seq. ID Method

47470

BLASTX

kl1701202593.h1



cds

```
47465
Seq. No.
                   kl1701202371.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g456713
                   236
BLAST score
                   1.0e-130
E value
                   236
Match length
                   33
% identity
                  Glycine max gene for ubiquitin, complete cds
NCBI Description
                   47466
Seq. No.
Seq. ID
                   kl1701202379.h1
                   BLASTN
Method
                   g4558521
NCBI GI
                   36
BLAST score
                   2.0e-11
E value
                   68
Match length
                   88
% identity
                   Genomic sequence for Arabidopsis thaliana BAC T10024,
NCBI Description
                   complete sequence
                   47467
Seq. No.
                   kl1701202416.h1
Seq. ID
                   BLASTN
Method
                   g3869075
NCBI GI
                   53
BLAST score
                   4.0e-21
E value
                   101
Match length
                   88
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXK3, complete sequence [Arabidopsis thaliana]
                   47468
Seq. No.
Seq. ID
                   k11701202570.h1
                   BLASTX
Method
NCBI GI
                   g3402677
                   203
BLAST score
                   3.0e-16
E value
                   83
Match length
% identity
                   (AC004697) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47469
Seq. No.
                   kl1701202579.h1
Seq. ID
                   BLASTN
Method
                   g3980263
NCBI GI
BLAST score
                   76
                   7.0e-35
E value
                   170
Match length
                   90
 % identity
                   Cicer arietinum mRNA for 20S proteasome beta subunit
NCBI Description
```

Seq. ID Method

NCBI GI



```
q4455192
NCBI GI
                  248
BLAST score
                  1.0e-21
E value
                  83
Match length
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  k11701202631.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3832512
                  138
BLAST score
                  8.0e-09
E value
                  63
Match length
                  57
% identity
                  (AF097922) granule-bound glycogen (starch) synthase
NCBI Description
                  [Astragalus membranaceus]
                  47472
Seq. No.
                  kl1701202742.hl
Seq. ID
                  BLASTX
Method
                  g3548801
NCBI GI
BLAST score
                  186
                  3.0e-14
E value
                  67
Match length
                   48
% identity
                  (AC005313) putative transmembrane protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4335768_gb AAD17445 (AC006284) putative
                   integral membrane protein [Arabidopsis thaliana]
                   47473
Seq. No.
                   kl1701202755.h1
Seq. ID
                  BLASTX
Method
                   g1172633
NCBI GI
                   435
BLAST score
                   2.0e-43
E value
                   87
Match length
% identity
                  PROLIFERA PROTEIN >gi_675491 (L39954) contains MCM2/3/5
NCBI Description
                   family signature; PROSITE; PS00847; disruption leads to
                   early lethal phenotype; similar to MCM2/3/5 family, most
                   similar to YBR1441 [Arabidopsis thaliana]
Seq. No.
                   47474
                   kl1701202803.h1
Seq. ID
                   BLASTX
Method
                   q3036805
NCBI GI
BLAST score
                   180
E value
                   9.0e-14
Match length
                   40
% identity
                  (AL022373) thaumatin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47475
```

kl1701202834.h1

BLASTX g3033401



```
BLAST score
                  2.0e-33
E value
                  86
Match length
                  81
% identity
                   (AC004238) putative potassium transporter [Arabidopsis
NCBI Description
                  thaliana]
                   47476
Seq. No.
                  kl1701202878.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4454042
BLAST score
                  146
                   1.0e-09
E value
                   45
Match length
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
                   47477
Seq. No.
                   kl1701202913.hl
Seq. ID
                   BLASTN
Method
                   q2511696
NCBI GI
BLAST score
                   108
                   7.0e-54
E value
                   212
Match length
                   88
% identity
                   Phaseolus vulgaris Moldavian encoding asparagine-specific
NCBI Description
                   endopeptidase precursor (clone cp6b)
                   47478
Seq. No.
Seq. ID
                   kl1701202927.h1
                   BLASTN
Method
                   q2827081
NCBI GI
BLAST score
                   124
                   2.0e-63
E value
                   262
Match length
                   90
% identity
                   Medicago sativa cytosolic malate dehydrogenase (cmdh) mRNA,
NCBI Description
                   complete cds
                   47479
Seq. No.
Seq. ID
                   kl1701202959.h1
Method
                   BLASTX
NCBI GI
                   g2462745
BLAST score
                   326
E value
                   1.0e-30
Match length
                   90
% identity
                   (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47480
Seq. No.
                   kl1701202973.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3982595
BLAST score
                   229
```

1.0e-126

277

96

E value

Match length

% identity





```
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
```

Seq. No. 47481

Seq. ID kl1701202978.h1

Method BLASTX
NCBI GI g1825693
BLAST score 139
E value 1.0e-15
Match length 87
% identity 42

NCBI Description (U88180) Similar to ubiquitin carboxyl-terminal hydrolase;

coded for by C. elegans cDNA yk126d11.5; coded for by C. elegans cDNA yk14g8.5; coded for by C. elegans cDNA

CEESI24R; coded for by C. elegans cDNA yk93d10.5; coded for

by C. elegans

Seq. No. 47482

Seq. ID kl1701203141.h1

Method BLASTN
NCBI GI g17847
BLAST score 32
E value 1.0e-08
Match length 56
% identity 89

NCBI Description B.napus mRNA for phosphatase 2A

Seq. No. 47483

Seq. ID kl1701203181.h1

Method BLASTX
NCBI GI g3386604
BLAST score 373
E value 4.0e-36
Match length 86
% identity 74

NCBI Description (AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.

Seq. ID kl1701203235.h1

47484

Method BLASTX
NCBI GI g4544449
BLAST score 150
E value 3.0e-11
Match length 79
% identity 54

NCBI Description (AC006592) putative peroxidase [Arabidopsis thaliana]

Seq. No. 47485

Seq. ID kl1701203247.h1

Method BLASTX
NCBI GI g3482972
BLAST score 242
E value 6.0e-21
Match length 82
% identity 61

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 47486



Seq. ID kl1701203260.h1

Method BLASTX
NCBI GI g3377507
BLAST score 172
E value 1.0e-12
Match length 54
% identity 61

NCBI Description (AF056026) auxin transport protein EIR1 [Arabidopsis thaliana] >gi 3661620 (AF093241) putative auxin efflux

carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana] >gi_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

Seq. No. 47487

Seq. ID kl1701203277.h1

Method BLASTX
NCBI GI g4512670
BLAST score 172
E value 2.0e-15
Match length 76
% identity 46

NCBI Description (AC006931) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.

47488

Seq. ID k11701203313.h1

Method BLASTN
NCBI GI g532704
BLAST score 44
E value 1.0e-15
Match length 48
% identity 38

NCBI Description Glycine max clone GMFP3 isoprenylated protein mRNA, partial

cds

Seq. No. 47489

Seq. ID kl1701203363.h1

Method BLASTN
NCBI GI g1326160
BLAST score 50
E value 3.0e-19
Match length 132
% identity 89

NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds

Seq. No. 47490

Seq. ID kl1701203376.h1

Method BLASTX
NCBI GI g3367534
BLAST score 316
E value 2.0e-29
Match length 59
% identity 58

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

thaliana]



```
47491
Seq. No.
                  kl1701203380.hl
Seq. ID
                  BLASTN
Method
                  g170048
NCBI GI
                  169
BLAST score
                  3.0e-90
E value
                  178
Match length
% identity
                  18
                  Glycine max SbPRP1 gene encoding a proline-rich protein,
NCBI Description
                  complete cds
                  47492
Seq. No.
                  kl1701203384.h1
Seq. ID
                  BLASTX
Method
                  g2388885
NCBI GI
                  144
BLAST score
                   2.0e-09
E value
                   37
Match length
                   78
% identity
NCBI Description (Y14762) glutathione peroxidase [Lycopersicon esculentum]
                   47493
Seq. No.
                   kl1701203385.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3982595
                  81
BLAST score
                   7.0e-38
E value
                   217
Match length
                   84
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   47494
Seq. No.
                   k11701203447.h1
Seq. ID
                   BLASTX
Method
                   q2245119
NCBI GI
                   279
BLAST score
                   3.0e-25
E value
                   93
Match length
% identity
                   65
                  (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   47495
Seq. No.
                   kl1701203487.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3982595
                   101
BLAST score
                   5.0e-50
E value
                   137
Match length
                   93
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   47496
Seq. No.
                   kl1701203525.h2
Seq. ID
```

Method BLASTX NCBI GI q2244836 BLAST score 322 3.0e - 30E value



```
81
Match length
                  70
% identity
NCBI Description (Z97337) RNA helicase homolog [Arabidopsis thaliana]
                   47497
Seq. No.
                  kl1701203537.h2
Seq. ID
                  BLASTX
Method
                   g2832658
NCBI GI
                   168
BLAST score
                   4.0e-12
E value
                   83
Match length
                   40
% identity
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
                   47498
Seq. No.
                   kl1701203589.h2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539345
                   152
BLAST score
                   3.0e-10
E value
                   61
Match length
                   56
% identity
                  (AL035539) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47499
Seq. No.
                   kl1701203604.h2
Seq. ID
                   BLASTX
Method
                   g1402878
NCBI GI
BLAST score
                   226
                   7.0e-19
E value
                   88
Match length
                   48
% identity
                  (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                   47500
Seq. No.
                   kl1701203618.h2
Seq. ID
                   BLASTN
Method
                   g927504
NCBI GI
                   105
BLAST score
                   4.0e-52
E value
                   197
Match length
                   88
% identity
                   P.sativum mRNA for fructose-1, 6-biphosphate aldolase
NCBI Description
                   (clone aldcyt2)
                   47501
Seq. No.
                   kl1701203690.h2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g435678
                   37
BLAST score
                   2.0e-11
E value
                   77
Match length
                   87
 % identity
                   L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein
NCBI Description
                   S25
```

7677

47502

Seq. No.



```
k11701203695.h2
Seq. ID
                  BLASTN
Method
                  g303900
NCBI GI
                  61
BLAST score
                  7.0e-26
E value
Match length
                  237
% identity
                  78
NCBI Description Soybean gene for ubiquitin, complete cds
                   47503
Seq. No.
Seq. ID
                   kl1701203743.h2
                   BLASTN
Method
                   q472849
NCBI GI
BLAST score
                   71
                   8.0e-32
E value
                   194
Match length
                   87
% identity
                   Glycine max Essex desiccation protectant protein Lea14
NCBI Description
                   homolog mRNA, complete cds
                   47504
Seq. No.
                   kl1701203807.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3176707
                   152
BLAST score
                   3.0e-10
E value
                   44
Match length
                   66
% identity
                   (AC002392) putative proline-rich protein APG [Arabidopsis
NCBI Description
                   thaliana]
                   47505
Seq. No.
Seq. ID
                   kl1701203828.h1
                   BLASTX
Method
                   g2809246
NCBI GI
BLAST score
                   365
                   3.0e-35
E value
Match length
                   81
% identity
                   (AC002560) F2401.15 [Arabidopsis thaliana]
NCBI Description
Seq. No. '
                   47506
Seq. ID
                   kl1701203902.h2
Method
                   BLASTN
NCBI GI
                   q3449322
BLAST score
                   37
E value
                   1.0e-11
                   89
Match length
% identity
                   85
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXC17, complete sequence [Arabidopsis thaliana]
```

 Seq. No.
 47507

 Seq. ID
 kl1701203907.h2

 Method
 BLASTX

NCBI GI g3559816 BLAST score 299

```
1.0e-27
E value
                  82
Match length
% identity
NCBI Description (Y15782) transketolase 2 [Capsicum annuum]
                  47508
Seq. No.
                  kl1701203979.h2
Seq. ID
                  BLASTX
Method
                  g1199467
NCBI GI
                  250
BLAST score
                  8.0e-22
E value
                  79
Match length
% identity
                  61
                  (D64155) possible aldehyde decarbonylase [Arabidopsis
NCBI Description
                  thaliana]
                  47509
Seq. No.
                  k11701204017.h1
Seq. ID
                  {\tt BLASTX}
Method
                  g3047082
NCBI GI
                  141
BLAST score
                   1.0e-14
E value
                  77
Match length
                   56
% identity
NCBI Description (AF058914) similar to Vigna radiata pectinacetylesterase
                  precursor (GB:X99348) [Arabidopsis thaliana]
                   47510
Seq. No.
                   kl1701204042.hl
Seq. ID
                   BLASTX
Method
                   g4559334
NCBI GI
                   192
BLAST score
                   5.0e-15
E value
                   65
Match length
                   51
% identity
NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]
                   47511
Seq. No.
                   kl1701204172.h1
Seq. ID
                   BLASTN
Method
                   q169090
NCBI GI
BLAST score
                   86
E value
                   8.0e-41
Match length
                   166
                   88
% identity
                   Pea glyceraldehyde-3-phosphate dehydrogenase (GapC1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   47512
                   kl1701204272.h2
Seq. ID
                   BLASTX
Method
                   g4098647
NCBI GI
BLAST score
                   174
E value
                   2.0e-14
Match length
                   52
                   83
 % identity
NCBI Description (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
```

Seq. No.

Seq. ID

Method

47518

BLASTN

kl1701204592.h2



thaliana]

```
47513
Seq. No.
                  kl1701204429.h2
Seq. ID
                  BLASTX
Method
                  g2894596
NCBI GI
                  137
BLAST score
E value
                   1.0e-08
                   43
Match length
% identity
                   (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   47514
Seq. No.
                   kl1701204451.h2
Seq. ID
                   BLASTN
Method
                   g2511696
NCBI GI
BLAST score
                   46
                   4.0e-17
E value
                   87
Match length
                   91
% identity
                   Phaseolus vulgaris Moldavian encoding asparagine-specific
NCBI Description
                   endopeptidase precursor (clone cp6b)
                   47515
Seq. No.
                   kl1701204504.h2
Seq. ID
                   BLASTX
Method
                   g3319353
NCBI GI
                   182
BLAST score
                   1.0e-16
E value
                   69
Match length
                   62
% identity
                   (AF077407) contains similarity to copper-binding proteins
NCBI Description
                   [Arabidopsis thaliana]
                   47516
Seq. No.
Seq. ID
                   kl1701204515.h2
                   BLASTN
Method
NCBI GI
                   g310560
                   279
BLAST score
                   1.0e-156
E value
                   279
Match length
                   100
% identity
                   Soybean ascorbate peroxidase mRNA, complete cds
NCBI Description
                   47517
Seq. No.
Seq. ID
                   kl1701204550.h2
                   BLASTN
Method
                   q2055227
NCBI GI
BLAST score
                   101
E value
                   1.0e-49
                   245
Match length
                   86
% identity
                   Glycine max mRNA for SRC1, complete cds
NCBI Description
```

7680



```
NCBI GI
BLAST score
                  66
                  7.0e-29
E value
                  158
Match length
                  85
% identity
                  A.thaliana DNA for S-adenosylmethionine synthetase gene
NCBI Description
                  sam-1 >gi 166871 gb_M55077_ATHSAM A.thaliana
                  S-adenosylmethionine synthetase gene, complete cds
                  47519
Seq. No.
                  k11701204642.h1
Seq. ID
                  BLASTX
Method
                  q4490310
NCBI GI
                  141
BLAST score
                   4.0e-09
E value
                   65
Match length
                   46
% identity
                  (AL035678) somatic embryogenesis receptor-like kinase-like
NCBI Description
                  protein [Arabidopsis thaliana]
                   47520
Seq. No.
                   kl1701204665.h1
Seq. ID
                   BLASTX
Method
                   g3135611
NCBI GI
                   163
BLAST score
                   1.0e-11
E value
                   54
Match length
% identity
                   63
NCBI Description (AF062485) cellulose synthase [Arabidopsis thaliana]
                   47521
Seq. No.
Seq. ID
                   k11701204730.h1
                   BLASTX
Method
                   q1931645
NCBI GI
                   170
BLAST score
                   2.0e-12
E value
                   56
Match length
% identity
                  (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]
NCBI Description
                   47522
Seq. No.
                   kl1701204771.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2832660
BLAST score
                   250
                   9.0e-22
E value
                   76
Match length
 % identity
                   (AL021710) lipase-like protein [Arabidopsis thaliana]
NCBI Description
                   47523
 Seq. No.
                   kl1701204783.h1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2459424
                   192
 BLAST score
                   6.0e-15
 E value
```

87

Match length

Seq. ID

Method



```
% identity
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
                  47524
Seq. No.
                  kl1701204785.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1556445
BLAST score
                  101
                  1.0e-49
E value
                  197
Match length
                  88
% identity
NCBI Description Hordeum vulgare alpha tubulin (tubA) mRNA, complete cds
                  47525
Seq. No.
                  kl1701205004.h1
Seq. ID
                  BLASTX
Method
                  g2407790
NCBI GI
                  297
BLAST score
                   3.0e-27
E value
                  93
Match length
                   62
% identity
NCBI Description (AF019910) grr1 [Glycine max]
                   47526
Seq. No.
                   kl1701205017.h1
Seq. ID
                  BLASTX
Method
                   g4490758
NCBI GI
                   152
BLAST score
E value
                   2.0e-11
                   73
Match length
% identity
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
                   47527
Seq. No.
Seq. ID
                   kl1701205044.h1
                   BLASTN
Method
                   g3982595
NCBI GI
BLAST score
                   202
                   1.0e-110
E value
Match length
                   265
                   95
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   47528
Seq. No.
                   kl1701205066.hl
Seq. ID
                   BLASTX
Method
                   q4204293
NCBI GI
BLAST score
                   294
E value
                   6.0e-27
                   89
Match length
% identity
                   66
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   47529
```

kl1701205078.h1

BLASTX



```
g4056433
NCBI GI
                  166
BLAST score
                  7.0e-12
E value
                  49
Match length
% identity
                  (AC005990) Similar to anter-specific proline-rich protein
NCBI Description
                  (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]
                  47530
Seq. No.
                  kl1701205083.h1
Seq. ID
                  BLASTX
Method
                  q2244836
NCBI GI
                  171
BLAST score
                  2.0e-12
E value
                  60
Match length
                  57
% identity
NCBI Description (Z97337) RNA helicase homolog [Arabidopsis thaliana]
Seq. No.
                  47531
                  k11701205160.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q728868
                  196
BLAST score
                  2.0e-15
E value
Match length
                  90
% identity
                  ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
NCBI Description
                  >gi_99824_pir__S16748 proline-rich protein - rape
                   (fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
                  protein [Brassica napus]
                   47532
Seq. No.
                  kl1701205161.h1
Seq. ID
                  BLASTN
Method
                  g3982595
NCBI GI
                  106
BLAST score
                   8.0e-53
E value
                  190
Match length
                   89
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   47533
Seq. No.
Seq. ID
                   kl1701205203.hl
                   BLASTX
Method
                   g2494174
NCBI GI
                   358
BLAST score
                   3.0e-34
E value
                   72
Match length
                   92
% identity
                   GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi .497979 (U10034)
NCBI Description
                   glutamate decarboxylase [Arabidopsis Thaliana]
                   47534
Seq. No.
Seq. ID
                   kl1701205354.h1
Method
                   BLASTX
```

q3355618

176

NCBI GI BLAST score



```
5.0e-13
E value
                  55
Match length
                  58
% identity
                  (AJ000232) unnamed protein product [Hordeum vulgare]
NCBI Description
                   47535
Seq. No.
                  kl1701205427.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3790569
BLAST score
                  166
                   7.0e-12
E value
                   67
Match length
                   43
% identity
                   (AF078822) RING-H2 finger protein RHA2a [Arabidopsis
NCBI Description
                   thaliana]
                   47536
Seq. No.
                   k11701205434.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4558591
BLAST score
                   154
E value
                   2.0e-10
                   47
Match length
                   72
% identity
                   (AC006555) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   47537
Seq. No.
                   kl1701205538.h1
Seq. ID
Method
                   BLASTX
                   g478809
NCBI GI
                   319
BLAST score
                   8.0e-30
E value
                   82
Match length
                   76
% identity
                   protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449)
NCBI Description
                   protein kinase [Glycine max] >gi_444789_prf__1908223A
                   protein kinase [Glycine max]
                   47538
Seq. No.
                   k11701205576.h1
Seq. ID
                   BLASTX
Method
                   g2347088
NCBI GI
                   156
BLAST score
                   2.0e-13
E value
Match length
                   65
% identity
                   65
                   (U72765) non-specific lipid transfer protein PvLTP-24
NCBI Description
                    [Phaseolus vulgaris]
                   47539
 Seq. No.
                   kl1701205586.h1
 Seq. ID
                   BLASTN
Method
                   g3982595
NCBI GI
BLAST score
                   210
E value
                   1.0e-115
```

257

Match length



```
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                  47540
Seq. No.
Seq. ID
                  kl1701205621.h1
                  BLASTX
Method
                  a349379
NCBI GI
                  282
BLAST score
                  1.0e-25
E value
                  88
Match length
                  65
% identity
NCBI Description (L22847) HAHB-1 [Helianthus annuus]
                  47541
Seq. No.
                  kl1701205633.h1
Seq. ID
                  BLASTX
Method
                  g3914441
NCBI GI
                  155
BLAST score
                  1.0e-10
E value
                  88
Match length
                   5
% identity
NCBI Description REPETITIVE PROLINE-RICH CELL WALL PROTEIN PRECURSOR (MSPRP)
                  >gi_166408 (M91078) MsPRP [Medicago sativa]
                   47542
Seq. No.
                  kl1701205691.h1
Seq. ID
                  BLASTX
Method
                   g3924596
NCBI GI
                   382
BLAST score
                   3.0e-37
E value
                   76
Match length
% identity
                   (AF069442) putative phospho-ser/thr phosphatase
NCBI Description
                   [Arabidopsis thaliana]
                   47543
Seq. No.
                   kl1701205720.hl
Seq. ID
                   BLASTX
Method
                   q3236238
NCBI GI
                   148
BLAST score
                   8.0e-10
E value
                   86
Match length
                   40
 % identity
                   (AC004684) putative ARF1 GTPase activating protein
 NCBI Description
                   [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_
                   (AB017876) Asp1 [Arabidopsis thaliana]
                   47544
 Seq. No.
 Seq. ID
                   kl1701205731.h1
                   BLASTX
 Method
                   g4249382
 NCBI GI
 BLAST score
                   194
                   3.0e-15
 E value
 Match length
                   48
 % identity
                   79
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
 NCBI Description
```

putative permease from Arabidopsis thaliana BAC

NCBI Description

thaliana]



gb AC004481. [Arabidopsis thaliana]

```
47545
Seq. No.
                  kl1701205747.h1
Seq. ID
                  BLASTX
Method
                  g2244940
NCBI GI
                  271
BLAST score
                  3.0e-24
E value
                  85
Match length
% identity
                   61
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]
                   47546
Seq. No.
                  kl1701205777.h1
Seq. ID
                  BLASTX
Method
                   g2118231
NCBI GI
                   316
BLAST score
                   1.0e-29
E value
                   73
Match length
                   78
% identity
                  H+-transporting ATPase (EC 3.6.1.35) AHA10 - Arabidopsis
NCBI Description
                   thaliana >gi_765354_bbs_157347 (S74033) plasma membrane
                   H(+)-ATPase isoform AHA10=P-type ATPase [Arabidopsis
                   thaliana, cv. Columbia, Peptide, 946 aa] [Arabidopsis
                   thaliana]
                   47547
Seq. No.
                   kl1701205779.h1
Seq. ID
                   BLASTX
Method
                   g3790575
NCBI GI
                   217
BLAST score
                   6.0e-18
E value
                   76
Match length
                   51
% identity
                   (AF078825) RING-H2 finger protein RHA3b [Arabidopsis
NCBI Description
                   thaliana]
                   47548
Seq. No.
                   kl1701205782.h1
Seq. ID
                   BLASTX
Method
                   g4467158
NCBI GI
                   141
BLAST score
                   5.0e-09
E value
                   45
Match length
% identity
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   47549
Seq. No.
Seq. ID
                   kl1701205935.h1
                   BLASTX
Method
                   g3859592
NCBI GI
BLAST score
                   205
                   5.0e-31
E value
                   91
Match length
                   71
 % identity
                   (AF104919) contains similarity to expansins [Arabidopsis
```



Seq. No. 47550

Seq. ID kll701205942.hl

Method BLASTN
NCBI GI g515691
BLAST score 180
E value 7.0e-97
Match length 191
% identity 99

NCBI Description Glycine max Forrest beta-tubulin (tubB3) mRNA, partial cds

Seq. No. 47551

Seq. ID kl1701205978.h1

Method BLASTX
NCBI GI g2708750
BLAST score 124
E value 8.0e-13
Match length 89
% identity 54

NCBI Description (AC003952) putative physical impedence protein [Arabidopsis

thaliana]

Seq. No. 47552

Seq. ID kl1701205980.h1

Method BLASTX
NCBI GI g136644
BLAST score 228
E value 8.0e-26
Match length 76
% identity 71

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 100765 pir A34506

23K ubiquitin carrier protein E2 - wheat >gi_170782 (M28059) ubiquitin carrier protein [Triticum vulgare]

Seq. No. 47553

Seq. ID kl1701206027.h1

Method BLASTN
NCBI GI g725331
BLAST score 304
E value 1.0e-171
Match length 304
% identity 100

NCBI Description Glycine max mitochondrion polymorphic marker DNA sequence

Seq. No. 47554

Seq. ID kl1701206085.h1

Method BLASTN
NCBI GI g602589
BLAST score 33
E value 4.0e-09
Match length 88
% identity 92

NCBI Description P.hybrida mRNA for triosephosphate isomerase

Seq. No. 47555

Seq. ID k11701206107.h1



```
BLASTN
Method
NCBI GI
                  g18646
                  129
BLAST score
                  2.0e-66
E value
                  189
Match length
                  92
% identity
NCBI Description Soybean mRNA for HMG-Y related protein, variant A
                   47556
Seq. No.
                   kl1701206168.hl
Seq. ID
                   BLASTX
Method
                   g4263722
NCBI GI
                   173
BLAST score
                   6.0e-13
E value
                   36
Match length
                   83
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
                   47557
Seq. No.
                   kl1701206221.h1
Seq. ID
                   BLASTX
Method
                   g3355465
NCBI GI
                   362
BLAST score
                   6.0e-35
E value.
                   85
Match length
                   78
% identity
                   (AC004218) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   47558
Seq. No.
                   kl1701206301.h1
Seq. ID
                   BLASTN
Method
                   g4566613
NCBI GI
BLAST score
                   46
                   7.0e-17
E value
                   122
Match length
% identity
                   84
                   Populus alba x Populus tremula actin depolymerizing factor
NCBI Description
                   mRNA, partial cds
                   47559
Seq. No.
Seq. ID
                   kl1701206349.h1
                   BLASTX
Method
NCBI GI
                   g2827549
                   235
BLAST score
                   5.0e-20
E value
                   48
Match length
                   90
% identity
                   (AL021635) glycoprotein endopeptidase - like protein
NCBI Description
                    [Arabidopsis thaliana]
                   47560
Seq. No.
                   kl1701206366.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4206196
```

230

2.0e-19

BLAST score

E value



```
72
Match length
% identity
                  54
                  (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47561
                  kl1701206396.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4324966
BLAST score
                  74
```

E value 1.0e-33
Match length 130
% identity 89

NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No. 47562 Seq. ID kl1701206410.hl

Method BLASTX
NCBI GI g1297359
BLAST score 294
E value 6.0e-27
Match length 67
% identity 81

NCBI Description (U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]

Seq. No. Seq. ID 47563 kl1701206538.h1

Method BLASTN

NCBI GI g929950
BLAST score 74
E value 1.0e-33
Match length 135
% identity 96

NCBI Description Glycine max homeobox-leucine zipper protein mRNA, partial

cds

Seq. No. 47564

Seq. ID kl1701206557.h1

Method BLASTX
NCBI GI g1865677
BLAST score 430
E value 7.0e-43
Match length 88
% identity 88

NCBI Description (Y08568) trehalose-6-phosphate synthase [Arabidopsis

thaliana]

Seq. No.

47565

Seq. ID kl1701206581.h1

Method BLASTX
NCBI GI g1084512
BLAST score 155
E value 1.0e-10
Match length 83
% identity 46

NCBI Description viral mRNA translation inhibitor SKI2 - yeast

(Saccharomyces cerevisiae) >gi_625114 (U19729) Ski2p:

Antiviral protein [Saccharomyces cerevisiae]

Seq. ID

Method



```
47566
Seq. No.
                  kl1701206586.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4115383
BLAST score
                  197
                  1.0e-15
E value
                  75
Match length
% identity
                  (AC005967) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                   47567
Seq. No.
Seq. ID
                   kl1701206604.h1
                   BLASTX
Method
                   q4508073
NCBI GI
BLAST score
                   154
                   3.0e-14
E value
Match length
                   78
% identity
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]
                   47568
Seq. No.
                   kl1701206618.h1
Seq. ID
                   BLASTN
Method
                   g16508
NCBI GI
                   105
BLAST score
                   4.0e-52
E value
                   149
Match length
                   93
% identity
                   A.thaliana DNA for S-adenosylmethionine synthetase gene
NCBI Description
                   sam-1 >gi 166871 gb M55077_ATHSAM A.thaliana
                   S-adenosylmethionine synthetase gene, complete cds
                   47569
Seq. No.
                   kl1701206656.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4335722
                   229
BLAST score
                   2.0e-19
E value
                   63
Match length
% identity
                   (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47570
Seq. No.
Seq. ID
                   k11701206658.h1
                   BLASTX
Method
                   g2583119
NCBI GI
BLAST score
                   284
                   8.0e-26
E value
                   80
Match length
% identity
                   (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47571
Seq. No.
```

kl1701206950.hl

BLASTX



```
g2911077
NCBI GI
                  146
BLAST score
                  1.0e-09
E value
                  54
Match length
                  52
% identity
                  (AL021960) gibberellin 20-oxidase - like protein
NCBI Description
                  [Arabidopsis thaliana]
                  47572
Seq. No.
                  kl1701206969.h1
Seq. ID
                  BLASTX
Method
                  g3367522
NCBI GI
                  201
BLAST score
                  4.0e-16
E value
                  82
Match length
                  51
% identity
                  (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                   47573
Seq. No.
                                                                  kl1701206975.hl
Seq. ID
                  BLASTX
Method
                   g3292815
NCBI GI
                   173
BLAST score
                   8.0e-13
E value
                   77
Match length
% identity
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]
                   47574
Seq. No.
                   kl1701206994.h1
Seq. ID
                   BLASTX
Method
                   g3290209
NCBI GI
                   210
BLAST score
                   4.0e-17
E value
                   70
Match length
                   63
 % identity
                   (U78947) MADS-box protein 1 [Malus domestica]
NCBI Description
                   47575
Seq. No.
                   kl1701207102.hl
Seq. ID
                   BLASTN
Method
                   q170053
NCBI GI
BLAST score
                   84
                   1.0e-39
E value
                   164
Match length
                   88
 % identity
NCBI Description Soybean ribosomal protein S11 mRNA, 3' end
                   47576
 Seq. No.
                   kl1701207126.hl
 Seq. ID
                   BLASTN
 Method
                   g256142
 NCBI GI
 BLAST score
                   249
 E value
                   1.0e-138
                   253
 Match length
```

100

% identity



NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var Prize, mRNA, 1450 nt]

47577 Seq. No.

kl1701207169.h1 Seq. ID

Method BLASTX NCBI GI g2245394 BLAST score 143 E value 3.0e-09 Match length 46 % identity 59

NCBI Description (U89771) ARF1-binding protein [Arabidopsis thaliana]

Seq. No.

47578 kl1701207219.h1 Seq. ID

Method BLASTX NCBI GI g4220524 BLAST score 232 1.0e-19

E value Match length 60 % identity 65

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 47579

Seq. ID kl1701207249.h1

Method BLASTX NCBI GI g3236254 BLAST score 216 1.0e-18 E value Match length 71

% identity

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

47580 Seq. No.

kl1701207255.h1 Seq. ID

Method BLASTN NCBI GI g757521 BLAST score 52 9.0e-21 E value Match length 144 % identity 84

NCBI Description A.glutinosa mRNA for subtilisin-like protein

47581 Seq. No.

Seq. ID kl1701207312.h1

Method BLASTX NCBI GI q4406819 BLAST score 248 E value 2.0e-21 Match length 58

(AC006201) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 47582

% identity

Seq. ID kl1701207361.h1

88

BLASTN Method NCBI GI g256142



BLAST score 249 E value 1.0e-138 Match length 257 % identity 99

NCBI Description cytosolic glutamine synthetase [Glycine max=soybeans, var

Prize, mRNA, 1450 nt]

Seq. No. 47583

Seq. ID kl1701207375.h1

Method BLASTX
NCBI GI g3264767
BLAST score 209
E value 3.0e-17
Match length 49
% identity 80

NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 47584

Seq. ID k11701207435.h1

Method BLASTN
NCBI GI g1707369
BLAST score 33
E value 3.0e-09
Match length 73
% identity 86

NCBI Description A.thaliana mRNA for arginine/serine-rich splicing factor,

RSp41

Seq. No.

47585

Seq. ID kl1701207462.h1

Method BLASTX
NCBI GI g2501182
BLAST score 151
E value 2.0e-10
Match length 32
% identity 78

NCBI Description OSMOTIN-LIKE PROTEIN PRECURSOR >gi_2129934_pir__JC5237

osmotin-like protein - tomato >gi_1220537 (L76632) osmotin-like protein [Lycopersicon esculentum]

Seq. No.

47586

Seq. ID kl1701207465.h1

Method BLASTX
NCBI GI g3738334
BLAST score 160
E value 3.0e-11
Match length 60
% identity 57

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.

47587

Seq. ID kl1701207526.h1

Method BLASTX
NCBI GI g3193306
BLAST score 171
E value 2.0e-12
Match length 58



% identity

(AF069300) contains similarity to Arabidopsis NCBI Description membrane-associated salt-inducible-like protein

(GB:AL021637) [Arabidopsis thaliana]

47588 Seq. No.

kl1701207529.h1 Seq. ID

Method BLASTN NCBI GI g1381675 135 BLAST score 5.0e-70 E value 243 Match length 89 % identity

Glycine max small GTP-binding protein (sra1) mRNA, partial NCBI Description

cds

47589 Seq. No.

kl1701207535.h1 Seq. ID

Method BLASTN g2924257 NCBI GI 91 BLAST score E value 9.0e-44185 Match length 90 % identity

NCBI Description Tobacco chloroplast genome DNA

47590 Seq. No.

kl1701207645.h1 Seq. ID

BLASTN Method g18764 NCBI GI 106 BLAST score 9.0e-53 E value 166 Match length 92 % identity

NCBI Description G.max tefS1 gene for elongation factor EF-1a

47591 Seq. No.

kl1701207668.h1 Seq. ID

BLASTN Method g2304954 NCBI GI 259 BLAST score 1.0e-144 E value 259 Match length 100 % identity

Glycine max aluminum induced sali5-4a mRNA, complete cds NCBI Description

47592 Seq. No.

k11701207680.hl Seq. ID

BLASTN

Method NCBI GI g16508 BLAST score 66 7.0e-29 E value 158 Match length % identity

A.thaliana DNA for S-adenosylmethionine synthetase gene NCBI Description

sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana

S-adenosylmethionine synthetase gene, complete cds



```
47593
Seq. No.
                  kl1701207748.h1
Seq. ID
                  BLASTX
Method
                  g3702332
NCBI GI
                  272
BLAST score
                  3.0e-24
E value
                  90
Match length
                  58
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  47594
Seq. No.
                  k11701207784.h1
Seq. ID
                  BLASTN
Method
                  g1370199
NCBI GI
                  63
BLAST score
                   3.0e-27
E value
                  185
Match length
                   88
% identity
NCBI Description L.japonicus mRNA for small GTP-binding protein, RAC1
                   47595
Seq. No.
                   k11701207809.h1
Seq. ID
                   BLASTN
Method
                   g1150683
NCBI GI
                   50
BLAST score
                   2.0e-19
E value
                   171
Match length
                   82
% identity
NCBI Description V.radiata atpB, rbcL and trnK genes
                   47596
Seq. No.
                   k11701207912.h1
Seq. ID
                   BLASTX
Method
                   q2959781
NCBI GI
                   447
BLAST score
                   9.0e-45
E value
                   95
Match length
 % identity
                   (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                   47597
 Seq. No.
Seq. ID
                   kl1701207942.h1
                   BLASTN
 Method
                   q1420935
 NCBI GI
                   130
 BLAST score
                   5.0e-67
 E value
                   199
 Match length
                   95
 % identity
NCBI Description Vigna unguiculata aspartic proteinase mRNA, complete cds
                    47598
 Seq. No.
                    kl1701207946.hl
 Seq. ID
 Method
                   BLASTX
                    q4432846
 NCBI GI
 BLAST score
                    156
```

2.0e-23

E value



Match length 104 % identity 70 NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 47599

Seq. ID kl1701207952.h1

Method BLASTX
NCBI GI 94406818
BLAST score 192
E value 6.0e-15
Match length 83
% identity 51

NCBI Description (AC006201) putative transcription factor-like protein

[Arabidopsis thaliana]

Seq. No. 47600

Seq. ID kl1701208025.h1

Method BLASTN
NCBI GI g2511696
BLAST score 108
E value 7.0e-54
Match length 212
% identity 88

NCBI Description Phaseolus vulgaris Moldavian encoding asparagine-specific

endopeptidase precursor (clone cp6b)

Seq. No. 47601

Seq. ID kl1701208060.h1

Method BLASTX
NCBI GI g2317901
BLAST score 341
E value 2.0e-32
Match length 80
% identity 82

NCBI Description (U89959) Similar to vesicle transport protein, PIR

Accession Number A55931 [Arabidopsis thaliana]

Seq. No. 47602

Seq. ID kl1701208091.h1

Method BLASTN
NCBI GI g16508
BLAST score 66
E value 7.0e-29
Match length 158
% identity 85

NCBI Description A.thaliana DNA for S-adenosylmethionine synthetase gene

sam-1 >gi_166871_gb_M55077_ATHSAM A.thaliana

S-adenosylmethionine synthetase gene, complete cds

Seq. No. 47603

Seq. ID kl1701208101.h1

Method BLASTX
NCBI GI g1762144
BLAST score 143
E value 3.0e-09
Match length 44
% identity 55



NCBI Description (U48435) putative cytochrome P450 [Solanum chacoense]

Seq. No.

47604

Seq. ID

kl1701208110.h1

Method

BLASTX

NCBI GI

g4567278

BLAST score

243

E value

6.0e-21

Match length

54

% identity

91 NCBI Description (AC006841) putative anthracycline associated resistance ARX

protein [Arabidopsis thaliana]

Seq. No. Seq. ID

47605 kl1701208144.h1

Method NCBI GI BLASTX g3080412

BLAST score E value

282 2.0e-25

Match length

81

% identity

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No.

47606

Seq. ID

kl1701208162.hl BLASTN

Method NCBI GI BLAST score

g1669590 160

E value

6.0e-85

Match length

264 90

% identity

Glycyrrhiza echinata mRNA for O-methyltransferase, complete NCBI Description

Seq. No.

47607

Seq. ID Method

kl1701208210.h1

NCBI GI

BLASTX g4115388

BLAST score

285

E value

6.0e-26

Match length

80

% identity NCBI Description

(AC005967) putative prolylcarboxypeptidase [Arabidopsis

thaliana]

Seq. No.

47608

Seq. ID

kl1701208280.hl

Method NCBI GI BLASTN g169928

BLAST score

255

E value

1.0e-141

Match length

255 100

% identity NCBI Description

Glycine max alpha'-type beta conglycinin storage protein

gene, complete cds, clone ch4A

Seq. No.

47609



```
Seq. ID
                   kl1701208281.h1
Method
                   BLASTX
NCBI GI
                   q4539333
BLAST score
                   226
                   5.0e-19
E value
Match length
                   66
% identity
                   62
NCBI Description
                   (AL035539) putative amino acid transport protein
                   [Arabidopsis thaliana]
Seq. No.
                   47610
Seq. ID
                   kl1701208341.h1
Method
                  BLASTX
NCBI GI
                  g2143290
BLAST score
                  166
E value
                   5.0e-12
                  77
Match length
% identity
                   40
NCBI Description
                  (Z95972) hypothetical protein Rv0669c [Mycobacterium
                   tuberculosis]
Seq. No.
                   47611
Seq. ID
                   k11701208348.h1
Method
                  BLASTX
NCBI GI
                  g1890317
BLAST score
                  175
E value
                   5.0e-20
Match length
                  78
% identity
                  (Y11791) peroxidase ATP26a [Arabidopsis thaliana]
NCBI Description
                   47612
Seq. No.
                   k11701208395.h1
Seq. ID
Method
                  BLASTX
                   g2347088
NCBI GI
BLAST score
                   168
                   3.0e-12
E value
Match length
                   54
% identity
                   57
NCBI Description
                   (U72765) non-specific lipid transfer protein PvLTP-24
                   [Phaseolus vulgaris]
Seq. No.
                   47613
Seq. ID
                  kl1701208415.hl
Method
                  BLASTX
NCBI GI
                  g3859116
BLAST score
                  187
E value
                  3.0e-14
Match length
                  44
                  75
% identity
NCBI Description
                  (AF031609) unknown [Oryza sativa]
```

47614

Seq. ID kl1701208468.h1

Method BLASTX NCBI GI g4263527 BLAST score 194



```
E value 9.0e-21
Match length 70
% identity 76
NCBI Description (AC004044) hypothetical
```

NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47615

Seq. ID kll701208478.hl

Method BLASTN
NCBI GI g19565
BLAST score 36
E value 4.0e-11
Match length 52
% identity 92

NCBI Description M.liliiflora GADPH mRNA for glycolytic

glyceraldehyde-3-phosphate dehydrogenase

Seq. No. 47616

Seq. ID kll701208531.hl

Method BLASTX
NCBI GI g1669655
BLAST score 208
E value 2.0e-21
Match length 83
% identity 60

NCBI Description (X95962) CER3 [Arabidopsis thaliana]

Seq. No. 47617

Seq. ID kl1701208536.h1

Method BLASTX
NCBI GI g3367537
BLAST score 293
E value 6.0e-27
Match length 85
% identity 63

NCBI Description (AC004392) Contains similarity to ANK repeat region of

Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375.

[Arabid

Seq. No. 47618

Seq. ID kl1701208568.h1

Method BLASTN
NCBI GI g218227
BLAST score 102
E value 2.0e-50
Match length 138
% identity 93

NCBI Description Rice mRNA for ras-related GTP binding protein, complete cds

Seq. No. 47619

Seq. ID kl1701208569.h1

Method BLASTN
NCBI GI g3982595
BLAST score 160
E value 5.0e-85
Match length 212



% identity

Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds NCBI Description

Seq. No.

47620

Seq. ID

kl1701208596.h1

Method NCBI GI BLASTN g2511696

BLAST score

80

E value

3.0e-37 148

Match length % identity

89

NCBI Description

Phaseolus vulgaris Moldavian encoding asparagine-specific

endopeptidase precursor (clone cp6b)

Seq. No.

47621

Seq. ID

kl1701208606.h1

Method NCBI GI BLASTX q3549665

BLAST score E value

233 6.0e-20

71

70

Match length % identity

(AL031394) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

47622

Seq. ID

kl1701208649.hl

Method NCBI GI BLASTX g1076287 165

BLAST score E value Match length

1.0e-11 49

63

% identity NCBI Description

amine acid permease - Arabidopsis thaliana

>gi_510236_emb_CAA50672_ (X71787) amine acid permease

[Arabidopsis thaliana]

Seq. No.

47623

Seq. ID

k11701208685.h1 BLASTX

Method NCBI GI BLAST score

q3894157 370

E value Match length 8.0e-36 92

% identity NCBI Description 71 (AC005312) putative protein kinase, 3' partial [Arabidopsis

thaliana]

Seq. No.

47624

Seq. ID

kl1701208778.h1

Method NCBI GI BLASTN g4457220

BLAST score

37

E value Match length 2.0e-11 125

% identity NCBI Description

Capsicum chinense putative bZIP DNA-binding protein mRNA,

complete cds



```
47625
Seq. No.
Seq. ID
                  kl1701208795.h1
Method
                  BLASTX
NCBI GI
                  g2104529
BLAST score
                  325
                  1.0e-30
E value
                  88
Match length
% identity
                  (AF001308) putative hexose transporter [Arabidopsis
NCBI Description
                  thaliana]
                  47626
Seq. No.
Seq. ID
                  kl1701208811.h1
Method
                  BLASTX
NCBI GI
                  g2791278
BLAST score
                  136
E value
                  5.0e-12
                  83
Match length
                  43
% identity
NCBI Description (Z69257) beta-xylosidase [Hypocrea jecorina]
Seq. No.
                  47627
                  kl1701208831.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3702328
BLAST score
                  182
                  8.0e-14
E value
                  56
Match length
% identity
                  57
NCBI Description (AC005397) putative cytochrome b5 [Arabidopsis thaliana]
Seq. No.
                   47628
Seq. ID
                   kl1701208891.h1
Method
                  BLASTX
NCBI GI
                   g2494064
BLAST score
                  230
E value
                   1.0e-21
Match length
                   84
% identity
                  RETINALDEHYDE-SPECIFIC DEHYDROGENASE TYPE 2 (RALDH(II))
NCBI Description
                   (RALDH-2) >qi 1403721 (U60063) aldehyde dehydrogenase
                   [Rattus norvegicus]
Seq. No.
                   47629
                   k11701208920.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3116019
BLAST score
                   43
                   4.0e-15
E value
                  123
Match length
% identity
                   84
NCBI Description Pisum sativum mRNA for ftsZ gene
```

7701

47630

BLASTN

kl1701208955.h1

Seq. No.

Seq. ID Method



NCBI GI g1675195 BLAST score 92 E value 2.0e-44 Match length 185 % identity 88

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

Seq. No.

47631

Seq. ID kl1701208959.h1

Method BLASTX
NCBI GI g2267567
BLAST score 149
E value 1.0e-17
Match length 58
% identity 75

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium

x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding

protein 2 [Pelargonium x hortorum]

Seq. No.

47632

Seq. ID kl1701209027.h1

Method BLASTX
NCBI GI g2281100
BLAST score 191
E value 5.0e-15
Match length 72
% identity 51

NCBI Description (AC002333) LecRK1 protein kinase isolog [Arabidopsis

thaliana]

Seq. No.

47633

Seq. ID

kl1701209049.hl

Method BLASTX
NCBI GI g3513727
BLAST score 229
E value 2.0e-19
Match length 79
% identity 54

NCBI Description (AF080118) contains similarity to TPR domains (Pfam:

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative

protein [Arabidopsis thaliana]

Seq. No. 47634

Seq. ID kll701209149.hl

Method BLASTX
NCBI GI g3582333
BLAST score 185
E value 4.0e-14
Match length 82
% identity 41

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47635

Seq. ID kl1701209165.h1



```
BLASTX
Method
NCBI GI
                  q4508077
BLAST score
                  131
                  5.0e-14
E value
Match length
                  58
% identity
                  74
                  (AC005882) 62114 [Arabidopsis thaliana]
NCBI Description
                  47636
Seq. No.
Seq. ID
                  kl1701209170.h1
Method
                  BLASTX
                  g135431
NCBI GI
                  239
BLAST score
                  1.0e-20
E value
                  70
Match length
                  69
% identity
                  TUBULIN ALPHA CHAIN >gi 84078_pir_ A28914 tubulin alpha
NCBI Description
                  chain - Naegleria gruberi >gi 9739 emb CAA31074 (X12561)
                  alpha-tubulin [Naegleria gruberi] >gi_9741_emb_CAA31075_
                   (X12562) alpha-tubulin [Naegleria gruberi]
                  >gi_9743_emb_CAA31076_ (X12563) alpha-tubulin [Naegleria
                  gruberi]
                   47637
Seq. No.
                  kl1701209369.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3928150
                   210
BLAST score
                   3.0e-17
E value
Match length
                   49
% identity
                  (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                   47638
Seq. No.
                   kl1701209443.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1246403
BLAST score
                   274
E value
                   1.0e-24
Match length
                   62
                   79
% identity
                   (X94698) TINY [Arabidopsis thaliana] >gi_3406035 (AC005405)
NCBI Description
                   TINY [Arabidopsis thaliana]
Seq. No.
                   47639
                   kl1701209458.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3818624
BLAST score
                   230
                   1.0e-33
E value
Match length
                   86
% identity
                   90
```

(AF095912) actin related protein 2; ARP2 [Arabidopsis NCBI Description

thaliana]

Seq. No.

47640

Seq. ID

kl1701209469.h1



```
Method
                  q3183088
NCBI GI
BLAST score
                  146
                  1.0e-09
E value
                  58
Match length
% identity
                  53
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                  (LTP) >gi 629658 pir S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
Seq. No.
                  47641
Seq. ID
                  kl1701209511.hl
                  BLASTN
Method
                  g170025
NCBI GI
BLAST score
                  88
E value
                  6.0e-42
                  136
Match length
                  91
% identity
NCBI Description Soybean malate synthase (MS) mRNA, 3' end
                  47642
Seq. No.
Seq. ID
                  kl1701209517.hl
                  BLASTX
Method
                  q3850569
NCBI GI
BLAST score
                  215
                  1.0e-17
E value
Match length
                  90
% identity
                  (AC005278) ESTs gb_T21276, gb_T45403, and gb_AA586113 come
NCBI Description
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   47643
Seq. ID
                   kl1701209560.h1
                  BLASTX
Method
                   q3367534
NCBI GI
BLAST score
                   431
E value
                   6.0e-43
                   88
Match length
% identity
                  (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                   (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                   thaliana]
                   47644
Seq. No.
```

Seq. ID kl1701209592.h1

Method BLASTX NCBI GI g3914239 BLAST score 324 2.0e-30 E value Match length 90 % identity 71

PROTEIN PHOSPHATASE 2C ABI2 (PP2C) NCBI Description

>gi 1945140_emb_CAA70163_ (Y08966) ABI2 protein phosphatase

2C [Arabidopsis thaliana] >gi_1945142_emb_CAA70162

(Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana]

>gi_2564213_emb_CAA72538_ (Y11840) ABI2 [Arabidopsis



thaliana]

47645 Seq. No. Seq. ID kl1701209603.h1 Method BLASTN

NCBI GI q3982595 209 BLAST score 1.0e-114 E value 237 Match length

% identity Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds NCBI Description

47646 Seq. No.

Seq. ID kl1701209652.h1

97

BLASTX Method NCBI GI q2498329 BLAST score 165 E value 2.0e-18 64 Match length % identity

PATTERN FORMATION PROTEIN EMB30 >gi 2129665_pir__S65571 NCBI Description pattern-formation protein GNOM - Arabidopsis thaliana

>qi 1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi 1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

Seq. No. 47647

Seq. ID kl1701209674.hl

BLASTX Method NCBI GI q4455177 BLAST score 251 7.0e-22 E value 83 Match length % identity

(AL035521) putative protein [Arabidopsis thaliana] NCBI Description

47648 Seq. No.

kl1701209775.h1 Seq. ID

Method BLASTX NCBI GI g3892709 BLAST score 276 7.0e-25 E value Match length 76 % identity

(AL033545) putative protein [Arabidopsis thaliana] NCBI Description

47649 Seq. No.

kl1701209890.h1 Seq. ID

BLASTX Method NCBI GI q3738230 BLAST score 241 1.0e-20 E value 67 Match length 61 % identity



```
(AB007790) DREB2A [Arabidopsis thaliana]
NCBI Description
                  >gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis
                  thaliana]
                  47650
Seq. No.
Seq. ID
                  kl1701209922.hl
                  BLASTX
Method
                  q2245136
NCBI GI
BLAST score
                  188
                  1.0e-14
E value
Match length
                  62
% identity
                  56
                  (Z97344) trehalose-6-phosphate synthase homolog
NCBI Description
                   [Arabidopsis thaliana]
                   47651
Seq. No.
Seq. ID
                   k11701209952.h1
Method
                  BLASTX
                  g3643611
NCBI GI
                   249
BLAST score
                   8.0e-22
E value
Match length
                   59
% identity
                  (AC005395) putative casein kinase [Arabidopsis thaliana]
NCBI Description
                   47652
Seq. No.
Seq. ID
                   kl1701210038.hl
                   BLASTX
Method
                   q3337367
NCBI GI
BLAST score
                   170
                   2.0e-12
E value
                   70
Match length
% identity
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   47653
Seq. No.
                   kl1701210052.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2961297
BLAST score
                   38
E value
                   4.0e-12
Match length
                   187
% identity
NCBI Description Cicer arietinum mRNA for unidentified protein
Seq. No.
                   47654
                   kl1701210095.h1
Seq. ID
```

Method BLASTX g1297359 NCBI GI 300 BLAST score 1.0e-27 E value 68 Match length % identity 81

(U53701) alcohol dehydrogenase 2d [Gossypium hirsutum] NCBI Description

47655 Seq. No.

kl1701210117.h1 Seq. ID



```
Method BLASTX
NCBI GI g2129742
BLAST score 164
E value 1.0e-11
Match length 43
% identity 65
```

NCBI Description stress-induced protein OZI1 precursor - Arabidopsis

thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No

definition line found [Arabidopsis thaliana]

Seq. No. 47656

Seq. ID kl1701210128.h1

Method BLASTN
NCBI GI g3869066
BLAST score 32
E value 1.0e-08
Match length 111
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MBM17, complete sequence [Arabidopsis thaliana]

 Seq. No.
 47657

 Seq. ID
 kl1701210145.h1

 Method
 BLASTN

 NCBI GI
 g18644

 BLAST score
 203

BLAST score 203 E value 1.0e-110 Match length 251 % identity 95

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 47658

Seq. ID kll701210195.hl

Method BLASTX
NCBI GI g3885340
BLAST score 225
E value 7.0e-19
Match length 80
% identity 53

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 47659

Seq. ID kl1701210221.h1

Method BLASTN
NCBI GI g1737221
BLAST score 125
E value 5.0e-64
Match length 265
% identity 87

NCBI Description Pisum sativum BP-80 vacuolar sorting receptor mRNA,

complete cds

Seq. No. 47660

Seq. ID kl1701210239.h1



```
BLASTX
Method
                  g2827143
NCBI GI
BLAST score
                  165
E value
                  8.0e-12
Match length
                  85
% identity
                  44
                   (AF027174) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  47661
Seq. ID
                  kl1701210258.h1
Method
                  BLASTX
NCBI GI
                  g1502430
BLAST score
                  235
                   4.0e-29
E value
Match length
                  72
% identity
                   (U62331) phosphate transporter [Arabidopsis thaliana]
NCBI Description
                  >gi_2564661 (AF022872) phosphate transporter [Arabidopsis
                  thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate
                  Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                  phosphate transporter, AtPT2 [Arabidopsis thaliana]
                   47662
Seq. No.
                   kl1701210267.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2995951
BLAST score
                   189
                   2.0e-20
E value
Match length
                   75
% identity
                   (AF053564) auxin-induced protein [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   47663
                   kl1701210278.h1
Seq. ID
Method
                   BLASTX
                   g2499624
NCBI GI
BLAST score
                   144
                   2.0e-09
E value
Match length
                   70
                   43
% identity
                   PROBABLE SERINE/THREONINE-PROTEIN KINASE YOL045W
NCBI Description
                   >gi_2132002_pir__S66730 hypothetical protein YOL045w -
                   yeast (Saccharomyces cerevisiae) >gi_1419848_emb_CAA99051_
                   (Z74788) ORF YOLO45w [Saccharomyces cerevisiae]
```

Seq. ID kl1701210281.h1

Method BLASTX
NCBI GI g3482978
BLAST score 278
E value 5.0e-25
Match length 74
% identity 73

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]



Seq. ID kll701210317.hl

Method BLASTN
NCBI GI g3982595
BLAST score 115
E value 5.0e-58
Match length 135
% identity 96

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 47666

Seq. ID kll701210352.hl

Method BLASTN
NCBI GI g170048
BLAST score 250
E value 1.0e-138
Match length 266
% identity 9

NCBI Description Glycine max SbPRP1 gene encoding a proline-rich protein,

complete cds

Seq. No. 47667

Seq. ID kl1701210360.h1

Method BLASTN
NCBI GI g506628
BLAST score 107
E value 2.0e-53
Match length 199
% identity 93

NCBI Description Glycine max cv. Dare photosystem II type I chlorophyll

a/b-binding protein (lhcb1*7) gene, complete cds

Seq. No.

Seq. ID kl1701210424.h1

47668

Method BLASTN
NCBI GI g12199
BLAST score 47
E value 5.0e-18
Match length 91
% identity 88

NCBI Description P.vulgaris chloroplast DNA for tRNA-His gene region

Seq. No. 47669

Seq. ID kl1701210487.h1

Method BLASTX
NCBI GI g2765093
BLAST score 288
E value 2.0e-26
Match length 75
% identity 67

NCBI Description (Y10983) putative cytochrome P450 [Glycine max]

Seq. No.

No. 47670

Seq. ID kl1701210515.h1

Method BLASTX
NCBI GI g3080397
BLAST score 139



```
6.0e-09
E value
Match length
                   37
% identity
                   (AL022603) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47671
                  kl1701210520.hl
Seq. ID
                  BLASTN
Method
NCBI GI
                   q170067
                   153
BLAST score
                   5.0e-81
E value
                   164
Match length
                   99
% identity
                  Soybean (G.max) proline-rich cell wall protein (SbPRP3)
NCBI Description
                   gene, complete cds
                   47672
Seq. No.
Seq. ID
                   kl1701210653.hl
                   BLASTN
Method
                   q3982595
NCBI GI
                   159
BLAST score
                   2.0e-84
E value
                   213
Match length
                   95
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   47673
Seq. No.
Seq. ID
                   k11701210695.h1
                   BLASTN
Method
NCBI GI
                   q472262
BLAST score
                   55
                   2.0e-22
E value
Match length
                   93
                   90
% identity
                   Glycine max 28S ribosomal RNA (28S rRNA), ca. bp 1612 to
NCBI Description
                   1803 in mature rRNA
                   47674
Seq. No.
Seq. ID
                   kl1701210707.h1
                   BLASTX
Method
NCBI GI
                   g3600033
BLAST score
                   226
E value
                   5.0e-19
Match length
                   79
% identity
                   56
                   (AF080119) contains similarity to the N terminal domain of
NCBI Description
                   the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis
                   thaliana]
```

Seq. ID kll701210719.hl

47675

Method BLASTX
NCBI GI g2688094
BLAST score 156
E value 1.0e-10
Match length 89
% identity 40





```
(AE001130) guanosine-3',5'-bis(diphosphate)
NCBI Description
                  3'-pyrophosphohydrolase (spoT) [Borrelia burgdorferi]
Seq. No.
                  47676
Seq. ID
                  kl1701210761.h1
Method
                  BLASTX
NCBI GI
                  q2244876
BLAST score
                  281
                  2.0e-25
E value
Match length
                  83
% identity
                  71
                  (Z97338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  47677
Seq. No.
                  kl1701210774.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642163
BLAST score
                  201
                  5.0e-16
E value
Match length
                  84
                  43
% identity
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  47678
Seq. No.
                  kl1701210780.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2961297
BLAST score
                   38
                   4.0e-12
E value
Match length
                  187
% identity
                   81
                  Cicer arietinum mRNA for unidentified protein
NCBI Description
                   47679
Seq. No.
                   kl1701210805.h1
Seq. ID
                   BLASTX
Method
                   g4406784
NCBI GI
                   148
BLAST score
                   5.0e-10
E value
                   74
Match length
% identity
                   38
                   (AC006532) putative oligopeptide transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   47680
Seq. No.
                   kl1701210871.h1
Seq. ID
                   BLASTX
Method
                   g3342249
NCBI GI
                   188
BLAST score
                   1.0e-14
E value
                   69
Match length
% identity
                   51
                  (AF047719) GA3 [Arabidopsis thaliana] >gi 3342251
NCBI Description
                   (AF047720) GA3 [Arabidopsis thaliana]
```

Seq. ID kl1701210896.hl



```
BLASTN
Method
                  g170048
NCBI GI
BLAST score
                  52
                  2.0e-20
E value
Match length
                  56
                  13
% identity
                  Glycine max SbPRP1 gene encoding a proline-rich protein,
NCBI Description
                  complete cds
                  47682
Seq. No.
                  kl1701210921.h1
Seq. ID
                  BLASTX
Method
                  g4314387
NCBI GI
BLAST score
                  333
E value
                  1.0e-31
Match length
                  64
% identity
                  97
                   (AC006232) putative beta-alanine synthetase [Arabidopsis
NCBI Description
                  thaliana]
                   47683
Seq. No.
                  kl1701210962.h1
Seq. ID
                  BLASTN
Method
                  g166379
NCBI GI
                   96
BLAST score
                   8.0e-47
E value
                   156
Match length
% identity
                   69
                  Alfalfa glucose-regulated endoplasmic reticular protein
NCBI Description
                  mRNA, complete cds
                   47684
Seq. No.
                   kl1701211001.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g125606
BLAST score
                   210
                   4.0e-17
E value
                   80
Match length
% identity
                   51
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
NCBI Description
                   pyruvate kinase (EC 2.7.1.40) - potato
                   >gi 22576 emb CAA37727_ (X53688) pyruvate kinase [Solanum
                   tuberosum]
                   47685
Seq. No.
                   kl1701211017.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4325370
BLAST score
                   322
                   2.0e-36
E value
Match length
                   87
                   87
% identity
```

NCBI Description (AF128396) similar to human phosphotyrosyl phosphatase

activator PTPA (GB:X73478) [Arabidopsis thaliana]

Seq. No. 47686

Seq. ID kl1701211110.hl



```
BLASTX
Method
                  g3892713
NCBI GI
BLAST score
                  189
                   2.0e-16
E value
Match length
                   58
% identity
                   71
                   (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                   47687
Seq. No.
                   k11701211127.h1
Seq. ID
Method
                   BLASTX
                   g3600035
NCBI GI
                   292
BLAST score
                   9.0e-27
E value
                   77
Match length
% identity
                   70
                   (AF080119) contains similarity to GTP-binding proteins
NCBI Description
                   [Arabidopsis thaliana]
                   47688
Seq. No.
                   kl1701211132.hl
Seq. ID
Method
                   BLASTN
                   g3873174
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   107
Match length
                   83
-% identity
                   Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   47689
Seq. No.
Seq. ID
                   kl1701211144.hl
Method
                   BLASTN
NCBI GI
                   q18662
BLAST score
                   78
                   4.0e-36
E value
Match length
                   213
% identity
                   86
NCBI Description Glycine max hsp 70 gene
Seq. No.
                   47690
Seq. ID
                   kl1701211271.hl
Method
                   BLASTN
                   q2921322
NCBI GI
                   176
BLAST score
                   1.0e-94
E value
                   180
Match length
 % identity
                   99
 NCBI Description Glycine max beta-1,3-glucanase 7 (SGlu7) gene, partial cds
                   47691
 Seq. No.
                   kl1701211289.h1
 Seq. ID
                   BLASTX
 Method
                   g2435519
 NCBI GI
```

210

62

3.0e-20

BLAST score

Match length

E value



% identity 84

NCBI Description (AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No. 47692
Seq. ID kl1701211315.h1

Method BLASTN
NCBI GI g1431628
BLAST score 40
E value 2.0e-13
Match length 88
% identity 86

NCBI Description V.radiata mRNA for pectinacetylesterase

Seq. No. 47693

Seq. ID kl1701211345.hl

Method BLASTX
NCBI GI g2196466
BLAST score 270
E value 4.0e-24
Match length 83
% identity 67

NCBI Description (Y13673) TATA binding protein-associated factor

[Arabidopsis thaliana]

Seq. No. 47694

Seq. ID kl1701211355.h1

Method BLASTX
NCBI GI g2288988
BLAST score 328
E value 6.0e-31
Match length 84
% identity 74

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47695

Seq. ID kl1701211361.h1

Method BLASTX
NCBI GI g3868853
BLAST score 134
E value 5.0e-09
Match length 58
% identity 66

NCBI Description (AB013853) GPI-anchored protein [Vigna radiata]

Seq. No. 47696

Seq. ID kl1701211386.h1

Method BLASTN
NCBI GI g437944
BLAST score 48
E value 4.0e-18
Match length 104
% identity 92

NCBI Description V.mungo gene for alpha-amylase

Seq. No. 47697

Seq. ID

Method

NCBI GI



```
kl1701211415.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q169978
                  98
BLAST score
E value
                  3.0e-48
Match length
                  158
% identity
                  10
NCBI Description Soybean (G.max) hydroproline-rich protein mRNA, partial cds
                  47698
Seq. No.
Seq. ID
                  kl1701211428.hl
                  BLASTX
Method
NCBI GI
                  g1220196
                  148
BLAST score
                  5.0e-10
E value
Match length
                  34
% identity
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                  47699
Seq. No.
                  kl1701211517.h1
Seq. ID
Method
                  BLASTN
                  g18764
NCBI GI
                  263
BLAST score
                  1.0e-146
E value
                  271
Match length
                  100
% identity
NCBI Description G.max tefS1 gene for elongation factor EF-1a
                  47700
Seq. No.
                  kl1701211541.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499931
BLAST score
                  191
                  7.0e-15
E value
Match length
                  43
% identity
                  86
                  ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT)
NCBI Description
                  >gi_2129534_pir__S71272 adenine phosphoribosyltransferase
                   (EC 2.4.2.7) - Arabidopsis thaliana
                  >gi 1321681 emb_CAA65609_ (X96866) adenine
                  phosphoribosyltransferase [Arabidopsis thaliana]
                   47701
Seq. No.
                  kl1701211544.h1
Seq. ID
                  BLASTX
Method
                  g4510424
NCBI GI
BLAST score
                  146
                  1.0e-09
E value
                  79
Match length
                   43
% identity
                  (AC006929) putative carboxypeptidase [Arabidopsis thaliana]
NCBI Description
                   47702
Seq. No.
```

kl1701211554.hl

BLASTX

g1717755



BLAST score 191 E value 7.0e-15 Match length 46 % identity 76

NCBI Description TROPINONE REDUCTASE HOMOLOG (P29X) >gi_539028_pir__C48674

tropinone reductase homolog - jimsonweed >gi_424158 (L20475) 29kDa protein; high homology to aa sequence of

tropinone reductases [Datura stramonium]

Seq. No. 47703

Seq. ID kll701211602.hl

Method BLASTX
NCBI GI g416638
BLAST score 226
E value 5.0e-19
Match length 77
% identity 56

NCBI Description OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

(INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1)

>gi_287562_dbj_BAA03306_ (D14410) ORF [Vigna radiata]

Seq. No. 47704

Seq. ID kl1701211649.h1

Method BLASTX
NCBI GI g2252634
BLAST score 221
E value 3.0e-18
Match length 78
% identity 53

NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47705

Seq. ID kll701211663.hl

Method BLASTX
NCBI GI g2505865
BLAST score 300
E value 1.0e-27
Match length 91
% identity 26

NCBI Description (Y12227) putative topoisomerase [Arabidopsis thaliana]

Seq. No. 47706

Seq. ID kl1701211691.h1

Method BLASTX
NCBI GI g1297359
BLAST score 219
E value 4.0e-22
Match length 78
% identity 74

NCBI Description (U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]

Seq. No. 47707

Seq. ID kll701211701.hl

Method BLASTX
NCBI GI g1076485
BLAST score 239
E value 1.0e-20



Match length 59 % identity 81

NCBI Description SAM-synthetase - chickpea (fragment)

>gi_732576_emb_CAA59508_ (X85252) SAM-synthetase [Cicer

arietinum]

Seq. No. 47708

Seq. ID kl1701211721.h1

Method BLASTN
NCBI GI g516853
BLAST score 183
E value 1.0e-98
Match length 239
% identity 28

NCBI Description Soybean SUBI-2 gene for ubiquitin, complete cds

Seq. No. 47709

Seq. ID kl1701211738.h1

Method BLASTX
NCBI GI 94567227
BLAST score 103
E value 2.0e-09
Match length 50
% identity 70

NCBI Description (AC007119) putative transport protein [Arabidopsis

thaliana]

Seq. No. 47710

Seq. ID kll701211741.hl

Method BLASTN
NCBI GI g1944341
BLAST score 241
E value 1.0e-133
Match length 278
% identity 98

NCBI Description Glycine max DNA for cysteine proteinase inhibitor, complete

cds

Seq. No. 47711

Seq. ID kl1701211811.hl

Method BLASTN
NCBI GI g2282583
BLAST score 115
E value 4.0e-58
Match length 199
% identity 89

NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete

cds

Seq. No. 47712

Seq. ID kl1701211856.h1

Method BLASTN
NCBI GI g886099
BLAST score 163
E value 1.0e-86
Match length 199
% identity 95



NCBI Description Glycine max putative water channel protein (Pip1) mRNA, complete cds

Seq. No. 47713

Seq. ID kl1701211888.h1

Method BLASTX
NCBI GI g3360291
BLAST score 141
E value 3.0e-10
Match length 61
% identity 54

% identity 54 NCBI Description (AF023165) leucine-rich repeat transmembrane protein kinase

2 [Zea mays]

Seq. No. 47714

Seq. ID kl1701211918.h1

Method BLASTX
NCBI GI g131399
BLAST score 257
E value 8.0e-23
Match length 68
% identity 76

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE

TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411

photosystem II 10K protein precursor - potato

>gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum

tuberosum]

Seq. No. 47715

Seq. ID kll701211934.hl

Method BLASTN
NCBI GI g2760173
BLAST score 32
E value 1.0e-08
Match length 116
% identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MYH19, complete sequence [Arabidopsis thaliana]

Seq. No. 47716

Seq. ID kl1701211947.h1

Method BLASTX
NCBI GI g2147484
BLAST score 286
E value 3.0e-26
Match length 58
% identity 93

NCBI Description homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)

homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No. 47717

Seq. ID kl1701212058.h1

Method BLASTN
NCBI GI g170061
BLAST score 278
E value 1.0e-155
Match length 282



```
% identity
                  Soybean (G.max L.) beta-tubulin (S-beta-2) gene, complete
NCBI Description
Seq. No.
                  47718
                  kl1701212065.hl
Seq. ID
                  BLASTN
Method
                  g4165487
NCBI GI
BLAST score
                  87
E value
                  2.0e-41
Match length
                  143
                  90
% identity
NCBI Description Hordeum vulgare mRNA for alpha-tubulin
                   47719
Seq. No.
                  kl1701212072.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3901294
BLAST score
                   174
                   8.0e-13
E value
                   92
Match length
% identity
                   45
                  (AF089711) rpp8 [Arabidopsis thaliana]
NCBI Description
                   47720
Seq. No.
Seq. ID
                   kl1701212081.h1
Method
                   BLASTX
                   q393707
NCBI GI
                   261
BLAST score
E value
                   6.0e-23
                   76
Match length
% identity
                   71
                  (X67696) acetyl-CoA acyltransferase [Cucumis sativus]
NCBI Description
                   47721
Seq. No.
                   k11701212090.h1
Seq. ID
Method
                   BLASTX
                   g3184283
NCBI GI
                   296
BLAST score
                   4.0e-27
E value
Match length
                   74
% identity
                   77
                   (AC004136) putative TBP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   47722
Seq. No.
                   kl1701212115.h1
Seq. ID
                   BLASTN
Method
                   g2252639
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   59
Match length
                   90
 % identity
                   Genomic sequence of Arabidopsis BAC F8A5, complete sequence
NCBI Description
                    [Arabidopsis thaliana]
```



```
kl1701212136.hl
Seq. ID
                  BLASTN
Method
                  g256142
NCBI GI
                  266
BLAST score
                  1.0e-148
E value
                  270
Match length
% identity
                   100
                  cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                   Prize, mRNA, 1450 nt]
                   47724
Seq. No.
                   kl1701212148.h1
Seq. ID
                   BLASTX
Method
                   g2828293
NCBI GI
                   242
BLAST score
                   8.0e-21
E value
                   91
Match length
                   54
% identity
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
                   47725
Seq. No.
                   kl1701212212.hl
Seq. ID
                   BLASTX
Method
                   g3184054
NCBI GI
                   215
BLAST score
                   1.0e-17
E value
                   64
Match length
                   72
% identity
NCBI Description (AJ223318) MADS-box transcription factor [Pisum sativum]
                   47726
Seq. No.
                   kl1701212213.hl
Seq. ID
                   BLASTX
Method
                   q3096945
NCBI GI
                   351
BLAST score
                   1.0e-33
E value
                   80
Match length
 % identity
                   (AL023094) putative auxin-regulated protein [Arabidopsis
 NCBI Description
                   thaliana]
                    47727
 Seq. No.
                    kl1701212220.h1
 Seq. ID
 Method
                   BLASTN
                    q170048
 NCBI GI
                    223
 BLAST score
                    1.0e-122
 E value
                    253
 Match length
 % identity
                    12
```

Glycine max SbPRP1 gene encoding a proline-rich protein, NCBI Description

complete cds

Seq. No. 47728

kl1701212238.h1 Seq. ID

BLASTN Method q1666233 NCBI GI

BLAST score 82



```
2.0e-38
E value
                  218
Match length
% identity
                  85
                  Pisum sativum actin (PEAc14) mRNA, complete cds
NCBI Description
                  >gi 1724142 gb_U81049_PSU81049 Pisum sativum actin (PEAc14)
                  mRNA, complete cds
                  47729
Seq. No.
                  kl1701212257.h1
Seq. ID
Method
                  BLASTN
                  g4324966
NCBI GI
                  152
BLAST score
                  4.0e-80
E value
                  164
Match length
% identity
                  98
NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds
                  47730
Seq. No.
                  kl1701212261.h1
Seq. ID
                  BLASTN
Method
                  g473604
NCBI GI
BLAST score
                  53
                   4.0e-21
E value
Match length
                   57
                   98
% identity
NCBI Description Zea mays W-22 histone H2B mRNA, complete cds
                   47731
Seq. No.
                   kl1701212327.h1
Seq. ID
                   BLASTX
Method
                   g3242722
NCBI GI
                   213
BLAST score
                   2.0e-17
E value
                   60
Match length
% identity
                   (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
NCBI Description
                   thaliana]
                   47732
Seq. No.
                   kl1701212337.h1
Seq. ID
                   BLASTN
Method
                   g347454
NCBI GI
                   101
BLAST score
                   1.0e-49
E value
                   101
Match length
                   100
% identity
                  Soybean hydroxyproline-rich glycoprotein (sbHRGP2) mRNA, 3'
NCBI Description
                   47733
Seq. No.
                   kl1701212361.h1
Seq. ID
                   BLASTX
Method
                   g585963
NCBI GI
```

244

68 76

5.0e-21

BLAST score

% identity

E value Match length





NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 47734

Seq. ID kl1701212376.h1

Method BLASTX
NCBI GI g4262153
BLAST score 159
E value 4.0e-11
Match length 34
% identity 85

NCBI Description (AC005275) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 47735

Seq. ID kl1701212405.h1

Method BLASTN
NCBI GI g4324966
BLAST score 163
E value 1.0e-86
Match length 175
% identity 98

NCBI Description Glycine max ADP-ribosylation factor mRNA, partial cds

Seq. No. 47736

Seq. ID kl1701212426.hl

Method BLASTX
NCBI GI g2335101
BLAST score 151
E value 1.0e-10
Match length 50
% identity 68

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 47737

Seq. ID kl1701212436.h1

Method BLASTN
NCBI GI g4193381
BLAST score 81
E value 9.0e-38
Match length 185
% identity 86

NCBI Description Arabidopsis thaliana ribosomal protein S27 (ARS27A) mRNA,

complete cds

Seq. No. 47738

Seq. ID kl1701212455.h1

Method BLASTX
NCBI GI g4510399
BLAST score 300
E value 1.0e-27
Match length 57
% identity 86

NCBI Description (AC006587) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 47739

Seq. ID kl1701212475.h1



```
BLASTN
Method
                  g2342665
NCBI GI
                  98
BLAST score
                  3.0e-48
E value
Match length
                  138
                  93
% identity
                  Glycine max seed coat peroxidase precursor (Ep) gene,
NCBI Description
                   complete cds
                   47740
Seq. No.
                   kl1701212496.h1
Seq. ID
                   BLASTN
Method
                   g1902893
NCBI GI
                   89
BLAST score
E value
                   1.0e-42
Match length
                   221
% identity
                   85
                  Solanum melongena mRNA for QM family protein, complete cds
NCBI Description
                   47741
Seq. No.
                   k11701212695.h1
Seq. ID
                   BLASTX
Method
                   g3747111
NCBI GI
                   138
BLAST score
                   1.0e-08
E value
Match length
                   44
% identity
                   55
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                   47742
Seq. No.
                   kl1701212711.h1
Seq. ID
                   BLASTX
Method
                   q4455335
NCBI GI
                   336
BLAST score
                   8.0e-32
E value
                   90
Match length
                   25
% identity
                   (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                   47743
Seq. No.
                   kl1701212714.hl
Seq. ID
                   BLASTX
Method
                   g4539390
NCBI GI
                   151
BLAST score
                   2.0e-10
E value
                   39
Match length
                   72
 % identity
                   (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
NCBI Description
                    [Arabidopsis thaliana]
                    47744
 Seq. No.
                   kl1701212721.h1
 Seq. ID
                   BLASTX
Method
                   g4572669
NCBI GI
                   246
 BLAST score
                   2.0e-22
E value
```

7723

90

Match length



```
% identity
                  (AC006954) putative glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  47745
                  kl1701212742.h1
Seq. ID
                  BLASTX
Method
                  q3024696
NCBI GI
BLAST score
                  298
                  1.0e-27
E value
Match length
                  74
% identity
                  81
                  T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA)
NCBI Description
                   (CCT-GAMMA) (CHAPERONIN SUBUNIT CCTV GAMMA)
                  >gi_1906364_emb_CAA72704_ (Y11967) chaperonin subunit CCTV
                  gamma [Oxytricha granulifera]
Seq. No.
                   47746
Seq. ID
                  kl1701212768.hl
                  BLASTN
Method
                  q1239962
NCBI GI
BLAST score
                   88
                   3.0e-42
E value
                   140
Match length
                   91
% identity
                  A.majus mRNA for MADS-box protein (DEFH72)
NCBI Description
                   47747
Seq. No.
                   kl1701212841.h1
Seq. ID
                   BLASTX
Method
                   q1946355
NCBI GI
                   218
BLAST score
                   5.0e-18
E value
                   81
Match length
                   49
% identity
                   (U93215) maize transposon MuDR mudrA protein isolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2880040 (AC002340) maize
                   transposon MuDR mudrA-like protein [Arabidopsis thaliana]
                   47748
Seq. No.
                   kl1701212869.hl
Seq. ID
                   BLASTN
Method
                   g169978
NCBI GI
                   85
BLAST score
                   3.0e-40
E value
                   85
Match length
% identity
                  Soybean (G.max) hydroproline-rich protein mRNA, partial cds
NCBI Description
                   47749
Seq. No.
                   k11701212876.h1
Seq. ID
                   BLASTX
```

Method BLASTX
NCBI GI g2129703
BLAST score 224
E value 2.0e-21
Match length 77
% identity 69



receptor kinase - Arabidopsis thaliana NCBI Description >gi_2129704_pir__S71184 receptor kinase - Arabidopsis thaliana >gi_166692 (M80238) receptor kinase [Arabidopsis thaliana] >qi 445123 prf__1908429A receptor kinase [Arabidopsis thaliana] 47750 Seq. No. kl1701212904.h1 Seq. ID BLASTX Method g1086249 NCBI GI BLAST score 148 8.0e-10 E value 79 Match length 41 % identity subtilisin-like protease - Alnus glutinosa NCBI Description >gi 757522_emb_CAA59964_ (X85975) subtilisin-like protease [Alnus glutinosa] 47751 Seq. No. Seq. ID kl1701212977.hl BLASTX Method NCBI GI q4454051 302 BLAST score 7.0e-28 E value 84 Match length % identity (AL035394) putative polygalacturonase [Arabidopsis NCBI Description 47752 Seq. No. kl1701213003.h1 Seq. ID BLASTN Method NCBI GI q170046 BLAST score 53 4.0e-21 E value 53 Match length 100 % identity NCBI Description Glycine max protein kinase (PK6) mRNA, complete cds 47753 Seq. No. kl1701213022.hl Seq. ID BLASTN Method q170048 NCBI GI 123 BLAST score 7.0e-63 E value 265 Match length % identity 17 NCBI Description Glycine max SbPRP1 gene encoding a proline-rich protein, complete cds

47754 Seq. No.

kl1701213070.hl Seq. ID

Method BLASTX g2605621 NCBI GI 150 BLAST score 4.0e-10 E value 52 Match length



```
% identity
                  (D88619) OSMYB3 [Oryza sativa]
NCBI Description
                  47755
Seq. No.
Seq. ID
                  kl1701213092.h1
Method
                  BLASTX
NCBI GI
                  g4567279
BLAST score
                  140
                  1.0e-14
E value
                  79
Match length
% identity
                  51
NCBI Description
                  (AC006841) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  47756
Seq. ID
                  kl1701213127.h1
Method
                  BLASTX
NCBI GI
                  g4415911
BLAST score
                  289
                  3.0e-26
E value
Match length
                  87
                  27
% identity
                  (AC006282) putative polyA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  47757
                  kl1701213178.h1
Seq. ID
Method
                  BLASTX
                  g2191182
NCBI GI
BLAST score
                  162
E value
                  2.0e-11
Match length
                  83
% identity
                  17
                  (AF007271) similar to N. tabacum membrane-associated
NCBI Description
                  salt-inducible protein (PID:g473874) [Arabidopsis thaliana]
                  47758
Seq. No.
Seq. ID
                  kl1701213201.h1
Method
                  BLASTX
NCBI GI
                  g4337197
BLAST score
                  150
                  2.0e-13
E value
Match length
                  74
                  62
% identity
NCBI Description (AC006403) putative AIG2 protein [Arabidopsis thaliana]
Seq. No.
                  47759
                  kl1701213204.h1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2388580
BLAST score 219
E value 2.0e-18
Match length 45
% identity 87

NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002

(gb_1253956). [Arabidopsis thaliana]



```
47760
Seq. No.
                  kl1701213214.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500724
BLAST score
                  165
                  9.0e-12
E value
                  85
Match length
% identity
                  PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR
NCBI Description
                  >gi_2129894_pir__S72453 secA protein precursor - garden pea
                  >gi_1122325_emb_CAA57798_ (X82404) chloroplast SecA protein
                   [Pisum sativum]
                   47761
Seq. No.
                   kl1701213324.h1
Seq. ID
Method
                   BLASTX
                   g4558672
NCBI GI
BLAST score
                   155
                   1.0e-10
E value
                   61
Match length
% identity
                   (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis
NCBI Description
                   thaliana]
                   47762
Seq. No.
                   kl1701213367.h1
Seq. ID
Method
                   BLASTN
                   q303900
NCBI GI
BLAST score
                   135
                   4.0e-70
E value
                   224
Match length
% identity
                   29
NCBI Description Soybean gene for ubiquitin, complete cds
                   47763
 Seq. No.
                   kl1701213383.h1
 Seq. ID
                   BLASTX
Method
                   g113361
NCBI GI
                   152
 BLAST score
                   2.0e-10
 E value
                   42
 Match length
                   69
 % identity
 NCBI Description ALCOHOL DEHYDROGENASE 1 >gi_81891_pir__S00912 alcohol
                   dehydrogenase (EC 1.1.1.1) 1 (clone lambda-PG8) - garden
                   pea >gi_20639_emb_CAA29609_ (X06281) alcohol dehydrogenase
                    [Pisum sativum]
                    47764
 Seq. No.
                   kl1701213389.h1
 Seq. ID
                   BLASTX
 Method
                   q3337352
 NCBI GI
                   137
```

Method BLASIX
NCBI GI g3337352
BLAST score 137
E value 1.0e-08
Match length 61
% identity 39

NCBI Description (AC004481) putative chromatin structural protein Supt5hp

[Arabidopsis thaliana]



47765

kl1701213434.h1

Seq. No.

```
Seq. ID
Method
                  BLASTX
                  q4521322
NCBI GI
                  148
BLAST score
                  9.0e-10
E value
                  54
Match length
                  59
% identity
                  (U11790) mitotic centromere-associated kinesin [Cricetulus
NCBI Description
                  griseus]
                   47766
Seq. No.
Seq. ID
                   kl1701213438.h1
Method
                   BLASTN
NCBI GI
                   g4249567
BLAST score
                   267
                   1.0e-149
E value
                   271
Match length
                   100
% identity
                  Glycine max A5A4B3 glycinin gene, complete cds
NCBI Description
                   47767
Seq. No.
                   k11701213453.h1
Seq. ID
                   BLASTX
Method
                   g1946367
NCBI GI
BLAST score
                   314
                   3.0e-29
E value
Match length
                   86
                   69
% identity
                   (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
                   47768
Seq. No.
                   kl1701213455.h1
Seq. ID
                   BLASTX
Method
                   g3201680
NCBI GI
                   297
BLAST score
                   3.0e-27
E value
                   90
Match length
                   60
 % identity
                   (AF060941) extra-large G-protein [Arabidopsis thaliana]
NCBI Description
                   47769
 Seq. No.
                   kl1701213472.h1
 Seq. ID
                   BLASTN
 Method
                   g1208702
 NCBI GI
                   79
 BLAST score
                   1.0e-36
 E value
                   155
 Match length
                   100
 % identity
                   Glycine max histone H3 gene, partial cds, clone H3-DMAX
 NCBI Description
                    47770
 Seq. No.
                    kl1701213491.hl
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                    g2961297
                    38
 BLAST score
```



E value 3.0e-12 Match length 62 % identity 90

NCBI Description Cicer arietinum mRNA for unidentified protein

Seq. No. 47771

Seq. ID kl1701213514.h1

Method BLASTX
NCBI GI g4567245
BLAST score 288
E value 2.0e-26
Match length 82
% identity 71

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

Seq. No. 47772

Seq. ID kl1701213520.h1

Method BLASTX
NCBI GI g1076812
BLAST score 204
E value 2.0e-16
Match length 68
% identity 63

NCBI Description initiator-binding protein - maize >gi_483490_emb_CAA55691_

(X79085) initiator binding protein [Zea mays]

Seq. No. 47773

Seq. ID kl1701213534.h1

Method BLASTX
NCBI GI g2791278
BLAST score 139
E value 8.0e-09
Match length 64

% identity 41

NCBI Description (Z69257) beta-xylosidase [Hypocrea jecorina]

Seq. No. 47774

Seq. ID kl1701213550.h1

Method BLASTX
NCBI GI g3482929
BLAST score 401
E value 1.0e-39
Match length 80
% identity 90

NCBI Description (AC003970) Putative transcription factor [Arabidopsis

thaliana]

Seq. No. 47775

Seq. ID kl1701213564.h1

Method BLASTN
NCBI GI g1568479
BLAST score 45
E value 2.0e-16
Match length 101
% identity 86

NCBI Description B.vulgaris partial cdc2-related protein kinase gene

```
Seq. No.
                   47776
Seq. ID
                  kl1701213585.h1
Method
                  BLASTX
NCBI GI
                  g3080367
BLAST score
                  166
                  5.0e-12
E value
Match length
                  64
                  48
% identity
NCBI Description (AL022580) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  47777
Seq. ID
                  k11701213605.h1
Method
                  BLASTX
NCBI GI
                  g4263821
BLAST score
                  164
E value
                  9.0e-12
Match length
                  69
% identity
                  48
                  (AC006067) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  47778
Seq. No.
                  kl1701213608.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1853968
BLAST score
                  158
E value
                  3.0e-11
Match length
                  56
                  57
% identity
NCBI Description
                  (D88121) CPRD12 protein [Vigna unquiculata]
Seq. No.
                  47779
Seq. ID
                  kl1701213654.h1
Method
                  BLASTX
NCBI GI
                  q3859592
BLAST score
                  401
E value
                  1.0e-39
                  79
Match length
```

85 % identity

(AF104919) contains similarity to expansins [Arabidopsis NCBI Description

thaliana]

Seq. No. 47780

Seq. ID kl1701213685.h1

Method BLASTX NCBI GI g2245004 BLAST score 228 E value 3.0e-19 63 Match length % identity 71

NCBI Description (Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

47781 Seq. No.

kl1701213787.h1 Seq. ID

Method BLASTN NCBI GI q2827513 BLAST score 32



```
E value 1.0e-08 Match length 80 % identity 85
```

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16

(ESSAII project)

Seq. No. 47782

Seq. ID kl1701213807.h1

Method BLASTN
NCBI GI g170048
BLAST score 129
E value 1.0e-66
Match length 209
% identity 12

NCBI Description Glycine max SbPRP1 gene encoding a proline-rich protein,

complete cds

Seq. No. 47783

Seq. ID kl1701213826.h1

Method BLASTN
NCBI GI 94574209
BLAST score 33
E value 4.0e-09
Match length 57
% identity 89

NCBI Description Tortula ruralis ribosomal protein S3 (rps3) mRNA, complete

cds

Seq. No. 47784

Seq. ID kl1701213842.h1

Method BLASTN
NCBI GI g2317728
BLAST score 43
E value 4.0e-15
Match length 83
% identity 88

NCBI Description Arabidopsis thaliana reversibly glycosylated polypeptide-1

(AtRGP) mRNA, complete cds

Seq. No. 47785

Seq. ID kl1701213892.h1

Method BLASTX
NCBI GI g1076414
BLAST score 241
E value 1.0e-20
Match length 88
% identity 58

NCBI Description subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis

thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974)

subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 47786

Seq. ID kl1701213893.h1

Method BLASTX
NCBI GI g4103324
BLAST score 299
E value 2.0e-27



```
Match length
                  66
                  91
% identity
                  (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                  tuberosum]
                  47787
Seq. No.
                  kl1701213935.hl
Seq. ID
                  BLASTX
Method
                  g3269287
NCBI GI
                  318
BLAST score
                  1.0e-29
E value
                  63
Match length
                  90
% identity
                  (AL030978) GH3 like protein [Arabidopsis thaliana]
NCBI Description
                  47788
Seq. No.
                  kl1701213996.h1
Seq. ID
                  BLASTN
Method
                  q3982595
NCBI GI
                  272
BLAST score
                  1.0e-152
E value
                  272
Match length
                  100
% identity
NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
                   47789
Seq. No.
                   kl1701214019.hl
Seq. ID
                   BLASTN
Method
                   g310575
NCBI GI
                   114
BLAST score
                   2.0e-57
E value
                   284
Match length
                   88
% identity
NCBI Description Glycine max nodulin-26 mRNA, complete cds
                   47790
Seq. No.
                   kl1701214057.h1
Seq. ID
                   BLASTX
Method
                   g3805962
NCBI GI
                   148
BLAST score
```

9.0e-10 E value 53 Match length 49 % identity

(Y13772) laccase [Populus balsamifera subsp. trichocarpa] NCBI Description

47791 Seq. No.

kl1701214130.hl Seq. ID

BLASTN Method q1675195 NCBI GI BLAST score 113 E value 7.0e-57 205 Match length 89 % identity

Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA, NCBI Description

complete cds

47792 Seq. No.



Seq. ID kl1701214219.h1 BLASTN Method NCBI GI g310575 BLAST score 111 1.0e-55 E value Match length 269 % identity 88 NCBI Description Glycine max nodulin-26 mRNA, complete cds 47793 Seq. No. Seq. ID kl1701214259.h1 Method BLASTX NCBI GI g3023527 BLAST score 142 E value 4.0e-09 Match length 55 % identity PUTATIVE UBIQUINONE BIOSYNTHESIS MONOOXGENASE COQ6 NCBI Description >gi 2088820 (AF003384) strong similarity to the E. coli VISC protein (SP:P25535) [Caenorhabditis elegans] Seq. No. 47794 kl1701214263.h1 Seq. ID Method BLASTX NCBI GI g2213629 BLAST score 339 4.0e-32 E value Match length 92 74 % identity (AC000103) F21J9.21 [Arabidopsis thaliana] NCBI Description 47795 Seq. No. Seq. ID kl1701214319.h1 BLASTN Method NCBI GI g1418989 BLAST score 36 6.0e-11 E value Match length 40 97 % identity NCBI Description L.esculentum partial mRNA (clone SENU5) Seq. No. 47796 Seq. ID kl1701214368.h1 Method BLASTX

NCBI GI g4185513 BLAST score 193 E value 3.0e-15 Match length 52 75 % identity

(AF102823) actin depolymerizing factor 5 [Arabidopsis NCBI Description

thaliana] >gi 4185517 (AF102825) actin depolymerizing

factor 5 [Arabidopsis thaliana]

Seq. No. 47797

kl1701214455.h1 Seq. ID

Method BLASTX NCBI GI g3044214



47798

```
BLAST score 312
E value 5.0e-29
Match length 85
% identity 73
```

NCBI Description (AF057044) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.

Seq. ID kl1701214472.h1

Method BLASTX
NCBI GI g3135273
BLAST score 174
E value 7.0e-13
Match length 46
% identity 74

NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]

>gi 4191773 (AC005917) putative WD-40 repeat protein

[Arabidopsis thaliana]

Seq. No.

Seq. ID kll701214547.hl

47799

Method BLASTX
NCBI GI g419760
BLAST score 314
E value 3.0e-29
Match length 79
% identity 76

NCBI Description P-glycoprotein atpgpl - Arabidopsis thaliana

>gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein

[Arabidopsis thaliana]

Seq. No.

47800

Seq. ID kl1701214589.h1

Method BLASTN
NCBI GI g3982595
BLAST score 141
E value 1.0e-73
Match length 159
% identity 98

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No.

47801

Seq. ID kl1701214648.h1 Method BLASTN

NCBI GI g2970653
BLAST score 41
E value 5.0e-14
Match length 96
% identity 86

NCBI Description Vigna unguiculata ferritin subunit cowpea2 precursor, mRNA,

nuclear gene encoding chloroplast protein, complete cds

Seq. No. 47802

Seq. ID kl1701214668.h1

Method BLASTX
NCBI GI g2625088
BLAST score 172
E value 9.0e-19



Match length 55 % identity

(AF030384) ADP-glucose pyrophosphorylase large subunit NCBI Description

[Cucumis melo var. markuwa Markino]

Seq. No. 47803

Seq. ID kl1701214709.h1

BLASTX Method NCBI GI g3201617 BLAST score 190 E value 5.0e-25 Match length 83 % identity

NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47804

Seq. ID kl1701214712.h1

Method BLASTN NCBI GI g2055227 BLAST score 39 8.0e-13 E value Match length 67 91 % identity

NCBI Description Glycine max mRNA for SRC1, complete cds

Seq. No. 47805

kl1701214731.h1 Seq. ID

Method BLASTX NCBI GI g3242715 BLAST score 133 E value 3.0e-18 Match length 87

% identity

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

47806 Seq. No.

Seq. ID kl1701214759.h1

BLASTN Method NCBI GI g2264316 BLAST score 33 E value 4.0e-09 Match length 72 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MRO11, complete sequence [Arabidopsis thaliana]

Seq. No. 47807

kl1701214760.h1 Seq. ID

Method BLASTX NCBI GI g3281868 BLAST score 194 E value 9.0e-30 Match length 85 % identity 76

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 47808



```
Seq. ID
                  kl1701214765.hl
Method
                  BLASTX
NCBI GI
                  g4176420
BLAST score
                  146
E value
                  9.0e-10
Match length
                  48
% identity
NCBI Description
                  (AB008097) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  47809
Seq. ID
                  kl1701214777.h1
Method
                  BLASTX
                  g2264382
NCBI GI
BLAST score
                  139
E value
                  9.0e-09
Match length
                  53
% identity
                  55
                  (AC002354) putative tetracycline transporter-like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  47810
                  kl1701214790.h1
Seq. ID
Method
                  BLASTX
                  g3269287
NCBI GI
BLAST score
                  167
                  2.0e-24
E value
Match length
                  66
                  83
% identity
NCBI Description
                  (AL030978) GH3 like protein [Arabidopsis thaliana]
Seq. No.
                  47811
Seq. ID
                  kl1701214813.h1
Method
                  BLASTX
NCBI GI
                  g4103757
BLAST score
                  265
                  2.0e-23
E value
Match length
                  57
                  91
% identity
NCBI Description (AF027376) MADS1 [Corylus avellana]
Seq. No.
                  47812
Seq. ID
                  kl1701214819.h1
Method
                  BLASTX
NCBI GI
                  q2499872
BLAST score
                  269
E value
                  5.0e-24
Match length
                  82
% identity
                  61
                  TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL
NCBI Description
                  AMINOPEPTIDASE) >gi 2137836 pir 148855
                  tripeptidyl-peptidase II (EC 3.4.14.10) - mouse
                  >gi_575955_emb_CAA57103 (X81323) tripeptidyl-peptidase ii
                  [Mus musculus]
```

Seq. No. 47813

Seq. ID kll701214822.hl

Method BLASTX



```
q3093294
NCBI GI
                  257
BLAST score
                  1.0e-22
E value
                  56
Match length
% identity
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
                  47814
Seq. No.
                  kl1701214839.hl
Seq. ID
                  BLASTX
Method
                  q542050
NCBI GI
                  249
BLAST score
                  1.0e-21
E value
                   64
Match length
                   72
% identity
                  catechol O-methyltransferase (EC 2.1.1.6) III - common
NCBI Description
                   tobacco >gi 429114_emb_CAA50561_ (X71430) catechol
                   O-methyltransferase [Nicotiana tabacum]
                   47815
Seq. No.
                   kl1701214851.hl
Seq. ID
                   BLASTX
Method
                   q3941494
NCBI GI
                   380
BLAST score
                   5.0e-37
E value
                   78
Match length
% identity
                   (AF062901) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   47816
Seq. No.
Seq. ID
                   kl1701214868.hl
                   BLASTX
Method
NCBI GI
                   a3212848
                   348
BLAST score
                   3.0e - 33
E value
                   84
Match length
                   74
 % identity
                   (AC004005) putative inositol polyphosphate-5-phosphatase
NCBI Description
                  [Arabidopsis thaliana]
                   47817
 Seq. No.
 Seq. ID
                   kl1701214887.hl
Method
                   BLASTN
                   q3982595
 NCBI GI
                   173
 BLAST score
                   1.0e-92
 E value
                   261
 Match length
 % identity
                   92
                   Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds
 NCBI Description
                   47818
 Seq. No.
                   kl1701214907.h1
 Seq. ID
 Method
                   BLASTX
                   g3983665
 NCBI GI
```

372

4.0e-36

BLAST score

E value



```
Match length
                   86
% identity
                   (AB011271) importin-beta2 [Oryza sativa]
NCBI Description
                   47819
Seq. No.
                   kl1701214959.hl
Seq. ID
Method
                   BLASTX
                   g2982320
NCBI GI
BLAST score
                   145
                   2.0e-09
E value
Match length
                   56
% identity
                   50
                  (AF051245) hypothetical protein [Picea mariana]
NCBI Description
                   47820
Seq. No.
Seq. ID
                   kl1701214996.hl
Method
                   BLASTN
NCBI GI
                   g3241920
                   69
BLAST score
                   1.0e-30
E value
                   121
Match length
                   89
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAE1, complete sequence [Arabidopsis thaliana]
                   47821
Seq. No.
                   k11701215128.h1
Seq. ID
                   BLASTX
Method
                   g3152595
NCBI GI
BLAST score
                   151
                   5.0e-21
E value
                   76
Match length
                   79
% identity
                   (AC002986) Similar to D. melanogaster sno gene gb_U95760.
NCBI Description
                   EST gb_N97148 and gb_Z26221 come from this gene.
                   [Arabidopsis thaliana]
                   47822
Seq. No.
                   kl1701215257.h1
Seq. ID
                   BLASTX
Method
                   g2880043
NCBI GI
                   167
BLAST score
                   5.0e-12
E value
                   62
Match length
                   52
 % identity
                   (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
NCBI Description
                   hydrolase [Arabidopsis thaliana]
                   47823
 Seq. No.
                   kl1701215286.hl
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3164115
                   151
 BLAST score
                    3.0e-10
 E value
```

7738

(AJ224145) major latex-like protein [Rubus idaeus]

76

39

Match length

NCBI Description

% identity



```
47824
Seq. No.
Seq. ID
                  k11701215327.h1
                  BLASTX
Method
NCBI GI
                  g542050
BLAST score
                  293
                  8.0e-27
E value
Match length
                  86
                  62
% identity
NCBI Description
                  catechol O-methyltransferase (EC 2.1.1.6) III - common
                  tobacco >gi 429114 emb CAA50561 (X71430) catechol
                  O-methyltransferase [Nicotiana tabacum]
Seq. No.
                  47825
Seq. ID
                  kl1701215356.hl
Method
                  BLASTN
                  g18644
NCBI GI
BLAST score
                  79
                  7.0e-37
E value
Match length
                  139
% identity
                  91
NCBI Description
                  Soybean mRNA for HMG-1 like protein
                  47826
Seq. No.
Seq. ID
                  kl1701215366.h1
Method
                  BLASTX
NCBI GI
                  g2642165
BLAST score
                  142
E value
                  5.0e-09
Match length
                  91
% identity
                  36
NCBI Description
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  47827
Seq. ID
                  kl1701215431.h1
                  BLASTX
Method
NCBI GI
                  g3885344
BLAST score
                  156
                  9.0e-11
E value
Match length
                  65
                  48
% identity
NCBI Description
                   (AC005623) unknown protein [Arabidopsis thaliana]
                  >gi_4557057_gb_AAD22497.1_AC007154_1 (AC007154) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  47828
Seq. ID
                  kl1701215483.h1
Method
                  BLASTX
NCBI GI
                  g3290020
```

Method BLASTX
NCBI GI g3290020
BLAST score 170
E value 2.0e-12
Match length 43
% identity 81

NCBI Description (AF044172) cysteine synthase; CS-A; O-acetylserine (thiol)

lyase; cytosolic isoform [Solanum tuberosum]

Seq. No. 47829



```
kmv700737733.h1
 Seq. ID
 Method
                   BLASTX
NCBI GI
                   g310921
BLAST score
                   211
                   3.0e-17
 E value
Match length
                   68
 % identity
                   (L19255) carbonic anhydrase [Nicotiana tabacum]
 NCBI Description
                   47830
 Seq. No.
 Seq. ID
                   kmv700737775,h1
                   BLASTX
 Method
 NCBI GI
                   g3935183
 BLAST score
                   190
 E value
                   9.0e-15
 Match length
                   77
 % identity
 NCBI Description
                   (AC004557) F17L21.26 [Arabidopsis thaliana]
 Seq. No.
                   47831
 Seq. ID
                   kmv700737789.h1
 Method
                   BLASTN
 NCBI GI
                   g12139
 BLAST score
                   44
 E value
                   8.0e-16
 Match length
                   107
 % identity
                   85
 NCBI Description
                   Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and
                   trnG coding for ribosomal protein S2, one CF(1) and three
                   CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly
 Seq. No.
                   47832
 Seq. ID
                   kmv700737813.h1
 Method
                   BLASTN
 NCBI GI
                   q169295
 BLAST score
                   78
 E value
                   5.0e-36
 Match length
                   158
 % identity
                   87
                   Pharbitis nil heat shock protein 83 (Hsp83) gene, complete
 NCBI Description
                   cds
 Seq. No.
                   47833
 Seq. ID
                   kmv700737843.h1
                   BLASTX
 Method
 NCBI GI
                   g3183088
 BLAST score
                   141
 E value
                   5.0e-09
 Match length
                   57
```

53

% identity

PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR NCBI Description

(LTP) >gi_629658_pir__S47084 lipid transfer like protein cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 47834

kmv700737922.h1 Seq. ID



Method BLASTX NCBI GI g2055228 220 BLAST score E value 2.0e-18 Match length 61 42 % identity NCBI Description (AB000129) SRC1 [Glycine max] 47835 Seq. No. Seq. ID kmv700737961.h1 Method BLASTX NCBI GI q2190540 BLAST score 224 E value 1.0e-18 Match length 70 % identity NCBI Description (AC001229) Similar to Arabidopsis TFL1 (gb U77674). [Arabidopsis thaliana]

47836 Seg. No.

Seq. ID kmv700738029.h1

Method BLASTN NCBI GI g288187 BLAST score 190 E value 1.0e-103 Match length 234 % identity 95

NCBI Description V.unguiculata cysteine proteinase inhibitor mRNA

47837 Seq. No.

kmv700738061.h1 Seq. ID

Method BLASTX NCBI GI g4455033 BLAST score 153 E value 2.0e-10 72 Match length

% identity

NCBI Description (AF116237) pseudouridine synthase 1 [Mus musculus]

47838 Seq. No.

Seq. ID kmv700738062.h1

Method BLASTX NCBI GI q2754849 BLAST score 213 2.0e-17 E value Match length 55 % identity

NCBI Description (AF039000) putative serine-glyoxylate aminotransferase

[Fritillaria agrestis]

Seq. No. 47839

Seq. ID kmv700738145.h1

Method BLASTN NCBI GI g4220631 BLAST score 34 5.0e-10 E value Match length 54



```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K5J14, complete sequence [Arabidopsis thaliana]
                  47840
Seq. No.
                  kmv700738195.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4530126
BLAST score
                  142
E value
                  4.0e-09
                  70
Match length
                  46
% identity
                  (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
                  47841
Seq. No.
                  kmv700738210.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3702316
BLAST score
                  272
E value
                  2.0e-24
Match length
                  78
% identity
                   (AC005397) putative Cop1 protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  47842
Seq. No.
                  kmv700738258.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2347208
BLAST score
                  161
                  2.0e-11
E value
Match length
                  79
% identity
                  42
                  (AC002338) APG protein isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  47843
                  kmv700738306.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1361983
BLAST score
                  141
E value
                  5.0e-09
Match length
                  53
                  57
% identity
                  ARP protein - Arabidopsis thaliana >gi 886434 emb CAA89858
NCBI Description
                   (Z49776) ARP protein [Arabidopsis thaliana]
Seq. No.
                  47844
                  kmv700738353.h1
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI g3877594
BLAST score 161
E value 2.0e-11
Match length 71
% identity 58

NCBI Description (279696) predicted using Genefinder; Similarity to Rat lipase (SW:LIPG_RAT); cDNA EST yk310f9.3 comes from this



gene; cDNA EST yk387d12.3 comes from this gene; cDNA EST yk300a8.3 comes from this gene; cDNA EST yk310f9.5 comes f

Seq. No. 47845

Seq. ID kmv700738475.h1

Method BLASTX
NCBI GI g3914472
BLAST score 251
E value 6.0e-22
Match length 63
% identity 78

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

>gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No. 47846

Seq. ID kmv700738515.h1

Method BLASTX
NCBI GI g2495699
BLAST score 139
E value 8.0e-09
Match length 65
% identity 9

NCBI Description HYPOTHETICAL PROTEIN KIAA0032 >gi 517115 dbj BAA04945

(D25215) KIAA0032 [Homo sapiens]

Seq. No. 47847

Seq. ID kmv700738517.h1

Method BLASTN
NCBI GI g1814402
BLAST score 124
E value 2.0e-63
Match length 188
% identity 91

NCBI Description Mesembryanthemum crystallinum methionine synthase (MetE)

mRNA, complete cds

Seq. No. 47848

Seq. ID kmv700738549.h1

Method BLASTN
NCBI GI g829118
BLAST score 105
E value 4.0e-52
Match length 205
% identity 88

NCBI Description P.vulgaris gene for cyclophilin

Seq. No. 47849

Seq. ID kmv700738568.h1

Method BLASTX
NCBI GI g3785994
BLAST score 236
E value 3.0e-20
Match length 77
% identity 61

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]



Seq. No. 47850

Seq. ID kmv700738631.h1

Method BLASTN
NCBI GI g20999
BLAST score 42
E value 1.0e-14
Match length 94
% identity 87

NCBI Description P.vulgaris gln-delta gene for plastid-located glutamine

synthetase (promotor region)

Seq. No. 47851

Seq. ID kmv700738664.h1

Method BLASTN
NCBI GI g20732
BLAST score 155
E value 6.0e-82
Match length 263
% identity 90

NCBI Description Pea chloroplast GAPB mRNA encoding

glyceraldehyde-3-phosphate dehydrogenase (GAPDH) subunit B

(EC 1.2.1.13)

Seq. No. 47852

Seq. ID kmv700738690.h1

Method BLASTX
NCBI GI g3914472
BLAST score 270
E value 4.0e-24
Match length 65
% identity 80

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

>gi_322764_pir__S32021 photosystem II 10K protein - common tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No. 47853

Seq. ID kmv700738702.h1

Method BLASTN
NCBI GI g3033512
BLAST score 185
E value 1.0e-100
Match length 256
% identity 93

NCBI Description Phaseolus vulgaris rubisco activase (Rcal) mRNA, complete

cds

Seq. No. 47854

Seq. ID kmv700738746.h1

Method BLASTX
NCBI GI g1709651
BLAST score 163
E value 9.0e-12
Match length 52
% identity 77

NCBI Description PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209



plastocyanin a precursor - black poplar
>gi_929813_emb_CAA90564_ (Z50185) plastocyanin a [Populus nigra]

Method BLASTX
NCBI GI g135053
BLAST score 144
E value 2.0e-09
Match length 79
% identity 49

NCBI Description SULFITE OXIDASE >gi_86440_pir__A34180 sulfite oxidase (EC

1.8.3.1), hepatic - chicken

Seq. No. 47856

Seq. ID kmv700738858.h1

Method BLASTN
NCBI GI g3184270
BLAST score 47
E value 1.0e-17
Match length 99
% identity 87

NCBI Description Arabidopsis thaliana chromosome II BAC T8K22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 47857

Seq. ID kmv700738889.h1

Method BLASTN
NCBI GI g984524
BLAST score 134
E value 2.0e-69
Match length 231
% identity 57

NCBI Description Zea mays high-methionine zein DZS18 (dzs18) gene, complete

cds

Seq. No. 47858

Seq. ID kmv700738902.h1

Method BLASTX
NCBI GI g4263522
BLAST score 215
E value 1.0e-17
Match length 46
% identity 76

NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47859

Seq. ID kmv700738921.h1

Method BLASTN
NCBI GI g4115336
BLAST score 75
E value 2.0e-34
Match length 149
% identity 18

NCBI Description Pisum sativum (Alaska) ubiquitin (PUB3) gene, complete cds



```
Seq. No.
                   47860
                  kmv700738927.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3150412
BLAST score
                  194
                  3.0e-15
E value
Match length
                  53
                  72
% identity
                  (AC004165) putative Fe(II) transport protein [Arabidopsis
NCBI Description
                  thaliana] >gi 3420044 (AC004680) putative Fe(II) transport
                  protein [Arabidopsis thaliana]
Seq. No.
                  47861
Seq. ID
                  kmv700738944.h1
Method
                  BLASTX
NCBI GI
                  g282873
BLAST score
                  145
E value
                  2.0e-09
Match length
                  29
% identity
                  83
NCBI Description
                  transforming protein (myb) homolog - Arabidopsis thaliana
                  >gi 217859 dbj BAA01730 (D10936) ATMYB1 protein
                   [Arabidopsis thaliana]
Seq. No.
                  47862
                  kmv700739034.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1673344
BLAST score
                  156
E value
                  9.0e-11
Match length
                  47
% identity
                  60
NCBI Description
                  (D64002) hypothetical protein [Synechocystis sp.]
Seq. No.
                  47863
Seq. ID
                  kmv700739046.h1
                  BLASTN
Method
                  g169036
NCBI GI
BLAST score
                  34
E value
                  8.0e-10
Match length
                  50
                  92
% identity
NCBI Description
                  Pisum sativum L. aldolase gene, 3' end cds
Seq. No.
                  47864
Seq. ID
                  kmv700739218.h1
Method
                  BLASTN
NCBI GI
                  g4406529
```

Method BLASTN
NCBI GI 9440652
BLAST score 166
E value 1.0e-88
Match length 245
% identity 92

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 47865

Seq. ID kmv700739323.h1



```
Method
                   BLASTX
NCBI GI
                   g1514643
BLAST score
                   286
                   5.0e-26
E value
                  82
Match length
% identity
                   30
NCBI Description
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
Seq. No.
                   47866
Seq. ID
                   kmv700739327.hl
Method
                  BLASTN
NCBI GI
                   q12158
BLAST score
                   37
                   7.0e-12
E value
Match length
                   68
% identity
                   91
                  Pea gpal gene for subunit A of chloroplast
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13)
                   47867
Seq. No.
Seq. ID
                   kmv700739380.hl
Method
                   BLASTN
NCBI GI
                   g4406529
BLAST score
                   55
E value
                   9.0e-23
Match length
                  79
% identity
                   92
                  Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene
NCBI Description
                   encoding chloroplast protein, complete cds
                   47868
Seq. No.
Seq. ID
                   kmv700739416.hl
Method
                   BLASTN
NCBI GI
                   g169036
BLAST score
                   50
E value
                   3.0e-19
                   70
Match length
                   93
% identity
NCBI Description Pisum sativum L. aldolase gene, 3' end cds
                   47869
Seq. No.
Seq. ID
                   kmv700739430.h1
Method
                   BLASTN
NCBI GI
                   q1020154
BLAST score
                   32
                   1.0e-08
E value
Match length
                   32
% identity
                   100
                  Arabidopsis thaliana clone myb6 DNA-binding protein mRNA,
NCBI Description
                   complete cds
```

Seq. No. 47870

Seq. ID kmv700739516.hl

Method BLASTX
NCBI GI g498902
BLAST score 284
E value 1.0e-25



```
Match length
                  58
% identity
                  (U10044) ribosomal protein L27 homolog [Pisum sativum]
NCBI Description
                  47871
Seq. No.
Seq. ID
                  kmv700739530.h1
                  BLASTN
Method
                  g2804153
NCBI GI
                  75
BLAST score
                  1.0e-34
E value
                  95
Match length
                  95
% identity
NCBI Description Lupinus albus mRNA for aquaporin, partial
                   47872
Seq. No.
Seq. ID
                  kmv700739595.h1
Method
                  BLASTX
NCBI GI
                  g1653513
BLAST score
                  183
                   6.0e-14
E value
Match length
                  66
% identity
                   48
                  (D90914) hypothetical protein [Synechocystis sp.]
NCBI Description
                   47873
Seq. No.
                   kmv700739607.h1
Seq. ID
                  BLASTX
Method
                   g2832652
NCBI GI
BLAST score
                   164
                   8.0e-12
E value
Match length
                   38
                   76
% identity
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47874
Seq. ID
                   kmv700739610.h1
Method
                   BLASTX
NCBI GI
                   q282929
BLAST score
                   179
                   2.0e-13
E value
                   89
Match length
% identity
                   46
                  carbonate dehydratase (EC 4.2.1.1) - garden pea
NCBI Description
                   47875
Seq. No.
                   kmv700739638.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q829118
BLAST score
                   43
                   4.0e-15
E value
Match length
                   119
```

% identity 84

P.vulgaris gene for cyclophilin NCBI Description

Seq. No.

47876

kmv700739693.hl Seq. ID

Method BLASTX

```
NCBI GI
                   q1117778
                   336
BLAST score
                   7.0e-32
E value
                  85
Match length
                  79
% identity
NCBI Description
                  (D49366) 4-coumarate:CoA ligase [Lithospermum
                  erythrorhizon]
                   47877
Seq. No.
Seq. ID
                  kmv700739761.h1
Method
                  BLASTX
NCBI GI
                  g4056489
BLAST score
                   203
                   3.0e-16
E value
                  78
Match length
% identity
                   53
                  (AC005896) putative white protein [Arabidopsis thaliana]
NCBI Description
                   47878
Seq. No.
Seq. ID
                   kmv700739781.h1
Method
                   BLASTN
NCBI GI
                  g20740
BLAST score
                   33
                   3.0e-09
E value
Match length
                  57
% identity
                  89
                  Pisum sativum mRNA for P protein, a part of glycine
NCBI Description
                  cleavage complex
Seq. No.
                   47879
                   kmv700739793.h1
Seq. ID
Method
                  BLASTX
                   g4336610
NCBI GI
BLAST score
                   210
E value
                   4.0e-17
Match length
                   76
% identity
NCBI Description
                  (AF099112) sigma factor; Sig3 [Zea mays]
Seq. No.
                   47880
Seq. ID
                   kmv700739813.h1
Method
                  BLASTX
                   g3914472
NCBI GI
BLAST score
                   256
E value
                   2.0e-22
Match length
                   64
```

% identity 77

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10) NCBI Description

> >gi 322764 pir S32021 photosystem II 10K protein - common tobacco >gi 22669 emb CAA49693 (X70088) NtpII10 [Nicotiana

tabacum]

Seq. No.

47881

Seq. ID

kmv700739904.h1

Method BLASTN NCBI GI g18561 BLAST score 225



E value 1.0e-124 Match length 256 100 % identity

G.max Gmachsl gene for chalcone synthase NCBI Description

47882 Seq. No.

Seq. ID kmv700739932.h1

Method BLASTN NCBI GI g3869087 BLAST score 117 E value 3.0e-59 Match length 177 92 % identity

NCBI Description Nicotiana paniculata mRNA for elongation factor-1 alpha,

complete cds

Seq. No. 47883

Seq. ID kmv700740059.h1

Method BLASTX NCBI GI q2088652 BLAST score 250 E value 6.0e-22 Match length 69 % identity 74

(AF002109) 26S proteasome regulatory subunit S12 isolog NCBI Description

[Arabidopsis thaliana] >gi 2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis

thaliana]

Seq. No. 47884

kmv700740077.h1 Seq. ID

Method BLASTX NCBI GI g2244868 BLAST score 211 E value 3.0e-17 Match length 76

% identity 49

(Z97337) cytochrome P450 [Arabidopsis thaliana] NCBI Description

Seq. No. 47885

Seq. ID kmv700740127.h1

Method BLASTN NCBI GI g516853 BLAST score 149 E value 2.0e-78 Match length 197 % identity 33

Soybean SUBI-2 gene for ubiquitin, complete cds NCBI Description

Seq. No. 47886

Seq. ID kmv700740157.h1

Method BLASTX NCBI GI g3482924 BLAST score 188 1.0e-14 E value Match length 65 % identity 60



NCBI Description (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

47887 Seq. No.

Seq. ID kmv700740175.h1

Method BLASTX NCBI GI q3914486 BLAST score 320 5.0e-30 E value Match length 80 % identity

PUTATIVE PSEUDOURIDYLATE SYNTHASE (PSEUDOURIDINE SYNTHASE) NCBI Description

>gi 2347206 (AC002338) pseudouridine synthase isolog

[Arabidopsis thaliana]

Seq. No. 47888

kmv700740255.h1 Seq. ID

Method BLASTX NCBI GI q2584787 BLAST score 137 1.0e-08 E value Match length 55 49 % identity

(X95762) Aminopeptidase P-like [Homo sapiens] NCBI Description

47889 Seq. No.

kmv700740308.h1 Seq. ID

Method BLASTX NCBI GI q4454042 BLAST score 365 E value 3.0e-35 Match length 82

% identity 82

(AL035394) putative protein [Arabidopsis thaliana] NCBI Description

47890 Seq. No.

Seq. ID kmv700740371.h1

Method BLASTN NCBI GI g2529369 BLAST score 62 E value 2.0e-26 Match length 158 85 % identity

Spinacia oleracea NADP-dependent glyceraldehydephosphate NCBI Description

dehydrogenase subunit A mRNA, chloroplast gene encoding

chloroplast protein, complete cds

Seq. No. 47891

Seq. ID kmv700740376.h1

Method BLASTX NCBI GI g3882183 BLAST score 186 E value 2.0e-14 Match length 77 45 % identity

NCBI Description (AB018274) KIAA0731 protein [Homo sapiens]



```
47892
Seq. No.
Seq. ID
                  kmv700740405.h1
                  BLASTX
Method
NCBI GI
                  g3128206
                  193
BLAST score
                  4.0e-15
E value
Match length
                  83
                  52
% identity
                  (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
                  47893
Seq. No.
Seq. ID
                  kmv700740425.h1
                  BLASTX
Method
NCBI GI
                  q4455367
BLAST score
                  138
E value
                   1.0e-08
Match length
                   52
% identity
                   58
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   47894
                  kmv700740472.h1
Seq. ID
Method
                  BLASTX
                   g2266985
NCBI GI
BLAST score
                   363
                   4.0e-35
E value
Match length
                  81
% identity
                  86
                  (Y13943) MEtRS [Arabidopsis thaliana]
NCBI Description
                   47895
Seq. No.
                   kmv700740528.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q462187
BLAST score
                   234
E value
                   4.0e-20
Match length
                   57
                   79
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 282928 pir A42906 serine
                   hydroxymethyltransferase - garden pea >gi_169158 (M87649)
                   serine hydroxymethyltransferase [Pisum sativum]
                   47896
Seq. No.
                   kmv700740565.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4263774
BLAST score
                   32
                   1.0e-08
E value
```

Match length 63 % identity 45

Arabidopsis thaliana chromosome II BAC T20F21 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

47897

Seq. No. kmv700740722.h1 Seq. ID



Method BLASTN
NCBI GI g4455290
BLAST score 85
E value 3.0e-40
Match length 145
% identity 90

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5

(ESSAII project)

Seq. No. 47898

Seq. ID kmv700740758.hl

Method BLASTN
NCBI GI g4406529
BLAST score 108
E value 5.0e-54
Match length 152
% identity 93

NCBI Description Vigna radiata rubisco activase (Rca) mRNA, chloroplast gene

encoding chloroplast protein, complete cds

Seq. No. 47899

Seq. ID kmv700740870.h1

Method BLASTN
NCBI GI g18695
BLAST score 110
E value 4.0e-55
Match length 186
% identity 90

NCBI Description Soybean nodulin 22 gene

Seq. No.

47900

Seq. ID kmv700740966.h1

Method BLASTX
NCBI GI g3033392
BLAST score 160
E value 4.0e-17
Match length 65
% identity 74

NCBI Description (AC004238) putative translation initiation factor

EIF-2B-epsilon subunit [Arabidopsis thaliana]

Seq. No. 47901

Seq. ID kmv700741020.h1

Method BLASTX
NCBI GI g81885
BLAST score 163
E value 6.0e-20
Match length 62
% identity 80

NCBI Description ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - kidney bean >gi_21050_emb_CAA42618_ (X60000)
ribulose bisphosphate carboxylase [Phaseolus vulgaris]
>gi_21053_emb_CAA40339_ (X57022) small subunit of ribulose
1,5-bisphosphate carboxylase/oxygenase [Phaseolus vulgaris]

Seq. No. 47902

Seq. ID kmv700741027.h1

Seq. No.

Seq. ID Method

NCBI GI

BLAST score



```
Method
                  BLASTX
NCBI GI
                  q3810596
BLAST score
                  128
E value
                  3.0e-09
Match length
                  87
% identity
                  31
                  (AC005398) reverse-transcriptase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  47903
Seq. No.
Seq. ID
                  kmv700741069.h1
                  BLASTX
Method
NCBI GI
                  g4455299
BLAST score
                  191
                  3.0e-25
E value
                  88
Match length
% identity
NCBI Description
                  (AL035528) putative protein [Arabidopsis thaliana]
                  47904
Seq. No.
Seq. ID
                  kmv700741111.h1
Method
                  BLASTX
NCBI GI
                  g1168411
BLAST score
                  163
E value
                  1.0e-11
Match length
                  51
% identity
                  69
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
Seq. No.
                  47905
                  kmv700741218.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1708313
BLAST score
                  158
E value
                  4.0e-11
Match length
                  38
% identity
                  89
                  HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs 163637
NCBI Description
                  (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                  thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                  thaliana]
Seq. No.
                  47906
Seq. ID
                  kmv700741350.h1
                  BLASTX
Method
NCBI GI
                  q4115357
BLAST score
                  168
E value
                  2.0e-16
Match length
                  76
% identity
                  51
NCBI Description
                  (AC005957) hypothetical protein [Arabidopsis thaliana]
                  47907
```

-- 7

kmv700741364.h1

BLASTX

220

q1773369



E value 3.0e-18 Match length 56 % identity 73

NCBI Description (U82633) Alt a I subunit [Alternaria alternata] >gi_1842045

(U86752) major allergen Alt a 1 subunit [Alternaria

alternata]

Seq. No. 47908

Seq. ID kmv700741381.hl

Method BLASTX
NCBI GI 94455158
BLAST score 205
E value 1.0e-16
Match length 53
% identity 74

NCBI Description (AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No. 47909

Seq. ID kmv700741421.h1

Method BLASTX
NCBI GI g1346526
BLAST score 275
E value 1.0e-24
Match length 57
% identity 91

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>gi_1076533_pir__S52218 methionine adenosyltransferase (EC
2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077)
methionine adenosyltransferase [Pisum sativum] >gi_609559
(L36681) S-adenosylmethionine synthase [Pisum sativum]

Seq. No. 47910

Seq. ID kmv700741544.hl

Method BLASTX
NCBI GI g1076678
BLAST score 312
E value 5.0e-29
Match length 73
% identity 88

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.

47911

Seq. ID kmv700741552.h1

Method BLASTX
NCBI GI g886100
BLAST score 226
E value 7.0e-19
Match length 45
% identity 91

NCBI Description (U27347) putative water channel protein; plasmalemma

intrinsic protein; similar to Arabidopsis Pip2a gene product, PIR Accession Number S44084 [Glycine max]

Seq. No. 47912

Seq. ID kmv700741592.h1

Method BLASTX



```
NCBI GI
                   g115800
BLAST score
                   396
E value
                   6.0e-39
Match length
                   84
                   90
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-3) (LHCP) >gi 81771 pir S01962 chlorophyll
                   a/b-binding protein 3 precursor - soybean
                  >gi_18552_emb_CAA31419_ (X12981) chlorophyll a/b binding preprotein (AA - 32 to 231) [Glycine max]
                   47913
Seq. No.
Seq. ID
                   kmv700741641.hl
Method
                   BLASTX
NCBI GI
                   q1296818
BLAST score
                   203
E value
                   3.0e-16
Match length
                   40
% identity
                   100
                   (X94706) naringenin-chalcone synthase [Juglans sp.]
NCBI Description
                   47914
Seq. No.
                   kmv700741735.h1
Seq. ID
Method
                   BLASTX
                   g231924
NCBI GI
BLAST score
                   393
E value
                   1.0e-38
Match length
                   76
% identity
                   96
NCBI Description
                  CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC181)
Seq. No.
                   47915
Seq. ID
                   kmv700741772.h1
Method
                   BLASTX
                   q3776005
NCBI GI
BLAST score
                   304
E value
                   3.0e-28
Match length
                   62
                   95
% identity
NCBI Description
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   47916
Seq. ID
                   kmv700741828.hl
Method
                   BLASTX
NCBI GI
                   q68200
BLAST score
                   170
                   2.0e-12
E value
Match length
                   52
                   69
% identity
NCBI Description
                   fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,
                   chloroplast - spinach >gi_22633_emb_CAA47293_ (X66814)
                   fructose-bisphosphate aldolase [Spinacia oleracea]
```

Seq. No. 47917

Seq. ID kmv700741829.h1

Method BLASTX NCBI GI g3023281



```
BLAST score 263
E value 3.0e-23
Match length 69
% identity 71
```

NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER

>gi_2065194_emb_CAA64475_ (X95098) ammonium transporter

[Lycopersicon esculentum]

Seq. No. 47918

Seq. ID kmv700741886.h1

Method BLASTX
NCBI GI g1076678
BLAST score 186
E value 2.0e-14
Match length 70
% identity 64

NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No. 47919

Seq. ID kmv700741967.h1

Method BLASTX
NCBI GI g131399
BLAST score 201
E value 4.0e-16
Match length 62
% identity 81

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE

TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi 82277 pir S00411

photosystem II 10K protein precursor - potato

>gi_21489_emb_CAA28450_ (X04753) ST-LS1 protein [Solanum

tuberosum]

Seq. No. 47920

Seq. ID kmv700741990.h1

Method BLASTX
NCBI GI g4098272
BLAST score 194
E value 2.0e-15
Match length 34
% identity 100

NCBI Description (U76558) alpha-tubulin [Triticum aestivum]

Seq. No. 47921

Seq. ID kmv700742244.h1

Method BLASTX
NCBI GI g131199
BLAST score 157
E value 4.0e-11
Match length 48
% identity 69

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)

>gi_81470_pir__S00453 photosystem I protein psaH precursor - spinach >gi_21287_emb_CAA34749 (X16858) psaH [Spinacia

oleracea]

Seq. No. 47922



```
kmv700742456.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3702327
BLAST score
                   225
E value
                   4.0e-19
Match length
                   63
% identity
NCBI Description
                   (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   47923
                   kmv700742692.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4322327
BLAST score
                   176
E value
                   3.0e-13
Match length
                   57
% identity
NCBI Description
                  (AF080545) peptide transporter [Nepenthes alata]
Seq. No.
                   47924
Seq. ID
                   kmv700742778.h1
Method
                   BLASTX
                   g3377822
NCBI GI
BLAST score
                   146
                   9.0e-10
E value
Match length
                   41
                   73
% identity
                   (AF076275) contains similarity to Caenorhabditis elegans
NCBI Description
                   MEL-26 (GB:U67737) [Arabidopsis thaliana]
Seq. No.
                   47925
Seq. ID
                   kmv700742786.h1
Method
                   BLASTX
NCBI GI
                   g3328221
BLAST score
                   148
E value
                   5.0e-10
Match length
                   32
% identity
                   91
                  (AF076920) thioredoxin peroxidase [Secale cereale]
NCBI Description
Seq. No.
                   47926
Seq. ID
                   kmv700742805.h1
Method
                   BLASTX
NCBI GI
                   g115765
BLAST score
                   127
                   8.0e-09
E value
Match length
                   56
                   62
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
                   (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_
```

CHLOROPHYLL A-B BINDING PROTEIN OF LHC1 TYPE 11 PRECURSOR (CAB-7) >gi_100201_pir__S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_(X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi_226546_prf__1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]



Seq. No. 47927

Seq. ID kmv700742812.h1

Method BLASTX
NCBI GI g461550
BLAST score 179
E value 1.0e-13
Match length 64
% identity 58

NCBI Description ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir_B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast -

Arabidopsis thaliana >gi_166632 (M61741) ATP synthase

gamma-subunit [Arabidopsis thaliana]

Seq. No. 47928

Seq. ID kmv700742848.h1

Method BLASTX
NCBI GI g2384669
BLAST score 253
E value 2.0e-22
Match length 63
% identity 68

NCBI Description (AF012656) putative potassium transporter AtKTlp

[Arabidopsis thaliana]

Seq. No. 47929

Seq. ID kmv700742863.h1

Method BLASTX
NCBI GI g4455293
BLAST score 178
E value 1.0e-13
Match length 62
% identity 63

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 47930

Seq. ID kmv700742867.h1

Method BLASTX
NCBI GI g3548802
BLAST score 178
E value 1.0e-13
Match length 62
% identity 55

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 47931

Seq. ID kmv700742882.h1

Method BLASTX
NCBI GI g2984004
BLAST score 242
E value 4.0e-21
Match length 63
% identity 68

NCBI Description (AE000750) threonyl-tRNA synthetase [Aquifex aeolicus]



```
47932
Seq. No.
Seq. ID
                  kmv700742914.h1
Method
                  BLASTX
NCBI GI
                  g131397
BLAST score
                  165
                  5.0e-12
E value
Match length
                  53
                  72
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi 81480 pir S00008 photosystem II oxygen-evolving
                  complex protein 3 precursor - spinach
                  >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                  oleracea] >gi 225597_prf_ 1307179B luminal protein 16kD
                  [Spinacia oleracea]
Seq. No.
                  47933
Seq. ID
                  kmv700743031.h1
Method
                  BLASTX
NCBI GI
                  g4006890
BLAST score
                  151
                  3.0e-10
E value
                  39
Match length
% identity
                  85
                  (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  47934
Seq. No.
                  kmv700743167.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3341696
BLAST score
                  208
E value
                  4.0e-17
Match length
                  63
% identity
                  67
                  (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
                  47935
Seq. No.
Seq. ID
                  kmv700743194.hl
Method
                  BLASTX
NCBI GI
                  q3600049
BLAST score
                  239
                  1.0e-20
E value
Match length
                  57
                  82
% identity
```

NCBI Description (AF080120) similar to initiation factor IF2-beta (Pfam: GTP EFTU.hmm, score: 226.67) [Arabidopsis thaliana]

Seq. No. 47936 kmv700743201.hl Seq. ID Method BLASTX g3327394 NCBI GI BLAST score 138 4.0e-22 E value 81 Match length % identity 71



```
NCBI Description
                  (AC004483) putative RNA helicase [Arabidopsis thaliana]
Seq. No.
                   47937
                   kmv700743352.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q99902
                  289
BLAST score
                  2.0e-26
E value
                  57
Match length
% identity
                   98
```

NCBI Description translation elongation factor eEF-1 alpha chain (gene tefS1) - soybean

 Seq. No.
 47938

 Seq. ID
 kmv700743401.h1

 Method
 BLASTX

 NCBI GI
 g2494131

 BLAST score
 235

BLAST score 235 E value 3.0e-20 Match length 67 % identity 64

NCBI Description (AC002376) Strong similarity to Lycopersicon aldehyde

oxidase (gb_U82559). [Arabidopsis thaliana]

Seq. No. 47939

Seq. ID kmv700743443.h1

Method BLASTX
NCBI GI g2702277
BLAST score 165
E value 5.0e-12
Match length 56
% identity 55

NCBI Description (AC003033) putative cyclin g-associated kinase [Arabidopsis

thaliana] >gi 2914689 (AC003974) putative cyclin

g-associated kinase [Arabidopsis thaliana]

Seq. No. 47940

Seq. ID kmv700743451.h1

Method BLASTX
NCBI GI 9730456
BLAST score 190
E value 6.0e-15
Match length 41
% identity 88

NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 47941

Seq. ID kmv700743483.h1

Method BLASTX
NCBI GI g4115538
BLAST score 148
E value 5.0e-10
Match length 63
% identity 54

NCBI Description (AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna

mungo]



Seq. No. 47942

Seq. ID kmv700743638.h1

Method BLASTX
NCBI GI g2073478
BLAST score 143
E value 3.0e-09
Match length 70
% identity 51

NCBI Description (Y11784) DNA polymerase I [Rickettsia prowazekii] >gi 3861304 emb CAA15203 (AJ235273) DNA POLYMERASE I

(polA) [Rickettsia prowazekii]

Seq. No. 47943

Seq. ID kmv700743675.h1

Method BLASTX
NCBI GI g4490336
BLAST score 211
E value 3.0e-17
Match length 70
% identity 61

NCBI Description (AL035656) auxin-induced protein-like [Arabidopsis

thaliana]

Seq. No. 47944

Seq. ID kmv700743703.h1

Method BLASTX
NCBI GI g3288821
BLAST score 106
E value 1.0e-13
Match length 58
% identity 72

NCBI Description (AF063901) alanine:glyoxylate aminotransferase;

transaminase [Arabidopsis thaliana]

Seq. No. 47945

Seq. ID kmv700743707.h1

Method BLASTX
NCBI GI g2435517
BLAST score 208
E value 4.0e-17
Match length 63
% identity 63

NCBI Description (AF024504) contains similarity to peptidase family A1

[Arabidopsis thaliana]

Seq. No. 47946

Seq. ID kmv700743721.h1

Method BLASTX
NCBI GI g1053216
BLAST score 212
E value 1.0e-17
Match length 42
% identity 98

NCBI Description (U39475) chlorophyll a/b-binding protein [Glycine max]

Seq. No. 47947

Seq. ID kmv700743734.h1

NCBI GI

E value

BLAST score



```
Method
                   BLASTX
NCBI GI
                   g1495802
BLAST score
                   157
E value
                   4.0e-11
Match length
                   67
                   43
% identity
NCBI Description (X96405) 13-lipoxygenase [Solanum tuberosum]
Seq. No.
                   47948
Seq. ID
                   kmv700743803.h1
                   BLASTX
Method
NCBI GI
                   q3885511
BLAST score
                   160
                   2.0e-11
E value
                   47
Match length
                   72
% identity
NCBI Description
                  (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
                   47949
Seq. No.
Seq. ID
                   kmv700743808.h1
Method
                   BLASTX
                   g3386611
NCBI GI
                   239
BLAST score
                  1.0e-20
E value
Match length
                  54
% identity
                   69
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                   47950
                   kmv700743838.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3776557
BLAST score
                   166
E value
                   4.0e-12
Match length
                   42
% identity
                   69
NCBI Description
                  (AC005388) Contains similarity to gi 2924495 hypothetical
                   protein Rv1920 from Mycobacterium tuberculosis genome
                   gb_AL022020. [Arabidopsis thaliana]
                   47951
Seq. No.
                   kmv700743872.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2104959
BLAST score
                   172
E value
                   8.0e-13
Match length
                   34
% identity
                   91
NCBI Description (U96925) immunophilin [Vicia faba]
                   47952
Seq. No.
Seq. ID
                   kmv700744095.h1
Method
                   BLASTX
```

q3183088

8.0e-12



Match length 57 % identity 53

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR (LTP) >gi_629658_pir__S47084 lipid transfer like protein - cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 47953

Seq. ID kwa701015555.h1

Method BLASTN
NCBI GI g1675195
BLAST score 73
E value 5.0e-33
Match length 152
% identity 88

NCBI Description Pisum sativum (clone PsRCI22-3) callus protein P23 mRNA,

complete cds

Seq. No.

47954

Seq. ID kwa701015564.h1

Method BLASTN
NCBI GI g169922
BLAST score 94
E value 8.0e-46
Match length 94
% identity 100

NCBI Description Soybean beta-1,3-endoglucanase mRNA, complete cds

Seq. No.

47955

Seq. ID kwa701015576.h1

Method BLASTX
NCBI GI g1041702
BLAST score 200
E value 2.0e-19
Match length 57

Match length 57 82

NCBI Description (U30476) expansin At-EXP1 [Arabidopsis thaliana]

Seq. No. 47956

Seq. ID kwa701015681.h1 Method BLASTN

NCBI GI g3449326 BLAST score 35 E value 1.0e-10 Match length 127 % identity 82

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K19M22, complete sequence [Arabidopsis thaliana]

Seq. No. 47957

Seq. ID leu701144321.h1

Method BLASTX
NCBI GI g2245131
BLAST score 142
E value 3.0e-09
Match length 48
% identity 65

Seq. No.

Seq. ID

47963

leu701144567.h1



```
NCBI Description (297344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  47958
                  leu701144373.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3953595
                  150
BLAST score
                  5.0e-10
E value
                  38
Match length
% identity
                  82
NCBI Description (AB008486) response regulator 3 [Arabidopsis thaliana]
                  47959
Seq. No.
Seq. ID
                  leu701144401.hl
Method
                  BLASTX
NCBI GI
                  g4263792
BLAST score
                  203
E value
                  9.0e-24
                  73
Match length
                  77
% identity
NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]
Seq. No.
                  47960
Seq. ID
                  leu701144405.h1
Method
                  BLASTX
NCBI GI
                  g99743
BLAST score
                  143
                  2.0e-09
E value
Match length
                  62
% identity
                  61
NCBI Description 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2
                  - Arabidopsis thaliana
                  47961
Seq. No.
Seq. ID
                  leu701144422.h1
Method
                  BLASTX
                  g3047104
NCBI GI
BLAST score
                  140
                  6.0e-09
E value
                  49
Match length
% identity
                  57
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
                  47962
Seq. No.
                  leu701144526.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g629692
BLAST score
                  150
E value
                  3.0e-10
Match length
                  39
% identity
                  77
NCBI Description hypothetical protein - common tobacco
                  >gi 506471 emb CAA56189 (X79794) unnamed protein product
                  [Nicotiana tabacum]
```



```
Method
                  BLASTX
NCBI GI
                  q4455232
BLAST score
                  358
                  2.0e-34
E value
                  83
Match length
                  75
% identity
                 (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                  47964
Seq. No.
Seq. ID
                  leu701144595.h1
                  BLASTN
Method
NCBI GI
                  g2351065
BLAST score
                  44
                  6.0e-16
E value
                  92
Match length
% identity
                  87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHF15, complete sequence [Arabidopsis thaliana]
                  47965
Seq. No.
Seq. ID
                  leu701144596.h1
                  BLASTX
Method
NCBI GI
                  g2160175
BLAST score
                  180
E value
                  8.0e-14
Match length
                  66
% identity
                  53
                  (AC000132) Strong similarity to Dianthus cysteine
NCBI Description
                  proteinase (gb_U17135). [Arabidopsis thaliana]
Seq. No.
                  47966
Seq. ID
                  leu701144660.h1
Method
                  BLASTN
NCBI GI
                  g3738275
BLAST score
                  61
E value
                  7.0e-26
Match length
                  149
                  85
% identity
                  Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  47967
                  leu701144671.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4033365
BLAST score
                  192
                  3.0e-15
E value
                  36
Match length
```

% identity 92

NCBI Description (AJ223499) ATP sulfurylase [Brassica juncea]

47968 Seq. No.

Seq. ID leu701144688.h1

Method BLASTX NCBI GI g1172811 BLAST score 175 E value 3.0e-13



```
Match length
                   45
% identity
NCBI Description
```

60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34) >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic - rice >gi_575355_emb_CAA57339_ (X81691) putative tumor

suppresser [Oryza sativa]

Seq. No.

47969

Seq. ID

leu701144692.h1

Method NCBI GI BLASTN g3212846

BLAST score

32

E value

1.0e-08

Match length % identity

56 89

NCBI Description

Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

47970

Seq. ID

leu701144713.h1

Method NCBI GI

BLASTN

BLAST score

g3492802 40

E value

2.0e-13

Match length

91

% identity

39

NCBI Description Medicago truncatula ENBP1 gene, exons 1 to

Seq. No.

47971

Seq. ID Method

leu701144725.h1

NCBI GI

BLASTN g22065

BLAST score

37

E value

8.0e-12

Match length

73 88

% identity

NCBI Description Vigna mungo gene for sulfhydryl-endopeptidase

Seq. No.

47972

Seq. ID

leu701144787.hl

Method NCBI GI BLASTX q1706082

BLAST score

192

E value Match length 3.0e-15

% identity

51 71

NCBI Description

SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)

>gi_629787_pir_S44191 serine-type carboxypeptidase (EC

3.4.16.1) II-3 - barley >gi_619350_bbs_153536

CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,

cv. Alexis, aleurone, Peptide, 516 aa]

>gi_474392_emb_CAA55478_ (X78877) serine carboxylase II-3

[Hordeum vulgare]

Seq. No.

47973

Seq. ID

leu701144889.h1

Method

BLASTN

```
g18737
NCBI GI
                  104
BLAST score
E value
                  1.0e-51
                  240
Match length
% identity
                  85
NCBI Description Glycine max RPRP3 gene for repetitive proline-rich protein
Seq. No.
Seq. ID
                  leu701144913.h1
Method
                  BLASTX
NCBI GI
                  g3935181
BLAST score
                  313
E value
                  4.0e-29
Match length
                  89
                  66
% identity
                 (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                  47975
Seq. No.
                  leu701144934.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3451068
BLAST score
                  247
E value
                  1.0e-22
Match length
                  92
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                  47976
Seq. No.
                  leu701144981.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1277163
BLAST score
                  231
E value
                  1.0e-127
Match length
                  235
% identity
                  100
NCBI Description Glycine max cysteine proteinase inhibitor mRNA, partial cds
                  47977
Seq. No.
Seq. ID
                  leu701145075.h1
```

Method BLASTX
NCBI GI g3860321
BLAST score 209
E value 4.0e-17
Match length 50
% identity 74

NCBI Description (AJ012687) beta-galactosidase [Cicer arietinum]

Seq. No. 47978

Seq. ID leu701145166.h1

Method BLASTX
NCBI GI g3876060
BLAST score 156
E value 8.0e-11
Match length 72
% identity 40

NCBI Description (Z72507) weak similarity with nitrogen fixation regulatory protein PIR accession number S52263; cDNA EST yk284f5.3

NCBI Description



comes from this gene; cDNA EST yk284f5.5 comes from this gene [Caenorhabditis elegans]

47979 Seq. No. Seq. ID leu701145218.h1 Method BLASTX NCBI GI g2344898 BLAST score 232 E value 1.0e-19 Match length 44 93 % identity (AC002388) 60S ribosomal protein L30 isolog [Arabidopsis NCBI Description thaliana] Seq. No. 47980 Seq. ID leu701145222.h1 Method BLASTN NCBI GI g170053 BLAST score 61 8.0e-26 E value Match length 109 89 % identity Soybean ribosomal protein S11 mRNA, 3' end NCBI Description Seq. No. 47981 Seq. ID leu701145235.h1 Method BLASTX NCBI GI q134777 BLAST score 234 E value 8.0e-20 Match length 84 % identity 56 NCBI Description STAGE V SPORULATION PROTEIN K >qi 98485 pir S16301 spoVJ protein - Bacillus subtilis >gi 40197 emb CAA42049 (X59412) spoVJ [Bacillus subtilis] 47982 Seq. No. Seq. ID leu701145283.h1 Method BLASTX g3063698 NCBI GI BLAST score 178 3.0e-13 E value Match length 84 % identity 43 (AL022537) putative protein [Arabidopsis thaliana] NCBI Description 47983 Seq. No. leu701145296.h1 Seq. ID Method BLASTN NCBI GI g2662468 BLAST score 34 E value 6.0e-10 Match length 58 % identity 90

complete cds

Arabidopsis thaliana ribosomal protein S6 (rps6) mRNA,

E value

Match length

5.0e-11



```
Seq. No.
                   47984
                  leu701145337.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469025
                  163
BLAST score
E value
                  1.0e-11
Match length
                  46
% identity
                  63
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                  47985
Seq. No.
Seq. ID
                  leu701145381.hl
                  BLASTN
Method
NCBI GI
                  g4106527
BLAST score
                  72
E value
                  2.0e-32
Match length
                  84
                  98
% identity
NCBI Description Mus musculus Pontin52 mRNA, complete cds
Seq. No.
                  47986
                  leu701145481.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341443
BLAST score
                  180
E value
                  1.0e-13
Match length
                  51
% identity
                  67
NCBI Description (AJ223074) acid phosphatase [Glycine max]
                  47987
Seq. No.
Seq. ID
                  leu701145575.h1
Method
                  BLASTX
                  q4455299
NCBI GI
BLAST score
                  258
E value
                  9.0e-23
Match length
                  82
                  56
% identity
NCBI Description
                 (AL035528) putative protein [Arabidopsis thaliana]
                  47988
Seq. No.
                  leu701145649.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3097320
BLAST score
                  48
E value
                   4.0e-18
Match length
                  124
% identity
                  90
NCBI Description Glycine max gene for Bd 30K, complete cds
                  47989
Seq. No.
Seq. ID
                  leu701145748.h1
Method
                  BLASTN
NCBI GI
                  g2673867
BLAST score
                  36
```



% identity 84

NCBI Description Antirrhinum majus mRNA for fimbriata-associated protein 1,

partial

Seq. No. 47990

Seq. ID leu701145750.hl

Method BLASTN
NCBI GI g170041
BLAST score 36
E value 5.0e-11
Match length 36
% identity 100

NCBI Description Glycine max cv Prize protein kinase mRNA

Seq. No.

Seq. ID leu701145794.h1

47991

Method BLASTX
NCBI GI g4558672
BLAST score 290
E value 1.0e-26
Match length 73
% identity 70

NCBI Description (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis

thaliana]

Seq. No. 47992

Seq. ID leu701145909.h1

Method BLASTX
NCBI GI g3702342
BLAST score 210
E value 4.0e-17
Match length 77
% identity 55

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 47993

Seq. ID leu701145928.h1

Method BLASTX
NCBI GI g1170949
BLAST score 310
E value 8.0e-29
Match length 78
% identity 73

NCBI Description SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir_S38327

protein kinase - Arabidopsis thaliana >gi_166811 (L07249)

protein kinase [Arabidopsis thaliana]

Seq. No. 47994

Seq. ID leu701145932.h1

Method BLASTN
NCBI GI g287567
BLAST score 38
E value 4.0e-12
Match length 62
% identity 90

NCBI Description Vigna radiata auxin-regulated mRNA



```
Seq. No. 47995
```

Seq. ID leu701146029.h1

Method BLASTX
NCBI GI \$2129662
BLAST score 170
E value 2.0e-12
Match length 73
% identity 41

NCBI Description ovule-specific homeotic protein homolog A20 - Arabidopsis thaliana >gi_1881536 (U37589) A20 [Arabidopsis thaliana]

Seq. No. 47996

Seq. ID leu701146109.hl

Method BLASTX
NCBI GI 94006855
BLAST score 95
E value 1.0e-09
Match length 47
% identity 65

NCBI Description (Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis

thaliana]

Seq. No.

47997

Seq. ID leu701146114.hl

Method BLASTN
NCBI GI g170053
BLAST score 73
E value 2.0e-33
Match length 105
% identity 92

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No.

47998

Seq. ID leu701146121.h1

Method BLASTN
NCBI GF g303900
BLAST score 105
E value 4.0e-52
Match length 122
% identity 27

NCBI Description Soybean gene for ubiquitin, complete cds

Seq. No.

47999

Seq. ID leu701146190.h1

Method BLASTX
NCBI GI g3451071
BLAST score 201
E value 4.0e-16
Match length 39
% identity 95

NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis

thaliana]

Seq. No.

48000

Seq. ID

leu701146261.h1

Method NCBI GI BLASTN g3097320



```
BLAST score
                  47
                  1.0e-17
E value
Match length
                  127
                  84
% identity
NCBI Description Glycine max gene for Bd 30K, complete cds
                  48001
Seq. No.
                  leu701146282.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160151
BLAST score
                  154
E value
                  9.0e-11
Match length
                  51
% identity
                  55
NCBI Description (AC000375) Strong similarity to Brassica aspartic protease
                  (gb_X77260). [Arabidopsis thaliana]
Seq. No.
                  48002
Seq. ID
                  leu701146319.h1
Method
                  BLASTN
NCBI GI
                  g1053050
BLAST score
                  35
                  2.0e-10
E value
Match length
                  91
% identity
                  91
NCBI Description Glycine max histone H3 gene, partial cds, clone S4
                  48003
Seq. No.
                  leu701146366.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1813328
BLAST score
                  32
E value
                  1.0e-08
Match length
                  135
% identity
                  82
NCBI Description Canavalia gladiata mRNA for HMG-1, complete cds
Seq. No.
                  48004
Seq. ID
                  leu701146380.h1
                  BLASTX
Method
NCBI GI
                  g4335864
BLAST score
                  162
E value
                  1.0e-11
```

Match length 32 91 % identity

NCBI Description (AF052040) calreticulin [Berberis stolonifera]

48005 Seq. No.

Seq. ID leu701146391.h1

Method BLASTN g170053 NCBI GI BLAST score 122 E value 3.0e-62 129 Match length 99 % identity

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end



Seq. No. 48006

Seq. ID leu701146410.h1

Method BLASTX
NCBI GI g1769901
BLAST score 202
E value 2.0e-16
Match length 69
% identity 55

NCBI Description (X95737) proline transporter 1 [Arabidopsis thaliana]

>gi_2088642 (AF002109) proline transporter 1 [Arabidopsis

thaliana]

Seq. No. 48007

Seq. ID leu701146415.h1

Method BLASTN
NCBI GI g296444
BLAST score 163
E value 6.0e-87
Match length 167
% identity 99

NCBI Description G.max ADR6 mRNA

Seq. No.

Seq. ID leu701146425.h1

48008

Method BLASTX
NCBI GI g2642450
BLAST score 330
E value 4.0e-31
Match length 86
% identity 72

NCBI Description (AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No. 48009

Seq. ID leu701146469.h1

Method BLASTN
NCBI GI g3241925
BLAST score 35
E value 2.0e-10
Match length 59
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MOK9, complete sequence [Arabidopsis thaliana]

Seq. No. 48010

Seq. ID leu701146483.h1

Method BLASTX
NCBI GI g4056457
BLAST score 149
E value 3.0e-10
Match length 40
% identity 75

NCBI Description (AC005990) ESTs gb 234051 and gb F13722 come from this

gene. [Arabidopsis thaliana]

Seq. No. 48011

NCBI GI

BLAST score



```
Seq. ID
                   leu701146516.h1
Method
                   BLASTN
NCBI GI
                   q218112
BLAST score
                   78
                   4.0e-36
E value
Match length
                  162
                   87
% identity
NCBI Description
                  Rice mRNA for ribosomal protein L41 (340 gene), partial
                  sequence >gi 3107899 dbj D42832 D42832 Rice callus cDNA,
                   48012
Seq. No.
Seq. ID
                   leu701146537.h1
Method
                  BLASTN
NCBI GI
                   q2995989
BLAST score
                  52
E value
                   2.0e-20
Match length
                   68
% identity
                   94
NCBI Description
                  Arabidopsis thaliana dormancy-associated protein (DRM1)
                  mRNA, complete cds
Seq. No.
                   48013
                   leu701146570.h1
Seq. ID
Method
                  BLASTX
                  g3947735
NCBI GI
BLAST score
                  186
E value
                   3.0e-14
Match length
                  76
% identity
                   46
NCBI Description
                  (AJ009720) NL27 [Solanum tuberosum]
Seq. No.
                   48014
Seq. ID
                  leu701146604.h1
Method
                  BLASTX
NCBI GI
                  g951449
BLAST score
                  182
                   1.0e-15
E value
Match length
                   64
                   59
% identity
NCBI Description
                  (L46681) aspartic protease precursor [Lycopersicon
                   esculentum]
                   48015
Seq. No.
Seq. ID
                  leu701146620.h1
Method
                  BLASTN
                  g170029
NCBI GI
BLAST score
                  41
E value
                  5.0e-14
Match length
                  77
% identity
                  88
NCBI Description Glycine max cv. Dare nodulin 26 gene fragment
                   48016
Seq. No.
Seq. ID
                  leu701146740.h1
Method
                  BLASTX
```

g3914435



```
1.0e-09
E value
                  36
Match length
                  75
% identity
                  PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin
NCBI Description
                  [Glycine max]
                  48017
Seq. No.
Seq. ID
                  leu701146743.h1
Method
                  BLASTN
NCBI GI
                  g3021374
```

NCBI GI g3021374
BLAST score 79
E value 1.0e-36
Match length 103
% identity 94

NCBI Description Glycine max mRNA for profilin, PRO1

Seq. No. 48018

Seq. ID leu701146761.h1

Method BLASTX
NCBI GI g1350680
BLAST score 147
E value 6.0e-10
Match length 49
% identity 49

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 48019

Seq. ID leu701146770.h1

Method BLASTN
NCBI GI g2264304
BLAST score 33
E value 3.0e-09
Match length 83
% identity 90

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBG8, complete sequence [Arabidopsis thaliana]

Seq. No. 48020

Seq. ID leu701146772.h1

Method BLASTX
NCBI GI g4454010
BLAST score 183
E value 4.0e-14
Match length 68
% identity 50

NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 48021

Seq. ID leu701146788.h1

Method BLASTX
NCBI GI g4335729
BLAST score 157
E value 5.0e-11
Match length 74
% identity 9

NCBI Description (AC006248) putative salt-inducible protein [Arabidopsis

thaliana]

E value

Match length

% identity

8.0e-09

36

64



```
Seq. No.
                   48022
                   leu701146852.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4165487
BLAST score
                   69
E value
                   1.0e-30
Match length
                   101
% identity
                   92
NCBI Description
                  Hordeum vulgare mRNA for alpha-tubulin
                   48023
Seq. No.
Seq. ID
                   leu701146887.h1
                   BLASTN
Method
NCBI GI
                   g3599418
BLAST score
                   173
                   9.0e-93
E value
                   232
Match length
% identity
                   93
                   Glycine max alternative oxidase precursor (Aox1) gene,
NCBI Description
                   nuclear gene encoding mitochondrial protein, complete cds
Seq. No.
                   48024
Seq. ID
                   leu701146922.h1
Method
                   BLASTX
NCBI GI
                   q1723780
BLAST score
                   139
                   1.0e-08
E value
Match length
                   78
                   40
% identity
                   HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC
NCBI Description
                   REGION >gi_2131716_pir__S64609 hypothetical protein YGR276c
                   - yeast (Saccharomyces cerevisiae)
                   >gi_1323503_emb_CAA97306_ (273061) ORF YGR276c
[Saccharomyces cerevisiae] >gi_2104899_emb_CAA58898_
                   (X84098) PIE553 [Saccharomyces cerevisiae]
Seq. No.
                   48025
Seq. ID
                   leu701146933.h1
                   BLASTX
Method
NCBI GI
                   g3806016
BLAST score
                   164
                   6.0e-12
E value
Match length
                   63
% identity
                   (AF053104) peroxisomal targeting signal 1 receptor; PTS1
NCBI Description
                   receptor; Pex5p [Nicotiana tabacum]
                   48026
Seq. No.
                   leu701146935.h1
Seq. ID
Method
                   BLASTX
                   g3451074
NCBI GI
BLAST score
                   139
```

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]



```
Seq. No. 48027
```

Seq. ID leu701146944.hl

Method BLASTN
NCBI GI g18644
BLAST score 172
E value 4.0e-92
Match length 196
% identity 97

NCBI Description Soybean mRNA for HMG-1 like protein

Seq. No. 48028

Seq. ID leu701146987.hl

Method BLASTX
NCBI GI g1170409
BLAST score 248
E value 2.0e-21
Match length 64
% identity 77

NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)

>gi 549887 (U09336) homeobox protein [Arabidopsis thaliana]
>gi 549888 (U09337) homeobox protein [Arabidopsis thaliana]
>gi 4490724 emb CAB38927.1 (AL035709) homeobox protein

HAT22 [Arabidopsis thaliana]

Seq. No. 48029

Seq. ID leu701147008.h1

Method BLASTN
NCBI GI g169974
BLAST score 34
E value 8.0e-10
Match length 94
% identity 84

NCBI Description Glycine max vspA gene, complete cds

Seq. No. 48030

Seq. ID leu701147041.h1

Method BLASTX
NCBI GI g3925363
BLAST score 328
E value 6.0e-31
Match length 83
% identity 70

NCBI Description (AF067961) homeodomain protein [Malus domestica]

Seq. No. 48031

Seg. ID leu701147169.hl

Method BLASTX
NCBI GI g3152587
BLAST score 410
E value 1.0e-40
Match length 77
% identity 38

NCBI Description (AC002986) Similar to CREB-binding protein homolog

gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]



```
Seq. No. 48032
```

Seq. ID leu701147176.h1

Method BLASTN
NCBI GI g1239960
BLAST score 54
E value 1.0e-21
Match length 162
% identity 83

NCBI Description A.majus mRNA for MADS-box protein (DEFH49

Seq. No. 48033

Seq. ID leu701147250.h1

Method BLASTN
NCBI GI g170053
BLAST score 210
E value 1.0e-115
Match length 234
% identity 97

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 48034

Seq. ID leu701147301.h1

Method BLASTX
NCBI GI g2498329
BLAST score 403
E value 1.0e-39
Match length 91
% identity 82

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__ S65571 pattern-formation protein GNOM - Arabidopsis thaliana

>gi_1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]

Seq. No. 48035

Seq. ID leu701147332.h1

Method BLASTN
NCBI GI g170053
BLAST score 219
E value 1.0e-120
Match length 255
% identity 96

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 48036

Seq. ID leu701147361.h1

Method BLASTX
NCBI GI g3169883
BLAST score 144
E value 2.0e-12
Match length 76
% identity 43

NCBI Description (AF033194) dehydroquinate dehydratase/shikimate:NADP



oxidoreductase [Lycopersicon esculentum] >gi_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum]

Seq. No. 48037 Seq. ID leu701147421.h1

Method BLASTX
NCBI GI g2829868
BLAST score 199
E value 9.0e-16
Match length 63

Match length 63 % identity 59

NCBI Description (AC002396) Unknown protein [Arabidopsis thaliana]

Seq. No. 48038

Seq. ID leu701147433.h1

Method BLASTX
NCBI GI g4262173
BLAST score 209
E value 6.0e-17
Match length 77
% identity 55

NCBI Description (AC005508) 3975 [Arabidopsis thaliana]

Seq. No. 48039

Seq. ID leu701147437.h1

Method BLASTN
NCBI GI g170053
BLAST score 125
E value 5.0e-64
Match length 125
% identity 100

NCBI Description Soybean ribosomal protein S11 mRNA, 3' end

Seq. No. 48040

Seq. ID leu701147440.h1

Method BLASTN
NCBI GI g2764805
BLAST score 83
E value 5.0e-39
Match length 187
% identity 86

NCBI Description G.max gene encoding epoxide hydrolase

Seq. No. 48041

Seq. ID leu701147512.h1

Method BLASTX
NCBI GI g3046693
BLAST score 229
E value 3.0e-19
Match length 39
% identity 100

NCBI Description (AL022140) receptor like protein (fragment) [Arabidopsis

thaliana]

Seq. No. 48042

Seq. ID leu701147553.h1



```
BLASTN
Method
                   g3341442
NCBI GI
                   155
BLAST score
E value
                   5.0e-82
Match length
                   243
                   91
% identity
NCBI Description Glycine max mRNA for root nodule acid phosphatase
Seq. No.
                   48043
Seq. ID
                   leu701147586.hl
                  BLASTX
Method
                   q2275202
NCBI GI
BLAST score
                   224
                   7.0e-19
E value
                  72
Match length
                   62
% identity
                  (AC002337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   48044
Seq. No.
                   leu701147650.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4138583
BLAST score
                   241
E value
                   8.0e-21
Match length
                   68
% identity
                   74
NCBI Description
                  (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
                   48045
Seq. No.
                   leu701147691.h1
Seq. ID
Method
                   BLASTX
                   g3834323
NCBI GI
BLAST score
                   184
                   5.0e-14
E value
Match length
                   90
% identity
                   43
NCBI Description
                  (AC005679) F9K20.25 [Arabidopsis thaliana]
Seq. No.
                   48046
Seq. ID
                   leu701147728.h1
                   BLASTN
Method
NCBI GI
                   g18551
BLAST score
                   163
                   9.0e-87
E value
                   231
Match length
% identity
                   95
                  Soybean Cab3 gene for PSII LHCII chlorophyll a/b binding
NCBI Description
                   protein
                   48047
Seq. No.
Seq. ID
                   leu701147744.h1
Method
                   BLASTN
NCBI GI
                   g505145
BLAST score
                   62
```

1.0e-26

130

E value Match length



% identity

Tobacco mRNA for protein-serine/threonine kinase, complete NCBI Description

Seq. No.

48048

Seq. ID

leu701147792.h1

Method

BLASTN g2331045

NCBI GI

53

BLAST score E value

3.0e-21

Match length

54

% identity

68

NCBI Description

Sambucus nigra ribosome inactivating protein precursor

mRNA, complete cds

Seq. No.

48049

Seq. ID Method

leu701147817.h1

NCBI GI

BLASTX g3386610

BLAST score

139

E value

9.0e-09

Match length

50

% identity

NCBI Description

(AC004665) hypothetical protein [Arabidopsis thaliana]

Seq. No.

48050

Seq. ID

leu701147831.h1

Method

BLASTX

NCBI GI

g4220469

BLAST score E value

176 3.0e-13

Match length

38

% identity

87

NCBI Description

(AC006069) putative receptor protein kinase, 5' partial

[Arabidopsis thaliana]

Seq. No.

48051

Seq. ID Method

leu701147852.h1

NCBI GI

BLASTX

BLAST score

q4263517

E value

149

Match length

4.0e-10

% identity

52 56

NCBI Description

(AC004044) similar to PHZF, catalyzing the hydroxylation of

phenazine-1-carboxylic acid to

2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis

thaliana]

Seq. No.

48052

Seq. ID

leu701147941.hl

Method NCBI GI BLASTX g1399303

BLAST score

E value

249 8.0e-22

Match length

59

% identity

71

3



```
(U41473) phosphoinositide-specific phospholipase C P12
NCBI Description
                   [Glycine max]
Seq. No.
                  48053
Seq. ID
                  leu701147943.hl
Method
                  BLASTX
NCBI GI
                  g2529663
BLAST score
                  159
E value
                  3.0e-11
Match length
                  57
                  53
% identity
                  (AC002535) putative lysophospholipase [Arabidopsis
NCBI Description
                  thaliana] >gi 3738277 (AC005309) putative lysophospholipase
                  [Arabidopsis thaliana]
Seq. No.
                  48054
Seq. ID
                  leu701147994.h1
Method
                  BLASTN
NCBI GI
                  g1419035
BLAST score
                  85
                  2.0e-40
E value
Match length
                  97
% identity
                  97
NCBI Description M.sativa mRNA for delta-1-pyrroline-5-carboxylate synthase,
                  P5CS-1
Seq. No.
                  48055
                  leu701148080.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3643082
                  270
BLAST score
                  3.0e-24
E value
Match length
                  75
% identity
                  64
NCBI Description
                  (AF075579) protein phosphatase-2C; PP2C [Mesembryanthemum
                  crystallinum]
Seq. No.
                  48056
Seq. ID
                  leu701148106.h1
                  BLASTX
Method
                  g629561
NCBI GI
BLAST score
                  143
                  3.0e-09
E value
Match length
                  39
% identity
                  69
                  SRG1 protein - Arabidopsis thaliana
NCBI Description
                  >gi 479047 emb CAA55654 (X79052) SRG1 [Arabidopsis
                  thaliana]
Seq. No.
                  48057
                  leu701148119.h1
Seq. ID
```

Method BLASTX g1350720 NCBI GI BLAST score 238 E value 1.0e-20 Match length 70 % identity 64



```
60s RIBOSOMAL PROTEIN L32
NCBI Description
                  48058
Seq. No.
                  leu701148140.h1
Seq. ID
Method
                  BLASTX
                  g4567235
NCBI GI
BLAST score
                  252
                  4.0e-31
E value
Match length
                  78
% identity
                  (AC007119) putative phosphatidylinositol/phophatidylcholine
NCBI Description
                  transfer protein [Arabidopsis thaliana]
Seq. No.
                  48059
Seq. ID
                  leu701148159.h1
                  BLASTN
Method
NCBI GI
                  g1694899
BLAST score
                  141
E value
                  1.0e-73
                  216
Match length
% identity
                  92
NCBI Description P.sativum mRNA for Cop1 protein
Seq. No.
                  48060
                  leu701148161.h1
Seq. ID
Method
                  BLASTN
                  q1575730
NCBI GI
BLAST score
                  96
                  1.0e-46
E value
Match length
                  222
% identity
                  87
                  Glycine max 14-3-3 related protein SGF14D mRNA, complete
NCBI Description
                  cds
                  48061
Seq. No.
Seq. ID
                  leu701148210.h1
Method
                  BLASTX
NCBI GI
                  q4325354
BLAST score
                  341
E value
                  2.0e-32
Match length
                  86
                  74
% identity
                  (AF128395) contains similarity to retrovirus-related
NCBI Description
                  polyproteins and to CCHC zinc finger protein (Pfam:
                  PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]
Seq. No.
                  48062
Seq. ID
                  leu701148217.h1
```

Method BLASTX NCBI GI g2961377 BLAST score 176 E value 4.0e-13 Match length 69 5 % identity

NCBI Description (AL022141) putative receptor protein kinase [Arabidopsis

thaliana]



```
Seq. No.
                   48063
Seq. ID
                   leu701148219.h1
Method
                  BLASTX
NCBI GI
                  g3860256
BLAST score
                  244
E value
                  5.0e-21
Match length
                  77
% identity
                  61
                 (AC005824) putative tRNA isopentenylpyrophosphate
NCBI Description
                  transferase [Arabidopsis thaliana]
Seq. No.
                  48064
Seq. ID
                  leu701148220.h1
                  BLASTN
Method
NCBI GI
                  g2764803
BLAST score
                  150
E value
                  5.0e-79
Match length
                  245
% identity
                  91
NCBI Description G.max mRNA for epoxide hydrolase
                  48065
Seq. No.
Seq. ID
                  leu701148223.h1
                  BLASTX
                                                 _ ****
30
Method
NCBI GI
                  g3914472
BLAST score
                  250
                  1.0e-21
E value
Match length
                   60
                  80
% identity
NCBI Description
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)
                  >gi 322764 pir S32021 photosystem II 10K protein - common
                   tobacco >gi_22669_emb_CAA49693_ (X70088) NtpII10 [Nicotiana
                  tabacum]
Seq. No.
                   48066
Seq. ID
                  leu701148244.h1
                  BLASTN
Method
NCBI GI
                  g3449316
BLAST score
                  34
                  8.0e-10
E value
                  46
Match length
                  93
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K9D7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  48067
Seq. ID
                  leu701148252.h1
Method
                  BLASTX
NCBI GI
                  g3777527
BLAST score
                  138
E value
                  1.0e-08
                  73
```

Match length % identity 44

NCBI Description (AF053008) gag-pol polyprotein [Glycine max]

48068 Seq. No.

leu701148281.h1 Seq. ID

٠. ت



```
Method
                  BLASTX
NCBI GI
                  g585876
BLAST score
                  263
                  2.0e-23
E value
                  69
Match length
% identity
                  80
NCBI Description
                  60S RIBOSOMAL PROTEIN L23A (L25) >gi 1084424 pir S48026
                  ribosomal protein L25 - common tobacco >gi 310935 (L18908)
                  60S ribosomal protein L25 [Nicotiana tabacum]
Seq. No.
                  48069
Seq. ID
                  leu701148282.h1
Method
                  BLASTN
NCBI GI
                  g436782
BLAST score
                  36
E value
                  3.0e-11
Match length
                  48
                  94
% identity
NCBI Description Rice mRNA for cyc07, complete cds
                  48070
Seq. No.
                  leu701148311.h1
Seq. ID
Method
                  BLASTX
                  g1769898
NCBI GI
BLAST score
                  219
                  4.0e-18
E value
Match length
                  83
% identity
                  51
NCBI Description
                  (Y08010) lectin receptor kinase [Arabidopsis thaliana]
Seq. No.
                  48071
Seq. ID
                  leu701148426.h1
Method
                  BLASTX
NCBI GI
                  g3319366
BLAST score
                  199
                  5.0e-16
E value
                  67
Match length
% identity
                  58
                  (AF077409) contains similarity to helicases [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  48072
Seq. ID
                  leu701148496.h1
Method
                  BLASTX
NCBI GI
                  q4454477
BLAST score
                  147
                  9.0e-10
E value
                  77
Match length
```

42 % identity

NCBI Description (AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No. 48073

Seq. ID leu701148502.h1

Method BLASTN NCBI GI g1854442 BLAST score 54 E value 1.0e-21



118 Match length 86 % identity

NCBI Description Vigna unguiculata mRNA for CPRD8 protein, complete cds

Seq. No.

48074

Seq. ID Method

leu701148625.h1

NCBI GI

BLASTX q2688839

BLAST score E value

321 5.0e-30

Match length % identity

91 67

NCBI Description

(AF003347) ATP phosphoribosyltransferase [Thlaspi

goesingense]

Seq. No.

48075

Seq. ID

leu701148689.h1

Method NCBI GI

BLASTX g3986296 157

BLAST score E value

6.0e-11

Match length % identity

67

51

(AB018419) mitotic checkpoint [Xenopus laevis] NCBI Description

Seq. No.

48076

Seq. ID

leu701148756.h1 BLASTX

Method NCBI GI

g3122323

BLAST score E value

168 3.0e-12

Match length

80

% identity

42

NCBI Description

LETHAL (2) DENTICLELESS PROTEIN (DTL83 PROTEIN)

>gi_1079099 pir_ S51748 lethal(2)denticleless - fruit fly (Drosophila melanogaster) >gi 603539 emb CAA58441 (X83414)

lethal(2)denticleless [Drosophila melanogaster]

>gi 4007010 emb CAA66723 (X98094) l(2)dlt [Drosophila

melanogaster]

Seq. No.

48077

Seq. ID

leu701148784.h1

Method

BLASTX

NCBI GI BLAST score g3702342

161

E value Match length 2.0e-11

% identity

51 53

NCBI Description

(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.

48078

Seq. ID

leu701148806.h1

Method NCBI GI BLASTX

BLAST score

g1362615

E value

269

Match length

5.0e-24 86



```
% identity
                  iswi protein - fruit fly (Drosophila melanogaster)
NCBI Description
                  >gi_439197 (L27127) ISWI protein [Drosophila melanogaster]
                  48079
Seq. No.
Seq. ID
                  leu701148825.h1
                  BLASTN
Method
NCBI GI
                  q19701
BLAST score
                  80
                  3.0e-37
E value
                  164
Match length
% identity
                  87
NCBI Description N.plumbaginifolia mRNA NeIF-5A2 for initiation factor 5A(2)
                  48080
Seq. No.
Seq. ID
                  leu701148834.h1
Method
                  BLASTX
NCBI GI
                  q4415931
BLAST score
                  301
                  1.0e-27
E value
Match length
                  89
% identity
                  62
                  (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
                  48081
Seq. No.
Seq. ID
                  leu701148881.h1
Method
                  BLASTX
NCBI GI
                  q4580389
BLAST score
                  143
E value
                  2.0e-09
Match length
                  63
% identity
                  49
NCBI Description
                  (AC007171) unknown protein [Arabidopsis thaliana]
                  48082
Seq. No.
Seq. ID
                  leu701148890.h1
                  BLASTX
Method
NCBI GI
                  g2346988
BLAST score
                  151
                  3.0e-10
E value
Match length
                  80
                  30
% identity
NCBI Description
                  (AB006606) ZPT4-4 [Petunia x hybrida]
                  48083
Seq. No.
                  leu701148915.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3982595
BLAST score
                  75
```

<u>. L.</u>

NCBI GI g3982595
BLAST score 75
E value 2.0e-34
Match length 127
% identity 90

NCBI Description Glycine max cationic peroxidase 2 (Prx2) mRNA, complete cds

Seq. No. 48084



leu701148987.h1 Seq. ID Method BLASTN NCBI GI q4103476 41 BLAST score 4.0e-14 E value Match length 41 100 % identity Glycine tomentella small subunit ribosomal RNA gene, NCBI Description partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, pa 48085 Seq. No. leu701149020.h1 Seq. ID BLASTN Method NCBI GI g170061 BLAST score 125 4.0e-64 E value 246 Match length 94 % identity Soybean (G.max L.) beta-tubulin (S-beta-2) gene, complete NCBI Description 48086 Seq. No. leu701149056.h1 Seq. ID BLASTN Method NCBI GI q20682 36 BLAST score 6.0e-11 E value Match length 44 % identity 95 P.sativum mRNA of cDNA clone 7a NCBI Description 48087 Seq. No. leu701149083.h1 Seq. ID BLASTX Method NCBI GI g4415933 197 BLAST score 2.0e-15 E value 88 Match length 59 % identity (AC006418) putative cellular apoptosis susceptibility NCBI Description protein [Arabidopsis thaliana] >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana] 48088 Seq. No. leu701149136.h1 Seq. ID BLASTX Method g2795805 NCBI GI

NCBI GI BLAST score g2795805 187 2.0e-14

47

E value Match length % identity

NCBI Description

77
(AC003674) putative protein kinase [Arabidopsis thaliana]
>gi_3355493 (AC004218) putative protein kinase [Arabidopsis

% identity

NCBI Description



thaliana]

```
48089
Seq. No.
                   leu701149174.hl
Seq. ID
                   BLASTX
Method
                   g509810
NCBI GI
BLAST score
                   365
                   3.0e - 35
E value
                   82
Match length
                   88
% identity
                  (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
                   48090
Seq. No.
                   leu701149238.hl
Seq. ID
                   BLASTX
Method
                   g625547
NCBI GI
                   174
BLAST score
                   2.0e-15
E value
                   53
Match length
                   64
% identity
                   chlorophyll a/b-binding protein type I - common tobacco
NCBI Description
                   >gi_493723_emb_CAA45523_ (X64198) photosystem I
                   light-harvesting chlorophyll a/b-binding protein [Nicotiana
                   tabacum]
                   48091
Seq. No.
                   leu701149268.h1
Seq. ID
                   BLASTN
Method
                   g886099
NCBI GI
BLAST score
                   153
                   1.0e-80
E value
                   180
Match length
% identity
                   Glycine max putative water channel protein (Pip1) mRNA,
NCBI Description
                   complete cds
                   48092
Seq. No.
                   leu701149289.h1
Seq. ID
                   BLASTX
Method
                   g3249110
NCBI GI
                   179
BLAST score
E value
                   2.0e-13
                   53
Match length
                   62
% identity
                   (AC003114) T12M4.6 [Arabidopsis thaliana]
NCBI Description
                   48093
Seq. No.
                   leu701149310.h1
Seq. ID
Method
                   BLASTX
                   q3193323
NCBI GI
BLAST score
                   373
                   3.0e-36
E value
Match length
                   78
                   94
```

(AF069299) similar to ribosomal protein S13 (Pfam; S15.hmm,

score: 78.35); identical to Arabidopsis 40S ribosomal protein S13 (fragment) (SW: P49203A) except the first 32





amino acids are different [Arabidopsis thaliana]

```
48094
Seq. No.
                  leu701149326.hl
Seq. ID
Method
                  BLASTN
                  q3116019
NCBI GI
                  112
BLAST score
                  2.0e-56
E value
                  232
Match length
                  87
% identity
NCBI Description Pisum sativum mRNA for ftsZ gene
                   48095
Seq. No.
                   leu701149383.h1
Seq. ID
                   BLASTX
Method
                   g4467126
NCBI GI
                   247
BLAST score
                   1.0e-21
E value
                   67
Match length
                   67
% identity
                   (AL035538) guanine nucleotide-exchange protein-like
NCBI Description
                   [Arabidopsis thaliana]
                   48096
Seq. No.
                   leu701149412.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4325355
                   93
BLAST score
                   1.0e-08
E value
Match length
                   76
                   41
% identity
                   (AF128395) contains similarity to retrovirus-related
NCBI Description
                   polyproteins [Arabidopsis thaliana]
                   48097
Seq. No.
                   leu701149445.h1
Seq. ID
Method
                   BLASTN
                   g2262200
NCBI GI
 BLAST score
                   56
                   6.0e-23
E value
Match length
                   76
                   93
 % identity
                   Phaseolus vulgaris gibberellin 20-oxidase mRNA, complete
 NCBI Description
                   48098
 Seq. No.
                   leu701149465.h1
 Seq. ID
                   BLASTX
 Method
                   g2244832
 NCBI GI
                   143
 BLAST score
                   2.0e-09
 E value
                   57
 Match length
 % identity
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
```

48099

leu701149620.h1

Seq. No.

Seq. ID

NCBI GI

BLAST score

g12616

100



```
BLASTX
Method
                  g3212871
NCBI GI
                  317
BLAST score
                  2.0e-37
E value
                  88
Match length
                  76
% identity
                   (AC004005) putative translation initiation factor
NCBI Description
                   [Arabidopsis thaliana]
                   48100
Seq. No.
                  leu701149623.hl
Seq. ID
                  BLASTX
Method
                   g2146731
NCBI GI
                   186
BLAST score
E value
                   2.0e-14
Match length
                   36
% identity
                   94
                   FK506-binding protein - Arabidopsis thaliana >gi_1354207
NCBI Description
                   (U49453) rof1 [Arabidopsis thaliana]
                   48101
Seq. No.
                   leu701149628.hl
Seq. ID
                   BLASTX
Method
                   g2499551
NCBI GI
                   139
BLAST score
                   7.0e-09
E value
                   76
Match length
% identity
                   42
                   PUTATIVE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE
NCBI Description
                   >gi 1001408 dbj BAA10030 (D63999) low molecular weight
                   phosphotyrosine protein phosphatase [Synechocystis sp.]
                   48102
Seq. No.
                   leu701149633.h1
Seq. ID
                   BLASTX
Method
                   g4097547
NCBI GI
                   148
BLAST score
                   5.0e-10
E value
                   59
Match length
                   21
% identity
                   (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
                   48103
Seq. No.
                   leu701149644.h1
Seq. ID
                   BLASTN
Method
                   g217902
NCBI GI
BLAST score
                   66
                   6.0e-29
E value
                   174
Match length
 % identity
 NCBI Description Catharanthus roseus cyc07 mRNA, complete cds
                   48104
 Seq. No.
                   leu701149645.h1
 Seq. ID
 Method
                   BLASTN
```



```
E value
                   3.0e-49
Match length
                  104
                   99
% identity
                  L.esculentum chloroplast trnY & trnD genes for tRNA-Tyr &
NCBI Description
                  tRNA-Asp
Seq. No.
                   48105
Seq. ID
                   leu701149647.h1
Method
                  BLASTN
NCBI GI
                  g1944341
BLAST score
                   43
                   2.0e-15
E value
Match length
                   51
```

% identity NCBI Description Glycine max DNA for cysteine proteinase inhibitor, complete

48106 Seq. No. leu701149674.h1 Seq. ID Method BLASTX NCBI GI g2827709 BLAST score 213 E value 1.0e-17 75

96

Match length % identity 57

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

48107 Seq. No. Seq. ID leu701149761.h1

Method BLASTN NCBI GI g166933 BLAST score 83 E value 4.0e-39 Match length 155 % identity 88

A.thaliana ubiquitin extension protein (UBQ5) gene, NCBI Description

complete cds

Seq. No. 48108

Seq. ID leu701149769.h1

Method BLASTN NCBI GI g296408 BLAST score 161 1.0e-85 E value Match length 185 97 % identity

NCBI Description G.max ADR12 mRNA

Seq. No.

48109

leu701149804.h1 Seq. ID

Method BLASTX NCBI GI g225280 257 BLAST score 1.0e-22 E value Match length 86 62 % identity

NCBI Description rpoC-like ORF 548 [Nicotiana tabacum]



```
48110
Seq. No.
                  leu701149811.hl
Seq. ID
Method
                  BLASTN
                  g169974
NCBI GI
                  138
BLAST score
                  7.0e-72
E value
                  224
Match length
                  91
% identity
NCBI Description Glycine max vspA gene, complete cds
                  48111
Seq. No.
                  leu701149882.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g256142
BLAST score
                  179
                   3.0e-96
E value
                   207
Match length
                   97
% identity
                  cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                   Prize, mRNA, 1450 nt]
                   48112
Seq. No.
                   leu701149901.hl
Seq. ID
                   BLASTX
Method
                   g3033399
NCBI GI
                   218
BLAST score
                   5.0e-18
E value
                   86
Match length
% identity
                  (AC004238) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   48113
Seq. No.
                   leu701149920.h1
Seq. ID
                   BLASTX
Method
                   g1663648
NCBI GI
                   186
BLAST score
                   3.0e-14
E value
                   70
Match length
                   56
% identity
                   (U75321) chromaffin granule ATPase II homolog [Mus
NCBI Description
                   musculus]
                   48114
Seq. No.
                   leu701149965.h1
Seq. ID
                   BLASTX
Method
                   g1345132
NCBI GI
                   325
BLAST score
                   1.0e-30
E value
                   80
Match length
% identity
                   72
                   (U47029) ERECTA [Arabidopsis thaliana]
NCBI Description
                   >gi 1389566 dbj BAA11869 (D83257) receptor protein kinase
                   [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
                   protein kinase, ERECTA [Arabidopsis thaliana]
```

Seq. No. 48115



```
leu701149981.hl
Seq. ID
                  BLASTN
Method
                  g18588
NCBI GI
                  227
BLAST score
                  1.0e-125
E value
                  238
Match length
% identity
                  71
NCBI Description Soybean gene 3 for chalcone synthetase protein
                  48116
Seq. No.
                  leu701149987.h1
Seq. ID
                  BLASTX
Method
                  g4539295
NCBI GI
                  157
BLAST score
                   6.0e-11
E value
                   37
Match length
                   76
% identity
                  (AL049480) putative protein [Arabidopsis thaliana]
NCBI Description
                   48117
Seq. No.
                   leu701149990.hl
Seq. ID
                   BLASTX
Method
                   g189422
NCBI GI
                   112
BLAST score
                   4.0e-12
E value
                   50
Match length
% identity
                   (M32110) proliferating cell nuclear protein P120 [Homo
NCBI Description
                   sapiens]
                   48118
Seq. No.
                   leu701150007.h1
Seq. ID
                   BLASTX
Method
                   g2765244
NCBI GI
                   155
BLAST score
                   1.0e-10
E value
                   46
Match length
                   63
 % identity
                   (Y12807) invertase inhibitor homolog [Arabidopsis thaliana]
NCBI Description
                   48119
Seq. No.
                   leu701150068.hl
 Seq. ID
                   BLASTN
Method
                   g710329
NCBI GI
                   51
BLAST score
                   6.0e-20
 E value
                   182
 Match length
                   88
 % identity
                   Arabidopsis thaliana 55 kDa B regulatory subunit of
 NCBI Description
                   phosphatase 2A mRNA, complete cds
                   48120
 Seq. No.
                   leu701150123.hl
 Seq. ID
                   BLASTX
 Method
                   g1039355
 NCBI GI
                   198
 BLAST score
```

1.0e-15

E value



Match length 64 % identity 59

NCBI Description (X92179) alcohol dehydrogenase [Solanum tuberosum]

Seq. No.

48121

Seq. ID leu701150129.h1

Method BLASTX
NCBI GI g3980380
BLAST score 355
E value 5.0e-34
Match length 83
% identity 82

NCBI Description (AC004561) putative enolase [Arabidopsis thaliana]

Seq. No.

48122

Seq. ID leu701150149.h1

Method BLASTN
NCBI GI g1236948
BLAST score 224
E value 1.0e-123
Match length 244
% identity 98

NCBI Description Glycine max lipoxygenase L-5 (vlxB) mRNA, complete cds

Seq. No.

48123

Seq. ID leu701150156.h1

Method BLASTX
NCBI GI g4455357
BLAST score 153
E value 2.0e-10
Match length 78
% identity 42

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No.

48124

Seq. ID leu701150291.h1

Method BLASTX
NCBI GI g1184075
BLAST score 142
E value 3.0e-09
Match length 72
% identity 2

NCBI Description (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon

esculentum]

Seq. No. 48125

Seq. ID leu701150334.h1

Method BLASTN
NCBI GI g169974
BLAST score 132
E value 3.0e-68
Match length 231
% identity 90

NCBI Description Glycine max vspA gene, complete cds

48126

Seq. No.



```
Seq. ID
                  leu701150343.h1
Method
                  BLASTX
NCBI GI
                  g4115916
BLAST score
                  144
E value
                  2.0e-09
Match length
                  87
% identity
                  (AF118222) F3H7.9 gene product [Arabidopsis thaliana]
NCBI Description
                  >qi 4539441 emb CAB40029.1 (AL049523) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  48127
```

Seq. ID leu701150350.hl Method BLASTX NCBI GI q3355620

BLAST score 361 E value 8.0e-35 Match length 84 % identity 82

(AJ000235) partial sequence, homology to NCBI Description

phosphoribosylformylglycinamidine synthase [Hordeum

vulgare]

48128 Seq. No.

leu701150368.h1 Seq. ID

Method BLASTX g3746058 NCBI GI BLAST score 343 E value 1.0e-32 Match length 75 77 % identity

(AC005311) myb-related protein [Arabidopsis thaliana] NCBI Description

>gi_4432813_gb_AAD20663_ (AC006593) putative transcription

factor MYB [Arabidopsis thaliana]

Seq. No. 48129

Seq. ID leu701150396.h1

BLASTN Method NCBI GI q170781 BLAST score 42 E value 1.0e-14 Match length 98 % identity 86

NCBI Description Wheat ubiquitin carrier protein (E2) mRNA, complete cds

Seq. No. 48130

Seq. ID leu701150402.h1

Method BLASTX g417148 NCBI GI BLAST score 170 E value 1.0e-12 Match length 52 % identity 63

NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)

(G2-4) >gi 99912 pir A33654 heat shock protein 26A soybean >gi 169981 (M20363) Gmhsp26-A [Glycine max]



```
48131
Seq. No.
                  leu701150464.hl
Seq. ID
                  BLASTN
Method
                  q295867
NCBI GI
                  35
BLAST score
                  2.0e-10
E value
                  67
Match length
                  88
% identity
NCBI Description E. coli transposon Tn1000 (gamma delta) tnpR and tnpA genes
                  for resolvase and transposase
                  48132
Seq. No.
                  leu701150503.hl
Seq. ID
                  BLASTN
Method
                  g2791947
NCBI GI
                  45
BLAST score
                  2.0e-16
E value
                  113
Match length
                  85
% identity
NCBI Description Lupinus luteus mRNA for ribosomal protein L13a
                  48133
Seq. No.
                  leu701150508.h1
Seq. ID
                  BLASTN
Method
                  g3341442
NCBI GI
                  214
BLAST score
                  1.0e-117
E value
                   214
Match length
                   100
% identity
NCBI Description Glycine max mRNA for root nodule acid phosphatase
                   48134
Seq. No.
                   leu701150522.h1
Seq. ID
                   BLASTN
Method
                   g1381675
NCBI GI
                   76
BLAST score
                   8.0e-35
E value
                   80
Match length
                   99
% identity
NCBI Description Glycine max small GTP-binding protein (sral) mRNA, partial
                   48135
Seq. No.
                   leu701150529.h1
Seq. ID
                   BLASTN
Method
                   g414833
NCBI GI
                   116
BLAST score
                   1.0e-58
E value
                   171
Match length
                   96
 % identity
NCBI Description Glycine max (Rab7p) mRNA, complete cds
                   48136
 Seq. No.
                   leu701150545.h1
 Seq. ID
                   BLASTN
 Method
```

g609224

53

NCBI GI

BLAST score



E value 3.0e-21 Match length 97 89 % identity P.sativum mRNA for SAMS-2 >gi_609558 gb L36681_PEADENSYNB NCBI Description Pisum sativum S-adenosylmethionine synthase mRNA, complete 48137 Seq. No. Seq. ID leu701150616.h1 Method BLASTN NCBI GI g169974 BLAST score 61 5.0e-26 E value 151 Match length 91 % identity NCBI Description Glycine max vspA gene, complete cds Seq. No. 48138 Seq. ID leu701150618.hl Method BLASTX NCBI GI g2388582 BLAST score 189 E value 8.0e-15 Match length 54 % identity 69 (AC000098) Contains similarity to Rattus O-GlcNAc NCBI Description transferase (gb_U76557). [Arabidopsis thaliana] Seq. No. 48139 Seq. ID leu701150683,h1 Method BLASTN g2921218 NCBI GI BLAST score 32 E value 6.0e-09 Match length 36 % identity 97 Asbestopluma hypogea heat-shock protein Hsp70 mRNA, partial NCBI Description 48140 Seq. No. Seq. ID leu701150734.h1 Method BLASTX NCBI GI g4220511 152 BLAST score E value 2.0e-10 Match length 46 67 % identity (AL035356) DNA polymerase III like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 48141

Seq. ID leu701150879.h1

Method BLASTX NCBI GI g4567251 BLAST score 286 E value 3.0e-26 74 Match length



```
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                  48142
Seq. No.
                  leu701150947.h1
Seq. ID
                  BLASTN
Method
                  g4519194
NCBI GI
BLAST score
                  72
                  2.0e-32
E value
                  224
Match length
                  83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHM17, complete sequence
                  48143
Seq. No.
                  leu701151005.h1
Seq. ID
                  BLASTN
Method
                  g169980
NCBI GI
BLAST score
                  47
                  2.0e-17
E value
                  78
Match length
                  90
% identity
NCBI Description Soybean heat-shock protein (Gmhsp26-A) gene, complete cds
Seq. No.
                  48144
                  leu701151009.h1
Seq. ID
                  BLASTN
Method
                  g669002
NCBI GI
                  163
BLAST score
                  9.0e-87
E value
                  179
Match length
                   98
% identity
NCBI Description Glycine max calnexin mRNA, complete cds
                   48145
Seq. No.
                   leu701151072.hl
Seq. ID
Method
                   BLASTX
                   q4455338
NCBI GI
                   178
BLAST score
E value
                   1.0e-13
                   63
Match length
                   57
% identity
                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                   48146
Seq. No.
                   leu701151171.h1
Seq. ID
                   BLASTX
Method
                   g2499411
NCBI GI
```

BLAST score 292 1.0e-26 E value Match length 66 88 % identity

PYRUVATE DEHYDROGENASE E1 COMPONENT >gi_1200524 (U47920) NCBI Description

pyruvate dehydrogenase [Pseudomonas aeruginosa]

Seq. No. 48147

leu701151201.hl Seq. ID